

Curriculum Vitae
Hiroshi Mamitsuka

February 1, 2024.

Bioinformatics Center
Institute for Chemical Research, Kyoto University.
Gokasho, Uji 6110011, Japan.

Phone: +81-774-38-3023
Fax: +81-774-38-3037
Email: hmamitsuka.work at gmail.com

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.

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 ¹H-NMR.

PROFESSIONAL EXPERIENCE

Jan. 2019–Dec. 2022: Visiting Professor, School of Science, Aalto University, Finland.

Jan. 2015–Dec. 2018: FiDiPro (Finland Distinguished Professor Programme) Professor, School of Science, Aalto University, Finland.

Apr. 2011–Mar. 2013, Apr. 2019–Mar. 2021, Apr. 2023–Present: Director, Bioinformatics Center, Institute for Chemical Research, Kyoto University, Japan.

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, Central Research Laboratories, NEC Corporation, Japan.

PUBLICATIONS

Books and Conference Proceedings

- Mamitsuka, H. *Machine Learning for Marketing*, Global Data Science Publishing, 2019 (Print ISBN:978-4-9910445-2-6, eBook ISBN:978-4-9910445-3-3). [Supporting Page]
- Mamitsuka, H. *Textbook of Machine Learning and Data Mining (with Bioinformatics Applications)*, Global Data Science Publishing, 2018 (Print ISBN:978-4-9910445-0-2, eBook ISBN:978-4-9910445-1-9). [Supporting Page]
- Mamitsuka, H. *Data Mining for Systems Biology: Methods and Protocols*, Second Edition, Methods in Molecular Biology, vol. 1807, Humana Press, 2018 (Hardcover ISBN:978-1-4939856-0-9, eBook ISBN:978-1-4939856-1-6). [DOI]
- Mamitsuka, H., DeLisi, C. and Kanehisa, M. *Data Mining for Systems Biology: Methods and Protocols*, Methods in Molecular Biology, vol. 939, Humana Press, 2013 (Print ISBN: 978-1-6270310-6-6, Online ISBN: 978-1-6270310-7-3). [DOI]
- Ng, S.-K., Mamitsuka, H. and Wong, L., *Genome Informatics Series, Vol. 19, (Proceedings of the 18th International Conference on Genome Informatics)*, Imperial College Press, 2007, ISBN: 978-1-8609498-4-5.
- Heinrich, R., Mamitsuka, H., Kanehisa, M., Takagi, T. and Miyano, S., *Genome Informatics, Vol. 16, No.2*, Universal Academy Press, Inc., 2005, ISBN: 4-9464439-6-7.
- 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: 4-9464438-8-6.

Book Chapters

- Nguyen, D. H., Nguyen, C. H. and Mamitsuka, H., Machine Learning for Metabolic Identification. Part of the *Creative Economy* book series (CRE), Creative Complex Systems, Chapter 20, 329–350, Eds. Nishimura, K., Murase, M. and Yoshimura, K., Springer Nature, 2021. [DOI]
- duVerle, D. and Mamitsuka, H., CalCleaveMKL: a Tool for Calpain Cleavage Prediction. *Calpain: Methods and Protocols*, Methods in Molecular Biology, vol. 1915, Chapter 11, 121–147, Ed. Messer, J. S., Humana Press, 2019. [DOI]
- Takahashi, K., duVerle, D. A., Yotsukura, S., Takigawa, I. and Mamitsuka, H., SiBIC: a Tool for Generating a Network of Biclusters Captured by Maximal Frequent Itemset Mining. *Data Mining for Systems Biology: Methods and Protocols*, Second Edition, Methods in Molecular Biology, vol. 1807, Chapter 8, 95–111, Ed. Mamitsuka, H., Humana Press, 2018. [DOI]
- Deng, J., Yuan, Q., Mamitsuka, H. and Zhu, S., DrugE-Rank: Predicting Drug-target Interactions by Learning to Rank. *Data Mining for Systems Biology: Methods and Protocols*, Second Edition, Methods in Molecular Biology, vol. 1807, Chapter 14, 195–202, Ed. Mamitsuka, H., Humana Press, 2018. [DOI]
- Peng, S., Mamitsuka, H. and Zhu, S., MeSHLabeler and DeepMeSH: Recent Progress in Large-scale MeSH Indexing. *Data Mining for Systems Biology: Methods and Protocols*, Second Edition, Methods in Molecular Biology, vol. 1807, Chapter 15, 203–209, Ed. Mamitsuka, H., Humana Press, 2018. [DOI]
- Yotsukura, S., Karasuyama, M., Takigawa, I. and Mamitsuka, H., A Bioinformatics Approach for Understanding Genotype-phenotype Correlation in Breast Cancer. *Big Data Analytics in Genomics*, Chapter 13, 397–428, Ed. Wong, K.-C., Springer, 2016. (Print ISBN: 978-3-319-41278-8, Online ISBN: 978-3-319-41279-5) [DOI]
- Xu, Y., Luo, C., Mamitsuka, H. and Zhu, S., MetaMHCpan, A Meta Approach for Pan-specific MHC Peptide Binding Prediction. *Vaccine Design: Methods and Protocols, Volume 2: Vaccines for Veterinary Diseases*, Methods in Molecular Biology, vol. 1404, 753–760, Ed. Sunil Thomas, Springer, 2016. (Print ISBN: 978-1-4939-3388-4, Online ISBN: 978-1-4939-3389-1) [DOI]

- Takigawa, I., Tsuda, K. and Mamitsuka, H., An *In Silico* Model for Interpreting Polypharmacology in Drug-Target Networks. *In Silico Models for Drug Discovery*, Methods in Molecular Biology, vol. 993, Chapter 5, 67–80, Ed. Kortagere, S., Humana Press, 2013. (Print ISBN: 978-1-62703-341-1, Online ISBN: 978-1-62703-342-8) [DOI]
- Hancock, T., Takigawa, I. and Mamitsuka, H., Identifying Pathways of Co-ordinated Gene Expression. *Data Mining for Systems Biology: Methods and Protocols*, Methods in Molecular Biology, vol. 939, Chapter 7, 69–85, Eds. Mamitsuka, H., DeLisi, C. and Kanehisa, M., Humana Press, 2013. (Print ISBN: 978-1-62703-106-6, Online ISBN: 978-1-62703-107-3) [DOI]
- 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. (Print ISBN: 978-1-60566-398-2, Online ISBN: 978-1-60566-399-9)
- 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. (Print ISBN: 978-3-540-43338-5, Online ISBN: 978-3-540-45884-5) [DOI]
- 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. (Print ISBN: 978-1-575-86338-2, Online ISBN: 978-1-684-00016-6)

Reviews

- Güvenç, B. P., Kaski, S. and Mamitsuka, H., Machine Learning Approaches for Drug Combination Therapies. *Briefings in Bioinformatics*, 22 (6), bbab293, 2021. [DOI]
- Güvenç, B. P., Mamitsuka, H. and Kaski, S., Improving Drug Response Prediction by Integrating Multiple Data Sources: Matrix Factorization, Kernel and Network-based Approaches. *Briefings in Bioinformatics*, 22 (1), 346–359, 2021. [DOI]
- Nguyen, D. A., Nguyen, C. H. and Mamitsuka, H., A Survey on Adverse Drug Reaction Studies: Data, Tasks, and Machine Learning Methods. *Briefings in Bioinformatics*, 22 (1), 164–177, 2021. [DOI]
- Nguyen, D. H., Nguyen, C. H. and Mamitsuka, H., Recent Advances and Prospects of Computational Methods for Metabolite Identification: A Review with Emphasis on Machine Learning Approaches. *Briefings in Bioinformatics*, 20 (6), 2028–2043, 2019. [DOI]
- Yotsukura, S., duVerle, D., Hancock, T., Natsume-Kitatani, Y. and Mamitsuka, H., Computational Recognition for Long Non-coding RNA (lncRNA): Software and Databases. *Briefings in Bioinformatics*, 18 (1), 9–27, 2017. [DOI]
- Mohamed, A., Nguyen, C. H., and Mamitsuka, H., Current Status and Prospects of Computational Resources for Natural Product Dereplication: A Review. *Briefings in Bioinformatics*, 17 (2), 309–312, 2016. [DOI]
- Yotsukura, S. and Mamitsuka, H., Evaluation of Serum-based Cancer Biomarkers: A Brief Review from a Clinical and Computational Viewpoint. *Critical Reviews in Oncology/Hematology*, 95 (2), 103–115, 2015. [DOI]
- Kayano, M., Shiga, M. and Mamitsuka, H., Detecting Differentially Coexpressed Genes from Labeled Expression Data: A Brief Review. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (1), 154–167, 2014. [DOI]
- Ding, H., Takigawa, I., Mamitsuka, H. and Zhu, S., Similarity-based Machine Learning Methods for Predicting Drug-target Interactions: A Brief Review. *Briefings in Bioinformatics*, 15 (5), 737–747, 2014. [DOI]
- Yamamoto, T., Nakayama, K., Hirano, H., Tomonaga, T., Ishihama, Y., Yamada, T., Kondo, T., Kodera, Y., Sato, Y., Araki, N., Mamitsuka, H. and Goshima, N., Integrated View of the Human Chromosome X-centric Proteome Project. *Journal of Proteome Research*, 12 (1), 58–61, 2013 (Perspectives, Invited Paper). [DOI]

- Takigawa, I. and Mamitsuka, H., Graph Mining: Procedure, Application to Drug Discovery and Recent Advance. *Drug Discovery Today*, 18 (1-2), 50–57, 2013 (Invited Paper). [DOI]
- Sorimachi, H., Mamitsuka, H. and Ono, Y., Understanding the Substrate Specificity of Conventional Calpains. *Biological Chemistry*, 393 (9), 853–871, 2012 (Invited Paper). [DOI]
- Mamitsuka, H., Mining from Protein-Protein Interactions. *WIREs Data Mining and Knowledge Discovery*, 2 (5), 400–410, 2012 (Invited Paper). [DOI]
- duVerle, D. and Mamitsuka, H., Machine Learning Sequence Classification Techniques: Application to Cysteine Protease Cleavage Prediction, 7 (4), 415–423, *Current Bioinformatics*, 2012 (Invited Paper).
- Zhang, L., Udaka, K., Mamitsuka, H. and Zhu, S., Toward More Accurate Pan-Specific MHC-Peptide Binding Prediction: A Review of Current Methods and Tools. *Briefings in Bioinformatics*, 13 (3), 350–364, 2012. [DOI]
- duVerle, D. and Mamitsuka, H., A Review of Statistical Methods for Prediction of Proteolytic Cleavage. *Briefings in Bioinformatics*, 13 (3), 337–349, 2012. [DOI]
- Shiga, M. and Mamitsuka, H., Clustering Genes with Expression and Beyond. *WIREs Data Mining and Knowledge Discovery*, 1(6), 496–511, 2011 (Invited paper). [DOI]
- Mamitsuka, H., Glycoinformatics: Data Mining-based Approaches. *Chimia*, 65 (1/2), 10-13, 2011 (Invited paper). [DOI]
- Mamitsuka, H., Informatic Innovations in Glycobiology: Relevance to Drug Discovery. *Drug Discovery Today*, 13 (3/4), 118–123, 2008 (Invited paper). [DOI]

Book/Journal (Special issue) Introduction

- Mamitsuka, H., Preface, *Machine Learning for Marketing*, i-ii, Global Data Science Publishing, 2019. [Supporting Page]
- Zhou, S., Chen, Y-P. P. and Mamitsuka, H., Editorial, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (March-April), 350–351, 2019. [DOI]
- Mamitsuka, H., Preface, *Textbook of Machine Learning and Data Mining, with Bioinformatics Applications*, i-ii, Global Data Science Publishing, 2018. [Supporting Page]
- Mamitsuka, H., Preface, *Data Mining for Systems Biology: Methods and Protocols*, Second Edition, Methods in Molecular Biology, vol. 1807, v–vi, Humana Press, 2018. [DOI]
- Zhou, S., Chen, Y-P. P. and Mamitsuka, H., Introduction to the Special Issue on GIW 2016, *Journal of Bioinformatics and Computational Biology*, 14 (5), 1602004, 2016. [DOI]
- Mamitsuka, H., DeLisi, C. and Kanehisa, M., Preface, *Data Mining for Systems Biology, Methods and Protocols*, Methods in Molecular Biology, vol. 939, v-vii, Humana Press, 2013. [DOI]
- 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. [DOI]

Refereed Journal/Magazine Papers

- Takahashi, K., Mamitsuka, H., Tosaka, M., Zhu, N. and Yamago, S., CoPolDB: A Copolymerization Database for Radical Polymerization. To appear in *Polymer Chemistry*. [DOI]
- Qu, W., You, R., Mamitsuka, H. and Zhu, S., DeepMHCI: An Anchor Position-aware Deep Interaction Model for Accurate MHC-I Peptide Binding Affinity Prediction. *Bioinformatics*, 39 (9), btad551, 2023. [DOI]
- Nguyen, D. A., Nguyen, C. H. and Mamitsuka, H., Central-Smoothing Hypergraph Neural Networks for Predicting Drug-Drug Interactions. To appear in *IEEE Transactions on Neural Networks and Learning Systems*. [DOI]
- Liao, Z., Xie, L., Mamitsuka, H. and Zhu, S., Sc2Mol: A Scaffold-based Two-step Molecule Generator with Variational Autoencoder and Transformer. *Bioinformatics*, 39 (1), btac814, 2023. [DOI]
- Nguyen, D. A., Nguyen, C. H., Petschner, P. and Mamitsuka, H., SPARSE: A Sparse Hypergraph Neural Network for Learning Multiple Types of Latent Combinations to Accurately Predict Drug-drug Interactions. *Bioinformatics (Proceedings of the 30th International Conference on Intelligent Systems for Molecular Biology (ISMB 2022))*, 38 (Supplement 1), i333–i341, 2022. [DOI]
- You, R., Qu, W., Mamitsuka, H. and Zhu, S., DeepMHCII: A Novel Binding Core-Aware Deep Interaction Model for Accurate MHC II-peptide Binding Affinity Prediction. *Bioinformatics (Proceedings of the 30th International Conference on Intelligent Systems for Molecular Biology (ISMB 2022))*, 38 (Supplement 1), i220–i228, 2022. [DOI]
- Güvenç, B. P., Kaski, S. and Mamitsuka, H., DIVERSE: Bayesian Data IntegratiVE learning for precise drug ResponSE prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (4), 2197–2207, 2022. [DOI]
- Liu, L., Mamitsuka, H. and Zhu, S., HPODNets: Deep Graph Convolutional Networks for Predicting Human Protein-phenotype Associations. *Bioinformatics*, 38 (3), 799–808, 2022. [DOI]
- Hiremath, S., Wittke, S., Palosuo, T., Kaivosoja, J., Tao, F., Proll, M., Puttonen, E., Peltonen-Sainio, P., Marttinen, P. and Mamitsuka, H., Crop Loss Identification at Field Parcel Scale using Satellite Remote Sensing and Machine Learning. *PLOS One*, 16 (12), e0251952, 2021. [DOI]
- Nguyen, D. H., Nguyen, C. H. and Mamitsuka, H., Learning Subtree Pattern Importance for Weisfeiler-Lehman based Graph Kernels. *Machine Learning*, 100 (7), 1585–1607, 2021. (Special Issue of the ECML PKDD 2021 Journal Track) [DOI]
- Nguyen, C. H. and Mamitsuka, H., Learning on Hypergraphs with Sparsity. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 43 (8), 2710–2722, 2021. [DOI]
- You, R., Yao, S., Mamitsuka, H. and Zhu, S., DeepGraphGO: Graph Neural Net for Large-scale, Multi-species Protein Function Prediction. *Bioinformatics (Proceedings of the 29th International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB 2021))*, 37 (Supplement 1), i262–i271, 2021. [DOI]
- Liu, L., Mamitsuka, H. and Zhu, S., HPOFiller: Identifying Missing Protein-phenotype Associations by Graph Convolutional Network. *Bioinformatics*, 37 (19), 3328–3336, 2021. [DOI]
- Cai, M., Nguyen, C. H., Mamitsuka, H. and Li, L., XGSEA: CROSS-species Gene Set Enrichment Analysis via Domain Adaptation. *Briefings in Bioinformatics*, 22 (5), bbaa406, 2021. [DOI]
- Kaneko, H., Blanc-Mathieu, R., Endo, H., Chaffron, S., Delmont, T. O., Gaia, M., Henry, N., Hernández-Velázquez, R., Nguyen, C.-H., Mamitsuka, H., Forterre, P., Jaillon, O., de Vargas, C., Sullivan, M. B., Suttle, C. A., Guidi, L. and Ogata, H., Eukaryotic Virus Composition Can Predict the Efficiency of Carbon Export in the Global Ocean. *iScience*, 24 (1), 102002, 2021. [DOI]

- Wimalawarne, K. and Mamitsuka, H., Reshaped Tensor Nuclear Norms for Higher Order Tensor Completion. *Machine Learning*, 110 (3), 507–531, 2021. [DOI]
- Yui, R., Liu, Y., Mamitsuka, H. and Zhu, S., BERTMeSH: Deep Contextual Representation Learning for Large-scale High-performance MeSH Indexing with Full Text. *Bioinformatics*, 37 (5), 684–692, 2021. [DOI]
- Liu, L., Huang, X., Mamitsuka, H. and Zhu, S., HPOLabeler: Improving Prediction of Human Protein-phenotype Associations by Learning to Rank. *Bioinformatics*, 36 (14), 4180–4188, 2020. [DOI]
- Dai, S., You, R., Lu, Z., Huang, X., Mamitsuka, H. and Zhu, S., FullMeSH: Improving Large-Scale MeSH Indexing with Full Text. *Bioinformatics*, 36 (5), 1533–1541, 2020. [DOI]
- Wimalawarne, K., Yamada, M. and Mamitsuka, H., Scaled Coupled Norms and Coupled Higher Order Tensor Completion. *Neural Computation*, 32 (2), 447–484, 2020. [DOI]
- You, R., Yao, S., Xiong, Y., Huang, X., Sun, F., Mamitsuka, H. and Zhu, S., NetGO: Improving Large-scale Protein Function Prediction with Massive Network Information. *Nucleic Acids Research*, 47 (W1), W379–W387, 2019. [DOI]
- Nguyen, D. H., Nguyen, C. H. and Mamitsuka, H., ADAPTIVE: LeArning DATA-dePendentT, ConcIse Molecular VEctors for Fast, Accurate Metabolite Identification from Tandem Mass Spectra. *Bioinformatics (Proceedings of the 27th International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB 2019))*, 35, i164–i172, 2019. [DOI]
- Gillberg, J., Marttinen, P., Mamitsuka, H. and Kaski, S., Modelling $G \times E$ with Historical Weather Information Improves Genomic Prediction in New Environments. *Bioinformatics*, 35 (20), 4045–4052, 2019. [DOI]
- Eid, A., Mamitsuka, H. and Wicker, N., A Metropolis-Hastings Sampling of Subtrees in Graphs. *Austrian Journal of Statistics*, 48 (5), 17–33, 2019. [DOI]
- Wicker, N., Nguyen, C. H. and Mamitsuka, H., A p-Laplacian Random Walk: Application to Video Games. *Austrian Journal of Statistics*, 48 (5), 11–16, 2019. [DOI]
- Gao, J., Liu, L., Yao, S., Huang, S., Mamitsuka, H. and Zhu, S., HPOAnnotator: Improving Large-scale Prediction of HPO Annotations by Low-rank Approximation with HPO Semantic Similarities and Multiple PPI Networks. *BMC Medical Genomics*, 12, 187, 2019. [DOI]
- Wimalawarne, K., Yamada, M. and Mamitsuka, H., Convex Coupled Matrix and Tensor Completion. *Neural Computation*, 30 (11), 3095–3127, 2018. [DOI]
- Nguyen, D. H., Nguyen, C. H. and Mamitsuka, H., SIMPLE: Sparse Interaction Model over Peaks of MoLEcules for Fast, Interpretable Metabolite Identification from Tandem Mass Spectra. *Bioinformatics*, 34 (13) (*Proceedings of the 26th International Conference on Intelligent Systems for Molecular Biology (ISMB 2018)*, Chicago, IL, USA, July, 2018), i323–i332, 2018. [DOI]
- You, R., Zhang, Z., Xiong, Y., Sun, F., Mamitsuka, H. and Zhu, S., GOLabeler: Improving Sequence-based Large-scale Protein Function Prediction by Learning to Rank. *Bioinformatics*, 34 (14), 2465–2478, 2018. [DOI]
- Yamada, M., Tang, J., Lugo-Martinez, J., Hodzic, E., Shrestha, R., Saha, A., Ouyang, H., Yin, D., Mamitsuka, H., Sahinalp, C., Radivojac, P., Menczer, F. and Chang, Y., Ultra High-Dimensional Nonlinear Feature Selection for Big Biological Data. *IEEE Transactions on Knowledge and Data Engineering*, 30 (7), 1352–1365, 2018. [DOI]
- Karasuyama, M. and Mamitsuka, H., Adaptive Edge Weighting for Graph-Based Learning Algorithms. *Machine Learning*, 106 (2), 307–335, 2017. [DOI]
- Takigawa, I. and Mamitsuka, H., Generalized Sparse Learning of Linear Models over the Complete Subgraph Feature Set. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 39 (3), 617–624, 2017. [DOI]

- Yotsukura, S., Karasuyama, M., Takigawa, I. and Mamitsuka, H., Exploring Phenotype Patterns of Breast Cancer within Somatic Mutations. *Briefings in Bioinformatics*, 18 (4), 619–633, 2017. [DOI]
- Gönen, M., Weir, B. A., Cowley, G. S., Vazquez, F., Guan, Y., Jaiswal, A., Karasuyama, M., Uzunangelov, V., Wang, T., Tsherniak, A., Howell, S., Marbach, D., Hoff, B., Norman, T. C., Airola, A., Bivol, A., Bunte, K., Carlin, D., Chopra, B., Deran, A., Ellrott, K., Gopalacharyulu, P., Graim, K., Kaski, S., Khan, S. A., Newton, Y., Ng, S., Pahikkala, T., Paull, E., Sokolov, A., Tang, H., Tang, J., Wennerberg, K., Xie, Y., Zhan, X., Zhu, F., Broad-DREAM Community, Aittokallio, T., Mamitsuka, H., Stuart, J. M., Boehm, J., Root, D., Xiao, G., Stolovitzky, G., Hahn, W. C. and Margolin, A. A., A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. *Cell Systems*, 5 (5), 485–497, 2017. [DOI]
- Wicker, N., Nguyen, C. H. and Mamitsuka, H., Some Properties of a Dissimilarity Measure for Labeled Graphs. *Publications Mathématiques de Besançon: Algèbre et Théorie des Nombres*, Issue 2016, 85–94, 2016.
- Peng, S., You, R., Wang, H., Zhai, C., Mamitsuka, H. and Zhu, S., DeepMeSH: Deep Semantic Representation for Improving Large-scale MeSH Indexing. *Bioinformatics*, 32 (12) (*Proceedings of the 24th International Conference on Intelligent Systems for Molecular Biology (ISMB 2016)*, Orland, FL, USA, July, 2016), i70–i79, 2016. [DOI]
- Yuan, Q.-J., Gao, J., Wu, D., Zhang, S., Mamitsuka, H. and Zhu, S., DrugE-Rank: Improving Drug-Target Interaction Prediction of New Candidate Drugs or Targets by Ensemble Learning to Rank. *Bioinformatics*, 32 (12) (*Proceedings of the 24th International Conference on Intelligent Systems for Molecular Biology (ISMB 2016)*, Orland, FL, USA, July, 2016), i18–i27, 2016. [DOI]
- Natsume-Kitatani, Y. and Mamitsuka, H., Classification of Promoters based on the Combination of Core Promoter Elements Exhibits Different Histone Modification Patterns. *PLOS One*, 11 (3), e0151917, 2016. [DOI]
- Mohamed, A., Nguyen, C. H. and Mamitsuka, H., NMRPro: An Integrated Web Component for Interactive Processing and Visualization of NMR Spectra. *Bioinformatics*, 32 (13), 2067–2068, 2016. [DOI]
- Shinkai-Ouchi, F., Koyama, S., Ono, Y., Hata, S., Ojima, K., Shindo, M., duVerle, D., Kitamura, F., Doi, N., Takigawa, I., Mamitsuka, H. and Sorimachi, H., Predictions of Cleavability of Calpain Proteolysis by Quantitative Structure-Activity Relationship Analysis Using Newly Determined Cleavage Sites and Catalytic Efficiencies of an Oligopeptide Array. *Molecular and Cellular Proteomics*, 15, 1262–1280, 2016. [DOI]
- Johnston, I., Hancock, T., Mamitsuka, H. and Carvalho, L., Gene-proximity Models for Genome-Wide Association Studies. *Annals of Applied Statistics*, 10 (3), 1217–1244, 2016. [DOI]
- Nakamura, A., Takigawa, I., Tosaka, H., Kudo, M. and Mamitsuka, H., Mining Approximate Patterns with Frequent Locally Optimal Occurrences. *Discrete Applied Mathematics*, 200, 123–152, 2016. [DOI]
- Liu, K., Peng, S., Wu, J., Zhai, C., Mamitsuka, H. and Zhu, S., MeSHLabeler: Improving the Accuracy of Large-scale MeSH indexing by Integrating Diverse Evidence. *Bioinformatics*, 31 (12) (*Proceedings of the 23rd International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB 2015)*, Dublin, Ireland, July, 2015), i339–i347, 2015. [DOI]
- Zhou, J., Shui, Y., Peng, S., Li, X., Mamitsuka, H., Zhu, S., MeSHSim: An R/Bioconductor Package for Measuring Semantic Similarity over MeSH Headings and MEDLINE Documents. *Journal of Bioinformatics and Computational Biology*, 13 (6), 1542002, 2015. [DOI]
- Baba, H., Takahara, J. and Mamitsuka, H., In Silico Predictions of Human Skin Permeability using Nonlinear Quantitative Structure-Property Relationship Models. *Pharmaceutical Research*, 32 (7), 2360–2371, 2015. [DOI]
- Shiga, M. and Mamitsuka, H., Non-negative Matrix Factorization with Auxiliary Information on Overlapping Groups. *IEEE Transactions on Knowledge and Data Engineering*, 27 (6), 1615–1628, 2015. [DOI]

- Wang, B., Chen, X., Mamitsuka, H. and Zhu, S., BMExpert: Mining MEDLINE for Finding Experts in Biomedical Domains Based on Language Model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (6), 1286–1294, 2015. [DOI]
- Mohamed, A., Hancock, T., Nguyen, C. H., and Mamitsuka, H., NetPathMiner:R/Bioconductor Package for Network Path Mining through Gene Expression. *Bioinformatics*, 30 (21), 3139–3141, 2014. [DOI]
- Nguyen, C. H., Wicker, N. and Mamitsuka, H., Selecting Graph Cut Solutions via Global Graph Similarity. *IEEE Transactions on Neural Networks and Learning Systems*, 25 (7), 1407–1412, 2014. [DOI]
- Takahashi, K., Takigawa, I. and Mamitsuka, H., SiBIC: A Web Server for Generating Gene Set Networks Based on Biclusters Obtained by Maximal Frequent Itemset Mining. *PLOS ONE*, 8 (12): e82890, 2013. [DOI]
- Karasuyama, M. and Mamitsuka, H., Multiple Graph Label Propagation by Sparse Integration. *IEEE Transactions on Neural Networks and Learning Systems*, 24 (12), 1999–2012, 2013. [DOI]
- Nakamura, A., Saito, T., Takigawa, I., Kudo, M. and Mamitsuka, H., Fast Algorithms for Finding a Minimum Repetition Representation of Strings and Trees. *Discrete Applied Mathematics*, 161 (10-11), 1556–1575, 2013. [DOI]
- Gu, J., Feng, W., Zeng, J., Mamitsuka, H. and Zhu, S., Efficient Semi-supervised MEDLINE Document Clustering with MeSH Semantic and Global Content Constraints. *IEEE Transactions on Cybernetics*, 43 (4), 1265–1276, 2013. [DOI]
- Wicker, N., Nguyen, C. H. and Mamitsuka, H., A New Dissimilarity Measure for Comparing Labeled Graphs. *Linear Algebra and its Applications*, 438 (5), 2331–2338, 2013. [DOI]
- Nguyen, C. H. and Mamitsuka, H., Latent Feature Kernels for Link Prediction on Sparse Graphs. *IEEE Transactions on Neural Networks and Learning Systems*, 23 (11), 1793–1804, 2012. [DOI]
- Hancock, T. and Mamitsuka, H., Boosted Network Classifiers for Local Feature Selection. *IEEE Transactions on Neural Networks and Learning Systems*, 23 (11), 1767–1778, 2012. [DOI]
- Shiga, M. and Mamitsuka, H., A Variational Bayesian Framework for Clustering with Multiple Graphs. *IEEE Transactions on Knowledge and Data Engineering*, 24 (4), 577–590, 2012. [DOI]
- Hancock, T., Wicker, N., Takigawa, I. and Mamitsuka, H. Identifying Neighborhoods of Coordinated Gene Expression and Metabolite Profiles. *PLOS ONE*, 7 (2), e31345, 2012. [DOI]
- Zhang, L., Chen, Y., Wong, H.-S., Zhou, S., Mamitsuka, H. and Zhu, S., TEPITOPEpan: Extending TEPITOPE for Peptide Binding Prediction Covering over 700 HLA-DR Molecules. *PLOS ONE*, 7 (2), e30483, 2012. [DOI]
- Shiga, M. and Mamitsuka, H., Efficient Semi-Supervised Learning on Locally Informative Multiple Graphs. *Pattern Recognition*, 45 (3), 1035–1049, 2012. [DOI]
- Natsume-Kitatani, Y., Shiga, M. and Mamitsuka, H., Genome-wide Integration on Transcription Factors, Histone Acetylation and Gene Expression Reveals Genes Co-regulated by Histone Modification Patterns. *PLOS ONE*, 6 (7), e22281, 2011. [DOI]
- Nguyen, C. H. and Mamitsuka, H., Discriminative Graph Embedding for Label Propagation. *IEEE Transactions on Neural Networks*, 22 (9), 1395–1405, 2011. [DOI]
- Kayano, M., Takigawa, I., Shiga, M., Tsuda, K. and Mamitsuka, H., ROS-DET: Robust Detector of Switching Mechanisms in Gene Expression. *Nucleic Acids Research*, 39 (11), e74, 2011. [DOI]
- Hu, X., Mamitsuka, H. and Zhu, S., Ensemble Approaches for Improving HLA Class I-peptide Binding Prediction. *Journal of Immunological Methods*, 374 (1/2), 47–52, 2011. [DOI]
- duVerle, D., Ono, Y., Sorimachi, H. and Mamitsuka, H., Calpain Cleavage Prediction Using Multiple Kernel Learning. *PLOS ONE*, 6 (5), e19035, 2011. [DOI]

- Takigawa, I., Tsuda, K. and Mamitsuka, H., Mining Significant Substructure Pairs for Interpreting Polypharmacology in Drug-Target Network. *PLOS ONE*, 6 (2), e16999, 2011. [DOI]
- Takigawa, I. and Mamitsuka, H., Efficiently Mining δ -Tolerance Closed Frequent Subgraphs. *Machine Learning*, 82 (2), 95–121, 2011. [DOI]
- Shiga, M., Takigawa, I. and Mamitsuka, H., A Spectral Approach to Clustering Numerical Vectors as Nodes in a Network. *Pattern Recognition*, 44 (2), 236–251, 2011. [DOI]
- Hancock, T., Takigawa, I. and Mamitsuka, H., Mining Metabolic Pathways through Gene Expression. *Bioinformatics*, 26 (17), 2128–2135, 2010. [DOI]
- Hu, X., Zhou, W., Uda, K., Mamitsuka, H. and Zhu, S., MetaMHC: A Meta Approach to Predict Peptides Binding to MHC Molecules. *Nucleic Acids Research*, 38, W474–W479, 2010. [DOI]
- Hancock, T. and Mamitsuka, H., A Markov Classification Model for Metabolic Pathways. *Algorithms for Molecular Biology*, 5 (1), 10, 2010. [DOI], Special Issue: Selected papers from WABI 2009.
- Li, L., Ching, W-K., Chan, Y-M. and Mamitsuka, H., On Network-based Kernel Methods for Protein-Protein Interactions with Applications in Protein Functions Prediction. *Journal of Systems Science and Complexity*, 23 (5), 917–930, 2010. [DOI]
- 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. [DOI]
- Zhu, S., Zeng, J. and Mamitsuka, H., Enhancing MEDLINE Document Clustering by Incorporating MeSH Semantic Similarity. *Bioinformatics*, 25 (15), 1944–1951, 2009. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- Takigawa, I. and Mamitsuka, H., Probabilistic Path Ranking Based on Adjacent Pairwise Coexpression for Metabolic Transcripts Analysis. *Bioinformatics*, 24 (2), 250–257, 2008. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]

- Mamitsuka, H., Selecting Features in Microarray Classification Using ROC Curves. *Pattern Recognition*, 39 (12), 2393–2404, 2006. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- Mamitsuka, H., Finding the Biologically Optimal Alignment of Multiple Sequences. *Artificial Intelligence in Medicine*, 35 (1), 9–18, 2005. [DOI]
- 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. [DOI]
- 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* (Currently, *IEEE Pulse*), 24 (3), 103–108, 2005. [DOI]
- 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. [DOI]
- 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. [DOI]
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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]

- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- Abe, N. and Mamitsuka, H., Predicting Protein Secondary Structures Using Stochastic Tree Grammars. *Machine Learning*, 29 (2-3), 275–301, 1997. [DOI]
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. [DOI]
- Mamitsuka, H., Representing Inter-residue Dependencies in Protein Sequences with Probabilistic Networks. *Computer Applications in the Biosciences (Currently, Bioinformatics)*, 11 (4), 413–422, 1995. [DOI]
- 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. [DOI]

Refereed Conference Papers

- Wang, X., Sun, L., Nguyen, C. H. and Mamitsuka, H., Multiplicative Sparse Tensor Factorization for Multi-View Multi-Task Learning. *Proceedings of the 26th European Conference on Artificial Intelligence (ECAI 2023)*, 2560–2567, Krakow, Poland, Sep. 2023, IOS Press. [DOI]
- Liao, Z., Huang, X., Mamitsuka, H. and Zhu, S., Drug3D-DTI: Improved Drug-target Interaction Prediction by Incorporating Spatial Information of Small Molecules. *Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM 2021)*, 340–347, Houston, TX, USA. Dec. 2021. [DOI]
- Strahl, J., Peltonen, J., Mamitsuka, H. and Kaski, S., Scalable Probabilistic Matrix Factorization with Graph-Based Priors. *Proceedings of the AAAI Conference on Artificial Intelligence (AAAI 2020)*, 34 (4), 5851–5858, New York, USA. Feb. 2020. [DOI]
- Nakamura, A., Takigawa, I. and Mamitsuka, H., Efficiently Enumerating Substrings with Statistically Significant Frequencies of Locally Optimal Occurrences in Gigantic String. *Proceedings of the AAAI Conference on Artificial Intelligence (AAAI 2020)*, 34 (4), 5240–5247, New York, USA. Feb. 2020. [DOI]
- You, R., Dai, S., Zhang, Z., Mamitsuka, H. and Zhu, S., AttentionXML: Label Tree-based Attention-Aware Deep Model for High-Performance Extreme Multi-Label Text Classification. *Proceedings of the 33rd Annual Conference on Neural Information Processing Systems (NeurIPS 2019)*, 5820–5830, Vancouver, Canada, Dec. 2019. [NeurIPS Paper Site]
- Sun, L., Nguyen, C. H. and Mamitsuka, H., Fast and Robust Multi-View Multi-Task Learning via Group Sparsity. *Proceedings of the 28th International Joint Conference on Artificial Intelligence (IJCAI 2019)*, 3499–3505, Macao SAR, Aug. 2019. [DOI]
- Sun, L., Nguyen, C. H. and Mamitsuka, H., Multiplicative Sparse Feature Decomposition for Efficient Multi-View Multi-Task Learning. *Proceedings of the 28th International Joint Conference on Artificial Intelligence (IJCAI 2019)*, 3506–3512, Macao SAR, Aug. 2019. [DOI]
- Wimalawarne, K. and Mamitsuka, H., Efficient Convex Completion of Coupled Tensors using Coupled Nuclear Norms. *Proceedings of the Thirty-Second Annual Conference on Neural Information Processing Systems (NIPS (NeurIPS) 2018)*, pp. 6902–6910, Montréal, Canada, Dec. 2018. [NeurIPS paper site]

- Gao, J., Shuwei, Y., Mamitsuka, H. and Zhu, S., AiProAnnotator: Low-rank Approximation with Network Side Information for High-performance, Large-scale Human Protein Abnormality Annotator. *Proceedings of the 2018 IEEE International Conference on Bioinformatics and Biomedicine*, pp. 13–20, Madrid, Spain, Dec. 2018. [DOI] (Best student Paper)
- Karasuyama, M. and Mamitsuka, H., Factor Analysis on a Graph. *Proceedings of the 21st International Conference on Artificial Intelligence and Statistics (AISTATS 2018) (JMLR: Workshop and Conference Proceedings (PMLR), Vol. 84)*, pp. 1117–1126, Playa Blanca, Lanzarote, Canary Islands, Apr. 2018, MIT Press. [PMLR paper site]
- Yamada, M., Lian, W., Goyal, A., Chen, J., Wimalawarne, K., Kahn, S., Kaski, S., Mamitsuka H. and Chang, Y., Convex Factorization Machine for Toxicogenomics Prediction. *Proceedings of the Twenty-third ACM SIGKDD International Conference On Knowledge Discovery and Data Mining (KDD 2017)*, pp. 1215–1224, Nova Scotia, Canada, Aug. 2017, ACM Press. [DOI]
- Gao, J., Yamada, M., Kaski, S., Mamitsuka, H. and Zhu, S., A Robust Convex Formulations for Ensemble Clustering. *Proceedings of the 25th International Joint Conference on Artificial Intelligence (IJCAI 2016)*, pp. 1476–1482, New York City, USA, Jul. 2016, AAAI Press. [IJCAI paper site]
- Nguyen, C. H. and Mamitsuka, H., New Resistance Distances with Global Information on Large Graphs. *Proceedings of the Nineteenth International Conference on Artificial Intelligence and Statistics (AISTATS 2016) (JMLR: Workshop and Conference Proceedings, Vol. 51)*, pp. 639–647, Cadiz, Spain, May 2016, MIT Press. [PMLR paper site]
- Zheng, X., Zhu, S., Gao, J. and Mamitsuka, H., Instance-wise Weighted Nonnegative Matrix Factorization for Aggregating Partitions with Locally Reliable Clusters. *Proceedings of the 24th International Joint Conference on Artificial Intelligence (IJCAI 2015)*, pp. 4091–4097, Buenos Aires, Argentina, Jul. 2015, AAAI Press. [IJCAI paper site]
- Karasuyama, M. and Mamitsuka, H., Manifold-based Similarity Adaptation for Label Propagation. *Proceedings of the Twenty-Seventh Annual Conference on Neural Information Processing Systems (NIPS 2013)*, pp. 1547–1555, Lake Tahoe, NV, USA, Dec. 2013. [NIPS paper site]
- Zheng, X., Ding, H., Mamitsuka, H. and Zhu, S., Collaborative Matrix Factorization with Multiple Similarities for Predicting Drug-Target Interactions. *Proceedings of the Nineteenth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD 2013)*, pp. 1025–1033, Chicago, IL, USA, Aug. 2013, ACM Press. [DOI]
- Nguyen, C. H. and Mamitsuka, H., Kernels for Link Prediction with Latent Feature Models. *Proceedings of the European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases (ECML PKDD 2011), Part II (Lecture Notes in Computer Science, vol. 6912)*, pp. 517–532, Athens, Greece, Sep. 2011, Springer. [DOI]
- Hancock, T. and Mamitsuka, H., Boosted Optimization for Network Classification. *Proceedings of the Thirteenth International Conference on Artificial Intelligence and Statistics (AISTATS 2010) (JMLR: Workshop and Conference Proceedings, Vol. 9)*, pp. 305–312, Sardinia, Italy, May 2010, MIT Press. [PMLR paper site]
- 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, Aug. 2007, ACM Press. [DOI]
- 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, Apr. 2007, Springer-Verlag. [DOI]

- 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, Aug. 2006, ACM Press. [DOI]
- 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, Aug. 2004, IEEE Computer Society Press. [DOI]
- 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, Apr. 2004, SIAM. [DOI]
- 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. [DOI]
- 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. [AAAI paper site]
- 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. [DOI]
- 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. [DOI]
- 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. [PDF]
- 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. [PDF]
- 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. [DOI]
- 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. [AAAI paper site]
- 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. [DOI]

Refereed Symposium Papers

- Nakamura, A., Saito, T., Takigawa, I., Mamitsuka, H. and Kudo, M., Algorithms for Finding a Minimum Repetition Representation of a String. *Proceedings of the Seventeenth Symposium on String Processing and Information Retrieval (SPIRE 2010)*. (*Lecture Notes in Computer Science*, vol. 6393), pp. 185–190, Los Cabos, Mexico, Oct. 2010, Springer-Verlag. [DOI]
- Wan, R., Anh, V. 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. [DOI]
- 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, P. R. China, Sep. 2009, APORC Press. [PDF]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]

Refereed Workshop Papers

- Shiga, M. and Mamitsuka, H., Variational Bayes Co-clustering with Auxiliary Information. *Proceedings of the 4th MultiClust Workshop on Multiple Clusterings, Multi-view Data, and Multi-source Knowledge-driven Clustering (MultiClust 2013)*, Article No. 5, Chicago, IL, USA, Aug. 2013. [DOI]
- Shiga, M. and Mamitsuka, H., Variational Bayes Learning over Multiple Graphs. *Proceedings of 2010 IEEE International Workshop on Machine Learning for Signal Processing (MLSP 2010)*, pp. 166–171, Kittilä, Finland, Aug. 2010, IEEE. [DOI]
- 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, Sep. 2009, Springer. [DOI]
- 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. [DOI]

- 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. [DOI]
- 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.) [DOI]

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. [DOI]
- Mamitsuka, H. and Abe, N., Active Ensemble Learning: Application to Data Mining and Bioinformatics, *Systems and Computers in Japan*, 38 (11), 100–108, 2007. [DOI]

Unrefereed Conference Proceedings Papers

- Kayano, M., Takigawa, I., Shiga, M., Tsuda, K. and Mamitsuka, H., On the Performance of Methods for Finding a Switching Mechanism in Gene Expression. *Proceedings of the Tenth Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2010)*. (*Genome Informatics*, 24), pp. 69–83, Kyoto, Japan, Jul. 2010, Imperial College Press. [DOI]
- Takigawa, I., Hashimoto, K., Shiga, M., Kanehisa, M. and Mamitsuka, H., Mining Patterns from Glycan Structures, *Proceedings of the Beilstein Symposium on Glyco-Bioinformatics*, 13-24, Potsdam, Germany, 2009.
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- 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. [DOI]
- Wan, R., Anh, V. N. 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., Anh, V. N. 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.
- 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. [DOI]

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

- Mamitsuka, H., Application of Machine Learning and Data Mining to Life Sciences, *Development of Biotechnology via Introduction of Artificial Intelligence*, 10–19, CMC Publishing, Co., Ltd. 2018. (in Japanese)
- Takahashi, K. and Mamitsuka, H., Application of Machine Learning (Data Mining) for Tribology, *Understanding and Controlling Tribology through Numerical and Surface Analysis*, Chapter 6, Section 13, 463–470, Technosystem Co., Ltd. 2018. (in Japanese)
- Mamitsuka, H., Machine Learning over Graphs, Network Sciences and Complex Systems. *Newsletter, International Research Unit of Integrated Complex System Science, Kyoto University*, 8 (Spring, 2017), 6–7, 2017. (in Japanese)
- Mamitsuka, H., Drug-target Interaction Prediction through Machine Learning. *SAR News*, 29, 2–8, 2015. (in Japanese)
- Kayano, M. and Mamitsuka, H., ROS-DET: Robust Detector of Switching Mechanisms in Gene Expression. *Jikken Igaku (Experimental Medicine)*, 30 (6), 969–974, 2012. (in Japanese)
- Takigawa, I. and Mamitsuka, H., Graph Algorithms for Chemistry. *Kagaku to Kyoiku (Chemistry and Education)*, 59 (9), 450–453, 2011. (in Japanese)
- Mamitsuka, H. and Yoneya, T., PURE: A System for Assisting PubMed Documents Retrieval. *Seimei Kenkyu he no Ouyou to Kaihatsu ga Susumu Biodatabase to Biosoftware Saizensen.*, pp. 201–206, Eds. Morishita, S. and Akutsu, T., Yodo-sya, 2008. (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-sya, 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 (already issued only)

- USA, #11533862, Gillberg, J., Kaski, S., Marttinen, P. and Mamitsuka, H.
- USA, #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

Professional Societies

- Membership
ACM, IEEE (currently senior member), IEEE Computer Society, ISCB, JSBi
- Services
AASBi (Association of Asian Societies for Bioinformatics)
Board Member (Jan. 2007–Mar. 2011)
IEEE Computational Intelligence Society
Bioinformatics and Bioengineering Technical Committee Member (Feb. 2013–Present)
JSBi
Co-founder (1999), Board Member (Apr. 2005–Mar. 2007, Apr. 2012–Mar. 2014), Secretary (Apr. 2007–Mar. 2008)

Research Experience

- Jan. 2019–Dec. 2022: Visiting Professor, Aalto University, Finland.
- Jan. 2018–Dec. 2018: Faculty member, Finnish Center for Artificial Intelligence (FCAI), Finland.
- Jan. 2015–Dec. 2018: Principal Investigator, HIIT (Helsinki Institute for Information Technology), Finland.
- Jan. 2015–Dec. 2018: FiDiPro Professor, Aalto University, Finland.
- Dec. 2014–Mar. 2016: Research Advisor, Kyoto Shisaku Center, Co. Ltd., Japan.
- Apr.–May 2014: Visiting Researcher, Aalto University, Finland.
- Apr.–May 2014: Erasmus Mundus Scholar, euSYSBIO, EACEA (Education, Audiovisual and Culture Executive Agency), European Commission.
- Mar. 2014: Visiting Scholar, Centre Européen pour les Mathématiques, la Physique et leurs interactions (CEMPI), France.
- Apr. 2011–Mar. 2012: Research Advisor, Kyowa Hakko Kirin, Co. Ltd., Japan.
- Apr. 2010–Present: Member, International Research Unit of Integrated Complex System Science (IRU-ICSS), Kyoto University, Japan.
- May 2009–Apr. 2011: Senior Visiting Scholar, Fudan University, P. R. China.
- May–Jun. 2009, May–Jun. 2011: Visiting Professor, University of Strasbourg, France.
- Dec. 2007: Visiting Researcher, School of Computing, National University of Singapore.
- Apr. 2006–Present: Professor, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan.
- Mar. 2006, Nov.–Dec. 2007 and Mar. 2009: Visiting Scientist, Institute for Infocomm Research (I2R), Agency for Science, Technology and Research (A*STAR), Singapore.
- 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. 1993–Dec. 2001: Member, Theory NEC Laboratory, Real World Computing (RWC) project (sponsored by METI (Ministry of Economy, Trade and Industry)), Japan.
- Apr. 1991–Mar. 2002: Research staff, Central Research Laboratories, NEC Corporation, Japan.

Book/Journal/Magazine Editing

Associate Editor, *IEEE Transactions on Neural Network and Learning Systems*, IEEE Computational Intelligence Society. Jan., 2020–Present.

Regional Editor, Editorial Board, *Network and Systems Medicine* (originally *Systems Medicine*), Mary Ann Liebert, Inc. Oct. 2017–Apr. 2021.

Editorial Board Member (Series Editor), *Advanced Information and Knowledge Processing* (Book Series), Springer. Oct., 2013–Present.

Associate Editor, *BMC Bioinformatics*, BioMed Central. Apr., 2010–Present.

Associate Editor, *Knowledge and Information Systems*, Springer. Nov., 2009–Jul., 2022.

Associate Editor, *International Journal of Knowledge Discovery in Bioinformatics*, IGI Global. Dec., 2008–Dec., 2018.

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

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

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

Book/Journal/Magazine Referee

- Post-publication assessment

PLOS One

- Regular referee

ACM Transactions on Knowledge Discovery from Data, Acta Biotheoretica, Amino Acids, Artificial Intelligence in Medicine, Bioinformatics, BMC Bioinformatics, BMC Medical Genomics, BMC Structural Biology, BMC Systems Biology, Briefings in Bioinformatics, Complexity, Computers in Biology and Medicine, Data and Knowledge Engineering, Data Mining and Knowledge Discovery, IEEE Intelligent Systems, IEEE IT Professional, IEEE/ACM Transactions on Computational Biology and Bioinformatics, IEEE Transactions on Information Technology in Biomedicine, IEEE Transactions on Knowledge and Data Engineering, IEEE Transactions on Neural Networks and Learning Systems, IEEE Transactions on Pattern Analysis and Machine Intelligence, Information Sciences, International Journal of Data Mining and Bioinformatics, International Journal of Foundation of Computer Science, Journal of Bioinformatics and Computational Biology, Journal of Biomedical Informatics, Journal of Chemical Information and Modeling, Journal of Clinical Bioinformatics, Journal of Computer Science and Technology, Journal of Machine Learning Research, Metabolites, Molecular Biosystems, Molecular Oncology, Molecular Pharmaceutics, New Generation Computing, Nucleic Acids Research, OMICS: A Journal of Integrative Biology, OR spectrum, Pattern Recognition, Pattern Recognition Letters, PeerJ, PLOS Computational Biology, PLoS ONE, Scientific Reports, Theoretical Computer Science, Wiley Encyclopedia of Chemical Biology

Conference Committee

- Conference Co-organizer

IBSB (2011, 2013, 2019), MLAB (2013)

- Program Committee Co-chair

BIBE (2009), GIW (2005, 2007, 2016), IBSB (2004)

- Senior Program Committee Member (Major conferences only)
IEEE BigData (2018), ICONIP (2020), ACM CIKM (2022-23)
- Program Committee Member (Major conferences only)
AAAI (2020–22), ACM CIKM (2010–11, 2017–21), ACM SIGKDD (2013–23), ECML–PKDD (2023), ICLR (2021–22), ICML (2018–19, 2023), IEEE BigData (2018–20), IEEE ICDM (2018–21), IJCAI (2020), ISMB (2007–09), NeurIPS (Reviewer, equivalent to Program Committee Member of regular conferences) (2011–15, 2018–20, 2022)

Grant Referee

Inserm (National Institute of Health and Medical Research), France (Mar.–Apr., 2023)

European Science Foundation (Aug. 2022)

National Science Centre, Poland (Mar. 2021)

Austrian Science Fund (FWF), Austria (Dec. 2020–Jan. 2021)

“Research Center Network for Realization of Regenerative Medicine” program, Japan Agency for Medical Research and Development (AMED), Japan (Aug. 2018–Mar. 2019)

“Research Fellowships for Young Scientists”, “Overseas Research Fellowships”, “Leading Initiative for Excellent Young Researchers (LEADER)” and all programs in International Collaborations, Japan Society for the Promotion of Science (JSPS), Japan (Aug., 2017–Jul., 2019)

NRF (National Research Foundation)-NSFC (National Science Foundation of China) Joint Grant Call in Data Science, Singapore (Aug.–Sep., 2016)

Fundamental Technology Development for Promoting the Industrial Application of iPS Cells, New Energy and Industrial Technology Development Organization (NEDO), Japan (Feb.–Mar., 2011)

Strategic Research Funding, City University of Hong Kong, Hong Kong SAR (Feb., 2008, Jan., 2012)

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

ORAL PRESENTATIONS (Since 2006)

Keynote/Invited Talks

- Sep. 28, 2023. Invited talk. *SFD (Structure, Function and Dynamics) Conference*, Honolulu, HI, USA.
- Oct. 12, 2022. Invited talk. *21st International Conference on Systems Biology (ICSB 2022)*, Berlin, Germany.
- Jun. 16, 2022. Invited Speech, *2nd International Congress of Asian Oncology Society (AOS 2022)*, Seoul, South Korea. (Online)
- Mar. 30, 2022. Invited talk, *Final Seminar of Novel Applications of Artificial Intelligence in Physical Sciences and Engineering Research (AIPSE) (AIPSE Closing Seminar)*, Academy of Finland, Helsinki, Finland. (Online)
- Nov. 24, 2021. Plenary talk, *1st International Conference on Computational Science and Data Analytics (COMDATA 2021)*, Kuala Lumpur, Malaysia. (Online)
- Jun. 28, 2021. Invited Speech, Symposium entitled with *Big biological data, data integration and learning algorithms in deciphering major depression and its treatments* at the *15th World Congress of Biological Psychiatry*, Vienna, Austria (Online)
- Nov. 27, 2019. Keynote talk, *DSx Conference 2019*, Perdana University, Selangor, Malaysia.
- Jun. 14, 2019: Invited talk, *Workshop on Bioinformatics and Data Analysis*, Xi'an, P. R. China.
- Nov. 16, 2018: Keynote Speech, *5th SHTP Annual International Conference 2018*, Ho Chi Minh City, Vietnam.
- Jul. 20, 2018: Invited talk, *Three Decades for Calpain for late Dr. Hiroyuki Sorimachi*, Tokyo, Japan.
- Jun. 21, 2018: Invited talk, *Second Belgrade Bioinformatics Conference (BelBi 2018)*, Belgrade, Serbia.
- Mar. 16, 2018: Invited talk, *Sixth International Symposium on Integrated Uncertainty in Knowledge Modelling and Decision Making (IUKM 2018)*, Hanoi, Vietnam.
- Dec. 12, 2016: Invited Speech, *102nd Meeting of Special Interest Group on Fundamental Problems on Artificial Intelligence, The Japanese Society of Artificial Intelligence*, Fukuoka, Japan.
- Nov. 30, 2016: Keynote Speech, *Fifth International Symposium on Integrated Uncertainty in Knowledge Modeling and Decision Making (IUKM 2016)*, Da Nang, Vietnam.
- Jul. 17, 2016: Invited Talk, *'The Biology of Calpain in Health and Disease'*, *FASEB Science Research Conference*, Big Sky, MT, USA.
- Dec. 1, 2015: Invited Speech, *Caroline von-Humboldt Professorship Award Ceremony*, Berlin, Germany.
- Oct. 24, 2015: Invited Talk, *Kick-off meeting, ACCEL SRT Project*, Imahama, Japan.
- Oct. 8, 2015: Invited Talk, *CIM Workshop on Machine Learning*, Uppsala, Sweden.
- Sep. 12, 2014: Invited Talk, *Sweden-Kyoto Symposium 2014*, Stockholm, Sweden.
- May 22, 2014: Keynote Speech, *2014 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology*, Honolulu, HI, USA.
- May 21, 2014: Panelist, *Roundtable: Future Directions in Computational Intelligence in Bioinformatics Research, 2014 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology*, Honolulu, HI, USA.
- Apr. 24, 25 and 28, 2014: Invited Lecture, *euSYSBIO, Erasmus Mundus Programme, Aalto University*, Espoo, Finland.
- Mar. 18, 2014: Invited Talk, *TML 2014 - "Trends in Machine Learning" workshop*, Kyoto, Japan.

- Dec. 17, 2013: Invited Talk, *AASBi Session, 24th International Conference on Genome Informatics*, Singapore.
- Sep. 19, 2013: Invited Talk, *The HUPO Initiative Assembly in Kyoto*, Uji, Japan.
- Sep. 17, 2013: Invited Talk, *Kyoto University–Koç University Symposium “New Frontiers in Health Sciences & Technologies”*, Kyoto, Japan.
- Sep. 11, 2013: Invited Talk, 17th Meeting of *JSBi-SGI, Pharmaco-Informatics*, Tokyo, Japan.
- Jul. 22, 2013: Invited talk, *FASEB Science Research Conference, “The Biology of Calpains in Health and Disease”*, Saxtons River, VT, USA.
- Feb. 8, 2013: Invited Talk, *Research Seminar at Kyushu Branch of JSBi*, Kyushu University, Japan.
- Jan. 18, 2013: Invited Talk, *1st JHUPO Satellite Symposium*, Kyoto, Japan.
- Nov. 28, 2012: Invited Lecture, *Kyoto University – Durham University Joint International Symposium*, Uji, Japan.
- Oct. 4, 2012: Invited Talk, *2012 Workshop on Pharmaco-Informatics for Drug Discovery in Conjunction with 2012 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012)*, Philadelphia, PA, USA.
- Nov. 23, 2011: Invited Talk, Seminar in Information Systems and Applications, *National Tsing Hua University*, Hsinchu, Taiwan (ROC).
- Nov. 13, 2011: Invited Tutorial, *2011 International Conference on Neural Information Processing (ICONIP)*, Shanghai, P. R. China.
- Oct. 26, 2011: Invited Talk, *13th Niigata Proteomics Forum*, Niigata, Japan.
- Aug. 24, 2011: Invited Lecture, *FICS (Finnish Doctoral Programme in Computational Sciences) Summer School*, Espoo, Finland.
- Jul. 28, 2011: Invited Talk, *Educational Seminar, 2011 Annual Meeting of Japanese Proteomics Society (The 9th JHUPO Conference)*, Niigata, Japan.
- Jul. 22, 2011: Invited Lecture, *Summer School, “Computational Systems Biology”*, Berlin, Germany.
- Feb. 28, 2011: Invited Talk, *2nd Workshop on Bioinformatics for Medical and Pharmaceutical Research*, Paris, France.
- Nov. 10, 2010: Invited Talk, *6th Research Achievement Report Meeting*, Institute for Bioinformatics Research and Development, Japan Science and Technology Agency, Shinagawa, Japan.
- Nov. 5, 2010: Plenary Lecture, *The 2010 Systems Biology and Bioinformatics Symposium (SBBS)*, Hsinchu, Taiwan (ROC).
- Oct. 24, 2010: Invited Talk, Open Lectures in *Institute for Chemical Research, Kyoto University*, Uji, Japan.
- Sep. 13, 2010: Keynote Speech, *Second International Seminar on Business and Information Management (ISBIM 2010)*, Wuhan, P. R. China.
- Aug. 5, 2010: Invited Talk, *Symposium on “Invitation to Integrated Complex System Sciences”*, Kyoto, Japan.
- Feb. 8, 2010: Invited Talk, *The Ninth Research Seminar at Hokkaido Branch of JSBi*, Sapporo, Japan.
- Oct. 5, 2009: Invited Lecture, *International Beilstein Symposium on Glyco-Bioinformatics*, Potsdam, Germany.

- Jun. 22 and 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, P. R. China.
- May 13, 2009: Keynote Speech, *Bioinformatics Workshop*, Fudan University, Shanghai, P. R. China.
- Jan. 15, 2009: Invited Talk, *Workshop, Bioinformatics on Herbal Medicine*, Toyama, Japan.
- Dec. 21, 2008: Keynote Speech, *IEEE International Symposium on Knowledge Acquisition and Modeling (KAM 2008)*, Huazhong Normal University, Wuhan, P. R. China.
- Jun. 22, 2008: Invited Talk, Workshop on *Relations with Computer Science, Foundations of Computational Mathematics (FoCM'08)*, City University of Hong Kong, Hong Kong SAR.
- Jun. 19, 2008: Invited Talk, *Research Meeting, The Institute of Electronics, Information and Communication Engineers (IEICE)*, Otaru, Japan.
- May 27, 2008: Keynote Speech, *Systems Biology Workshop: From Molecules to Life*, Melbourne, Australia.
- Dec. 2, 2007: Invited Talk, *AASBi Symposium 2007*, Biopolis, 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, P. R. China.
- Dec. 8, 2006: Invited Talk, *International Workshop on Scientific Computing: Models, Algorithms and Applications*, University of Hong Kong, Hong Kong SAR.
- Nov. 9, 2006: Invited Talk, *Second Taiwan-Japan Bilateral Symposium on Bioinformatics*, National Cheng Kung University, Tainan, Taiwan (ROC).
- Nov. 3, 2006: Invited Talk, *Third Japan-Germany Frontiers of Sciences Symposium*, Heidelberg, Germany.
- Mar. 14, 2006: Invited Talk, *First Japan-Taiwan Bilateral Symposium on Bioinformatics*, University of Tokyo, Japan.

Seminars

- May 24, 2023: Computer Science Colloquium, *City University of Hong Kong*, Hong Kong SAR.
- Mar. 24, 2023: Seminar, *University of Malaya*, Kuala Lumpur, Malaysia.
- Mar. 21, 2023: Seminar, *University of Malaya*, Kuala Lumpur, Malaysia.
- Feb. 27, 2023: Seminar, *Forest Workshop*, Sapporo, Japan (Online).
- Feb. 17, 2023: Seminar, *Hokkaido University*, Sapporo, Japan.
- Oct. 19, 2022: Seminar, *Humboldt University Berlin*, Germany.
- Apr. 15, 2021: Seminar, *Hokkaido University*, Sapporo, Japan.
- Feb. 13, 2020: Seminar, *IBM T. J. Watson Research Center*, Yorktown Heights, NY, USA.
- Jan. 23, 2020: Seminar, *Humboldt University Berlin*, Germany.
- Dec. 3, 2019: Seminar, *University of Malaya*, Kuala Lumpur, Malaysia.
- Aug. 20, 2019: Seminar, *Shenzhen University*, Shenzhen, P. R. China.
- Jun. 28, 2019: Seminar, *Perdana University*, Selangor, Malaysia.

Jun. 26, 2019: Seminar, *University of Malaya*, Kuala Lumpur, Malaysia.

Jun. 21, 2019: Seminar, *Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences*, Shanghai, P. R. China.

Jun. 20, 2019: Seminar, *Fudan University*, Shanghai, P. R. China.

May. 10, 2019: Seminar, *Kyushu Institute of Technology*, Iizuka, Japan.

Nov. 29, 2018: Seminar, *Research Institute at National Center for Global Health and Medicine*, Tokyo, Japan.

Nov. 28, 2018: Seminar, 1245th Seminar of Department of Biological Sciences, *University of Tokyo*, Tokyo, Japan.

Nov. 17, 2018: Seminar, *Ho Chi Minh City National University of Science*, Ho Chi Minh City, Vietnam.

Mar. 22, 2018: Seminar, *Hanoi University of Water Resources (ThuyLoi University)*, Hanoi, Vietnam.

Mar. 20, 2018: Seminar, *Hanoi University of Science and Technology*, Hanoi, Vietnam.

Apr. 20, 2017: Seminar, *Institute for Advanced Biosciences, Keio University*, Tsuruoka, Japan.

Mar. 27, 2017: Seminar, Machine Learning Coffee Seminars, *University of Helsinki*, Finland.

Nov. 29, 2016: Seminar, *University of Engineering and Technology, National University of Vietnam in Hanoi*, Hanoi, Vietnam.

Nov. 28, 2016: Seminar, *Hanoi University of Science and Technology*, Hanoi, Vietnam.

Jul. 27, 2016: Seminar, *Kyowa Hakko Kirin*, Mishima, Japan.

Dec. 3, 2015: Seminar, *Humboldt University Berlin*, Germany.

Jan. 21, 2015: Seminar, *National Tsing Hua University*, Hsinchu, Taiwan (ROC).

Oct. 24, 2014: Seminar, *Fudan University*, Shanghai, P. R. China.

Sep. 30, 2014: Seminar, *Lille 1 University*, Lille, France.

Mar. 26, 2014: Seminar, *Lille 1 University*, Lille, France.

Feb. 3, 2014: Seminar, *Aalto University*, Espoo, Finland.

Dec. 20, 2013: Seminar, *National University of Singapore*, Singapore.

Dec. 19, 2013: Seminar, *Institute for Infocomm Research (I2R)*, Singapore.

Mar. 8, 2013: Seminar, *Mitsubishi Electric Research Laboratories*, Boston, MA, USA.

Dec. 17, 2012: Seminar, *Noah's Ark Lab, Huawei*, Hong Kong SAR.

Nov. 20, 2012: Seminar, *Niigata University*, Niigata, Japan.

Oct. 8, 2012: Seminar, *IBM T. J. Watson Research Center*, Yorktown Heights, NY, USA.

Jul. 26, 2012: Seminar, *Faculty Lab Presentation, International Workshop of Bioinformatics and Systems Biology 2012*, Boston, MA, USA.

Feb. 2, 2012: Seminar, *Kyowa Hakko Kirin Co., Ltd.*, Mishima, Japan.

Jan. 30, 2012: Seminar, *Kochi Medical School*, Kochi, Japan.

Nov. 22, 2011: Seminar, *National Tsing Hua University*, Hsinchu, Taiwan (ROC).

Nov. 14, 2011: Seminar, *Fudan University*, Shanghai, P. R. China.

Jun. 21, 2011: Seminar, *Kyowa Hakko Kirin Co., Ltd.*, Mishima, Japan.

May 26, 2011: Seminar, *University of Strasbourg*, France.

May 24, 2011: Seminar, *IGBMC (Institute of Genetics and Molecular and Cellular Biology)*, *University of Strasbourg*, France.

May 16, 2011: Seminar, *Fudan University*, Shanghai, P. R. China.

Feb. 23, 2011: Seminar, *Humboldt University Berlin*, Germany.

Jan. 20, 2011: Seminar, *National Cheng Kung University*, Tainan, Taiwan (ROC).

Jan. 19, 2011: Seminar, *National Cheng Kung University*, Tainan, Taiwan (ROC).

Dec. 30, 2010: Seminar, *Fudan University*, Shanghai, P. R. China.

Dec. 28, 2010: Seminar, *Shanghai Jiao Tong University*, Shanghai, P. R. China.

Dec. 27, 2010: Seminar, *Shanghai Institutes for Biological Sciences*, Shanghai, P. R. China.

Dec. 10, 2010: Seminar, *Boston College*, MA, USA.

Dec. 8, 2010: Seminar, *Boston University*, MA, USA.

Oct. 18, 2010: Seminar, *Fudan University*, Shanghai, P. R. China.

Oct. 15, 2010: Seminar, *Soochow University*, Suzhou, P. R. China.

May 13, 2010: Seminar, *Fudan University*, Shanghai, P. R. China.

Mar. 22, 2010: Seminar, *Curie Institute*, Paris, France.

Mar. 16, 2010: Seminar, *Fudan University*, Shanghai, P. R. China.

Oct. 9, 2009: Seminar, *Humboldt University Berlin*, Germany.

Sep. 29, 2009: Seminar, *Fudan University*, Shanghai, P. R. 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.

Mar. 24, 2009: Seminar, *I2R, A*STAR*, Singapore.

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. 17, 2008: Seminar, *Nara Institute of Science and Technology*, Nara, Japan

May 27, 2008: Seminar, *University of Melbourne*, Australia.

Dec. 13, 2007: Seminar, *Helsinki University of Technology*, Finland.

Dec. 3, 2007: Opening Address, *Eighteenth International Conference on Genome Informatics*, Biopolis, Singapore.

Nov. 28, 2007: Seminar, *I2R, A*STAR*, Singapore.

Aug. 10, 2007: Seminar, *University of California Berkeley*, CA, USA.

Dec. 17, 2006: Closing Remark, *International Symposium on Bioinformatics Education and Research*, Yokohama, Japan.

Sep. 26, 2006: Seminar, *BioFrontier Laboratories, Kyowa Hakko Kogyo Co., Ltd.*, Machida, Japan.

Aug. 24, 2006: Seminar, *IBM T. J. Watson Research Center*, Yorktown Heights, NY, USA.

Aug. 23, 2006: Talk, *Twelfth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD 2006)*, Philadelphia, PA, 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.

AWARDS AND HONORS

- SCI (School of Science) Awards 2018: Innovation of the Year, Using Machine Learning to Tackle the Impending Food Crisis, Jussi Gilberg, Pekka Marttinen, Hiroshi Mamitsuka and Samuel Kaski, *School of Science, Aalto University*, Espoo, Finland, Dec. 2018.
- Best Student Paper, AiProAnnotator: Low-rank Approximation with network side information for high-performance, large-scale human Protein abnormality Annotator, Junning Gao, Shuwei Yao, Hiroshi Mamitsuka and Shanfeng Zhu, *2018 IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM 2018)*, Barcelona, Spain, Dec. 2018.
- FiDiPro Professor, Hiroshi Mamitsuka, *Tekes (Finnish Funding Agency for Technology and Innovation)*, Finland, Jan. 2015–Dec. 2018.
- Best Performer, Masayuki Karasuyama and Hiroshi Mamitsuka, *DREAM 9: DREAM Challenges and Cytoscape Workshops 2014*, “Broad-DREAM Gene Essentiality Prediction Challenge Sub-Challenge 1”, San Diego, CA, USA, Nov. 2014.
- Student Travel Award, Hierarchical Gene-Proximity Models for Genome-Wide Association Studies, Ian Johnston, Timothy Hancock, Hiroshi Mamitsuka and Luis Carvalho, *Section on Bayesian Statistical Science, JSM (Joint Statistical Meetings) 2014*, Boston, MA, USA, Aug. 2014.
- IEEE Kansai Section Medal recipient, Hiroshi Mamitsuka, *IEEE Kansai Section*, Feb. 2014.
- Best Poster Award, Reverse-engineering Gene Regulatory Networks Using Time Series, David duVerle and Hiroshi Mamitsuka, *The 11th Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2011)*, Berlin, Germany, Jul. 2011.
- Recipient of ‘Certificate of Appreciation’, Service Award, Hiroshi Mamitsuka, *IEEE Computer Society*, 2009.

TEACHING

Postdocs Adviser

Duc Anh Nguyen, Apr.–Aug. 2023.

Péter Petschner, Nov. 2020–Nov. 2022.

Lu Sun (Currently, Assistant Professor, ShanghaiTech University, P. R. China), Oct. 2017–Oct. 2019.

Sohiya Yotsukura, Oct. 2016–Sep. 2017.

Kishan Wimalawarne (Currently, Postdoctoral Fellow, University of Tokyo, Japan), Apr. 2016–Mar. 2020.

Canh Hao Nguyen (Currently, Senior Lecturer (equivalent to Associate Professor), Kyoto University, Japan), Apr. 2009–May 2013.

Mitsunori Kayano (Currently, Associate Professor, Obihiro University of Agriculture and Veterinary Medicine, Japan), Apr. 2008–Sep. 2010.

Yayoi Natsume (Currently, Project Leader (Group Head), National Institute of Biomedical Innovation, Japan), Apr. 2008–Sep. 2010.

Timothy Peter Hancock (Currently, Senior Scientist, Department of Primary Industries, New South Wales Trade and Investment, Austraria), Jul. 2007–Mar. 2011.

Motoki Shiga (Currently, Professor, Tohoku University, Japan), Apr. 2006–Mar. 2008.

Shanfeng Zhu (Currently, Professor, Fudan University, P. R. China), May 2004–May 2008.

Raymond Wan (Currently, Research Associate, University of Manchester, United Kingdom), Apr. 2004–Mar. 2009

Nicolas Majeux, Apr. 2003–Jan. 2004

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

PhD Thesis Adviser

Duc Anh Nguyen, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan, Oct. 2018–Mar. 2023.

Dai Hai Nguyen, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan, Oct. 2017–Sep. 2020.

Sohiya Yotsukura, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan, Oct. 2013–Sep. 2016.

Ahmed Mohamed Fathi Youssef Mohamed, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan, Apr. 2012–Mar. 2016.

David duVerle, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan, Apr. 2009–Mar. 2012.

PhD Thesis (External) Examiner/ Opponent

Ata Kircali Sezin, School of Computer Science and Engineering, Nanyang Technological University, Singapore, Aug.-Oct. 2019.

Bernard Lee Kok Bang, Institute of Mathematical Sciences, University of Malaya, Malaysia, Aug.–Sep. 2019.

Ong Huey Fang, Faculty of School of Graduate Studies, University Putra Malaysia, Malaysia. Jan.–Mar. 2019.

Weijia Zhang, School of Information Technology and Mathematical Sciences, University of South Australia, Adelaide, Australia, May–Jul. 2018.

Asif Khan, National University of Computer and Emerging Sciences, Islamabad, Pakistan, Feb.–Mar. 2018.

Aly Mohamed Alaafldin Aly Ezzat, Nanyang Technological University, Singapore, Oct. 2017.

Catherine Chang Ching Han, School of Engineering, Monash University, Malaysia, Aug.–Nov. 2016.

Ali Faisal, Department of Information and Computer Science, School of Science, Aalto University, Finland, Aug. 2014.

Koh Chuan Hock, Graduate School for Integrative Sciences and Engineering, National University of Singapore, Jan. 2013.

Ulavappa B. Angadi, Faculty of Science and Humanities, Kalasalingam University, India, Jun. 2011.

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

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

PhD Internship Supervisor

Kinga Gecse, Department of Pharmacodynamics, Semmelweis University, Hungary, Aug.–Oct. 2022.

Yufei Li, Department of Computer Science and Technology, Xi'an Jiaotong University, P. R. China, Apr. 2022 – Mar. 2023.

Antti Kangasräsiö, Department of Computer Science, Aalto University, Finland, Oct.–Dec. 2015.

Ian Johnston, School of Mathematics and Statistics, Boston University, USA, May–Aug. 2012, Jun–Aug. 2013.

Limin Li, Department of Mathematics, University of Hong Kong, Hong Kong SAR, Jun.–Sep. 2007.

Masters Thesis/ Internship Adviser

Abdul-Rashid III Sampaco, *Short internship adviser*, Institute of Chemistry, University of the Philippines, Diliman, Jun.–Jul. 2019.

Morgane Nadal, *Internship adviser*, École Normale Supérieure (ÉNS), France, Jun.–Aug. 2019.

Momoko Ishii, *Short internship adviser*, School of Public Health, Yale University, USA, Mar. 2019.

Beatriz Neves Mano, *Adviser*, Department of Computer Science, Aalto University, Finland, Jan. 2016–Nov. 2018.

Sinan Kaplan, *Summer internship adviser*, Leppera University of Technology, Finland, Jun.–Aug. 2015.

Xiaodong Zheng, *Internship adviser*, School of Computer Science, Fudan University, P. R. China, Apr.–Jul. 2012.

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

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

Visitors Adviser

- Avleen Kaur Malhi (Senior Lecturer, Bournemouth University, UK), May–Aug. 2022.
- Björn Goldenbogen (Postdoctoral Fellow, Humboldt University Berlin, Germany), Apr.–May 2022.
- Tong Gao (Undergraduate Student, University of Toronto, Canada), Jul.–Aug. 2015.
- Hiromi Baba (Researcher, Maruho Co., Ltd., Japan), Apr. 2014–Sep. 2014.
- Ia Kusradze (Research Associate, G. Eliava Institute of Bacteriophages, Georgia), Apr.–Jul. 2013.
- Hanaa Hibishy (Lecturer, Department of Biochemistry, Faculty of Pharmacy, Tanta University, Egypt), Feb.–Aug. 2013.
- Shanfeng Zhu (Associate Professor, Fudan University, P. R. China), Mar.–Aug. 2012
- Fang Wang (Associate Professor, Southwest University, P. R. China), Sep. 2011–Mar. 2012
- Nicolas Wicker (Assistant Professor, University of Strasbourg, France), Feb.–Mar. 2010
- Vo Ngoc Anh (Research Fellow, University of Melbourne, Australia), Jun.–Jul. 2008
- Kei-ichiro Takahashi (Senior Researcher, Olympus Corporation, Japan), Apr. 2008–Sep. 2009
- Nikolaos Angelopoulos (Postdoctoral Fellow, University of Edinburgh, UK), Oct. 2006
- Takashi Yoneya (Senior Scientist, Kirin Brewery Co., Ltd., Japan), Oct. 2005–Sep. 2006

Courses Taught

- Graduate School of Global Environmental Studies, Kyoto University, Japan (2012, 2014, 2017)
Clustering over Gene Networks (2012), *Mining from Metabolic Networks* (2014, 2017)
- Faculty of Medicine, Niigata University, Japan (2010–2012)
Systems Biology
- Kyoto Sustainability Initiative (KSI), The Integrated Research System for Sustainability Science (IR3S), Japan (2009)
Biological Sequence Alignment
- Graduate School of Pharmaceutical Sciences, Kyoto University (2003–2023)
Introduction to Bioinformatics, Advanced Bioinformatics, Information Sciences, Information Sciences for Drug Discovery
- 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