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Education

B.S. Molecular Biology, University of Washington, 1989.
M.S. Biophysics, Kyōto University, 1992.
Ph.D. Computer Science, UC Berkeley, 1997.

Academic Positions

Prime Senior Researcher, AIST, 2015–present
Research Team Leader, Computational Biology Research Center, 2003–2014
Visiting Associate Professor, The University of Tokyo, 2008–present
Staff Scientist, Real World Computing Partnership, 1998–2000

Selected Publications

Journal Articles

MitoFates: improved prediction of mitochondrial targeting sequences and their cleavage sites, Fukasawa et al., Mol Cel Proteomics, 14(4):1113–26, 2014.

Mammalian NUMT insertion is non-random, Junko Tsuji, Martin C. Frith, Kentaro Tomii & Paul Horton, Nucleic Acids Research, doi:10.1093/nar/gks424, 2012.

Prediction of leucine-rich nuclear export signal containing proteins with NESsential, Nucleic Acids Research, doi:10.1093/nar/gkr493, 2011.

Incorporating sequence quality data into alignment improves DNA read mapping, Martin C. Frith, Raymond Wan & Paul Horton, Nucleic Acids Research, 38(7):e100, 2010.

(Correspondence) Mitochondrial β-Barrel Proteins, an Exclusive Club?, Kenichiro Imai, M. Michael Gromiha & Paul Horton, Cell, 135(7):1158–9, 2008.

An Upper Bound on the Hardness of Exact Matrix Based Motif Discovery, Paul Horton & Wataru Fujibuchi, Journal of Discrete Algorithms, 5(4):706–13, 2007.

WoLF PSORT: Protein Localization Predictor, Paul Horton, Keun-Joon Park, Takeshi Obayashi, Naoya Fujita, Hajime Harada, C.J. Adams-Collier, & Kenta Nakai, Nucleic Acids Research, Web Server Issue, 2007.

PSORT: a Program for Detecting Sorting Signals in Proteins and Predicting their Subcellular Localization, Kenta Nakai & Paul Horton, Trends in Biochemical Sciences, 24(1):34-5, 1999.
Better Prediction of Protein Cellular Localization Sites with the $k$ Nearest Neighbors Classifier, Paul Horton & Kenta Nakai, Proceedings of Intelligent Systems in Molecular Biology (ISMB-97), pp. 368–383, Halkidiki, Greece 1997.

A Probabilistic Classification System for Predicting the Cellular Localization Sites of Proteins, Paul Horton & Kenta Nakai, Proceedings of Intelligent Systems in Molecular Biology (ISMB-96), pp. 368–383, St. Louis, USA, 1996.

An Assessment of Neural Network and Statistical Approaches for Prediction of E.coli Promoter Sites, Paul Horton & Minoru Kanehisa, Nucleic Acid Research, 20(16):4331–8, 1992.

Research Interest and Accomplishments

Protein Subcellular Localization

I collaborated with Kenta Nakai to develop the popular prediction program PSORT II [ISMB-97] and with him and others to develop WoLF PSORT [NAR 07]. Afterwards I collaborated with Kenichiro Imai to suggest a new hypothesis about the paucity of mitochondrial outer membrane protein families [Cell 08, BMC Genom. 11]. I think this work represents a good example of how computational biologists can contribute to biology by applying recent wet-lab discoveries to global analyses. Sometimes I do practical work.

Motif Discovery Algorithms

Motif discovery with a Markov-model representation (PWM) is almost exclusively done with heuristic algorithms such as Gibbs Sampling and Expectation Minimization. I was perhaps foolhardy to try to develop exact algorithms for this problem, but I did make fair progress. In a series of papers [PSB-96, JCB 01, JDA 07] I developed exact algorithms which are surprisingly close to practical (although not really there yet), moreover in the final paper [JDA 07] I proved what I believe is the only non-trivial lower-bound known for the complexity of this problem. Sometimes I tackle hard theoretical problems.

Recent Research Interests

Recently I have become interested in medial applications of bioinformatics. In this context I have started working on more accurate algorithms for indel variant calling and hope to apply my experience in predicting protein subcellular localization signals to the help understand the role of mislocalized proteins in disease.

Teaching and Educating

I currently advise two graduate students through my position at the University of Tokyo.

Community Service

I serve on the board of directors of the ISCB. I have served on the board of the Japanese Society of Bioinformatics. I was conference chair of ISCB-Asia/SCCG 2012, GIW/InCoB 2015 and co-chair of GIW/ISCB-Asia 2014. I served on the steering committee for ISMB from 2012–2014.

Languages: Japanese near-native, Mandarin semi-fluent