

## Kevin Karplus

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### Education

Ph. D.	1983	Computer Science	Stanford University
M. S.	1976	Mathematics	Stanford University
B. S.	1974	Mathematics	Michigan State University

### Research Interests

Modeling proteins, RNA, and DNA using Markov models, hidden Markov models, stochastic context-free grammars, and other statistical techniques. Mixtures of Dirichlet distributions for estimating amino-acid frequencies. Protein structure prediction and remote homology detection. Multi-purpose high-speed hardware for biosequence analysis.

### Research Summary

In 1993 I switched my research focus from logic minimization to biosequence analysis. I have worked extensively with hidden Markov models and Dirichlet mixtures, and to a lesser extent with neural networks. In summer 1998 and summer 2000, I lead teams of researchers doing protein structure prediction for the CASP3 and CASP4 experiments. We did well in both.

Richard Hughey and I have built a high-speed single-board computer (Kestrel) that can accelerate the dynamic programming for sequence alignment and hidden Markov model training. I have been developing other algorithms for Kestrel that can be used in protein structure prediction. For this project (which we have named Kestrel) we have designed and fabricated full-custom CMOS chips in order to get 512 simple processors on a board.

### Selected Refereed Journal articles

- [1] Kevin Karplus, Rachel Karchin, Christian Barrett, Spencer Tu, Melissa Cline, Mark Diekhans, Leslie Grate, Jonathan Casper, and Richard Hughey. What is the value added by human intervention in protein structure prediction? *Proteins: Structure, Function, and Genetics*, 2001. submitted.
- [2] Chang Zhu, Kevin Karplus, Leslie Grate, and Philip Coffino. A homolog of mammalian antizyme is present in fission yeast *schizosaccharomyces pombe* but not detected in budding yeast *saccharomyces cerevisiae*. *Bioinformatics*, 16(5):478–481, 2000.
- [3] Kevin Karplus, Christian Barrett, Melissa Cline, Mark Diekhans, Leslie Grate, and Richard Hughey. Predicting protein structure using only sequence information. *Proteins: Structure, Function, and Genetics*, Supplement 3(1):121–125, 1999.

- [4] Kevin Karplus, Christian Barrett, and Melissa Cline. Getting the most out of hidden Markov models. In *ISMB99 tutorial*, Heidelberg, Germany, August 1999.
- [5] Kevin Karplus, Christian Barrett, and Richard Hughey. Hidden markov models for detecting remote protein homologies. *Bioinformatics*, 14(10):846–856, 1998.
- [6] J. Park, K. Karplus, C. Barrett, R. Hughey, D. Haussler, T. Hubbard, and C. Chothia. Sequence comparisons using multiple sequences detect twice as many remote homologues as pairwise methods. *Journal of Molecular Biology*, 284(4):1201–1210, 1998. [http://www.mrc-lmb.cam.ac.uk/genomes/jong/assess\\_paper/assess\\_paperNov.html](http://www.mrc-lmb.cam.ac.uk/genomes/jong/assess_paper/assess_paperNov.html).
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- [8] Christian Barrett, Richard Hughey, and Kevin Karplus. Scoring hidden Markov models. *CABIOS*, 13(2):191–199, 1997.
- [9] Kevin Karplus, Kimmen Sjölander, Christian Barrett, Melissa Cline, David Haussler, Richard Hughey, Liisa Holm, and Chris Sander. Predicting protein structure using hidden Markov models. *Proteins: Structure, Function, and Genetics*, Suppl. 1:134–139, 1997.
- [10] K. Sjölander, K. Karplus, M. P. Brown, R. Hughey, A. Krogh, I. S. Mian, and D. Haussler. Dirichlet mixtures: A method for improving detection of weak but significant protein sequence homology. *Computer Applications in the Biosciences*, 12(4):327–345, August 1996.
- [11] Philipp Bucher, Kevin Karplus, Nicolas Moeri, and Kay Hoffman. A flexible motif search technique based on generalized profiles. *Computers and Chemistry*, 20(1):3–24, January 1996.
- [12] Kevin Karplus. Regularizers for estimating distributions of amino acids from small samples. In *Proceedings, 3rd International Conference on Intelligent Systems for Molecular Biology*, pages 188–196, Cambridge, England, July 1995.
- [13] Søren Søe and Kevin Karplus. Logic minimization using two-column rectangle replacement. In *ACM IEEE 28<sup>th</sup> Design Automation Conference Proceedings*, pages 470–473, San Francisco, CA, 17–21 June 1991.
- [14] Kevin Karplus. Xmap: a technology mapper for table-lookup field-programmable gate arrays. In *ACM IEEE 28<sup>th</sup> Design Automation Conference Proceedings*, pages 240–243, San Francisco, CA, 17–21 June 1991.
- [15] Kevin Karplus and Habib Krit. A semi-systolic decoder for the PDSC-73 error-correcting code. *Discrete Applied Math*, 33(1–3):109–28, 7 Nov 1991.
- [16] Susan Hertz, Kevin Karplus, and Jim Kadin. The Delta rule development system for speech synthesis from text. *Proceedings of the IEEE*, 73(11):1589–1601, November 1985.
- [17] Kevin Karplus and Alex Strong. Digital synthesis of plucked-string and drum timbres. *Computer Music Journal*, 7(2):43–55, Summer 1983. Reprinted in *The Music Machine* edited by Curtis Roads.

## Patents

- [1] Kevin Karplus. A semi-systolic architecture for decoding error-correcting codes. United States Patent 5,157,671, 20 October 1992. Rights owned by Space Systems/Loral, application filed 29 May 1990.
- [2] Alexander R. Strong and Kevin Karplus. Wavetable-modification instrument and method for generating musical sound. United States Patent 4,649,783, 17 March 1987. Also Australian Patent 570,669, 3 March 1988 and Canadian Patent 1,215,869, 30 December 1986 and Japanese Patent 6-139341, 1996.