

Curriculum Vitæ

Name Michael Zuker

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Nationality USA (naturalized)
born 1 April 1949 (Montréal, Canada)

Education 1974: Massachusetts Institute of Technology, Ph.D Mathematics
Thesis title: “Speeds of Convergence of Random Probability Measures”
1970: McGill University, B.Sc. (1st class honours) Mathematics

Employment 9/2000–present: Professor of Mathematical Sciences
Rensselaer Polytechnic Institute (RPI)

12/26/2007 - 1/10/2008: Visiting Fellow
Faculty of Natural Sciences Distinguished Scientist Visitors Program
Ben Gurion University of the Negev, Be’er Sheva, Israel

9/2006 - 6/2007: Visiting Investigator
Howard Hughes Medical Institute (HHMI),
Janelia Farm Research Campus

1994–2000: Associate Professor of Biomedical Computing
Institute for Biomedical Computing
Washington University in St. Louis

1991–1992: Visiting scholar; Department of Mathematics
Stanford University

1974–1994: Research Officer, Biomathematics & Computational Biology
(1987–1994: Senior Research Officer)
Institute for Biological Sciences
National Research Council of Canada

Publications 86 (list appended)

Invited & Plenary Lectures 123 since 1984
(list appended)

Professional Activities and Associations

- March 2007: Founding member of the Hudson Valley RNA Club (HVRC)
- May 2005 – October 2008: Member, Scientific Advisory Board (SAB), CODA Genomics, Inc., Laguna Hills, CA
- June 2003: Participated in a meeting of the Canada Foundation for Innovation (CFI) to discuss future directions. Invited as a special guest by the Board of Directors.
- June 2002: Member of an NIH study section (National Heart, Lung, and Blood Institute) reviewing contract proposals for proteomics centers.
- January 2000: Member of an NIH site visit panel reviewing a structural biology computational Research Resource.
- November 1999: *Ad hoc* member of an NIGMS Training Grant study section (Took part in one site visit in October)
- December 1997: Member of a team that evaluated the scientific program of the Laboratory for Experimental and Computational Biology (LECB) at the National Cancer Institute.
- March 1996: *Ad hoc* member of the Molecular and Cellular Study Section (BBCA) of the NIH.
- July 1994–present: Associate member of the Evolutionary Biology Program of the Canadian Institute for Advanced Research (CIAR)
- June 1994: Member of a Medical Research Council site visit team that reviewed a structural biology initiative in Montréal, Québec involving the Université de Montréal, Mc Gill University, the Federal Biotechnology Research Institute and several local companies.
- December 1993: Traveled to England and Germany with a Medical Research Council (MRC) team to study Bioinformatics and to make recommendations on what should be done about Bioinformatics in Canada.
- June 1993: Participant in a retreat in Toronto to plan the future of the Canadian Genome Analysis and Technology (CGAT) Program. Member of a discussion group assembled to form recommendations for an informatics program.
- July 1990: Senior lecturer at the Leonardo Fibonacci Institute for Theoretical Computer Science, Trento, Italy. Course on *String Algorithmics and Molecular Sequence Analysis*.
- July 1990: Member of a special study section of the NIH reviewing grant proposals in the area of computational molecular biology.
- April 1989: Participant in an “Informal Discussion Meeting on Large-Scale Mapping and DNA Sequencing in Canada” in Toronto.
- 1995–1998: Editorial Board member, GENE-COMBIS
- 1987–1996: Editorial Board member, Computer Applications in the Biological Sciences
- 1984–1986: Editorial Board member, Bulletin of Mathematical Biology

Honors

- 1989–94: Fellow of the Evolutionary Biology program of the Canadian Institute for Advanced Research (CIAR)
- 1970–74: MIT Graduate Tuition Scholarships

- 1970: Woodrow Wilson Fellowship
- 1969: Prince of Wales Scholarship
- 1966–70: McGill University Scholarships
- 1966: Sun Life Scholarship

Current Research Interests

Dr. Zuker works on the development of algorithms to predict nucleic acid folding and hybridization by free energy minimization using empirically derived thermodynamic parameters. Modeling and algorithm development have been closely coupled with the derivation of “nearest neighbor” and related energy rules in the laboratories of D. H. Turner, (RNA parameters, Department of Chemistry, University of Rochester, Rochester, NY) and of J. SantaLucia (DNA parameters, Department of Chemistry, Wayne State University, Detroit, MI). More recently, a comprehensive set of energy parameters for both RNA and DNA have been made available by D. H. Mathews (U. Rochester).

Recent work focused on the computation of partition functions for systems containing two molecules in solution that can fold as well as hybridize with each other. Ensemble free energies, mole fractions of different monomer and dimer species and base pair probabilities are computed over a range of temperatures. These computations lead to the prediction of UV absorbance (optical density) and heat capacity (C_p) melting profiles that can be directly compared with experimental data. The resulting UNAFold software package combines these computations with energy minimization methods that replace the older and well-known `mfold` package for RNA and DNA secondary structure prediction.

Closely related to this work has been the development of an algorithm named “FASTH” that searches RNA or DNA sequence databases for optimal hybridization sites for nucleic acid query sequences. Unlike traditional search algorithms, such as BLASTN and FASTA, “FASTH” uses hybridization free energy as the primary criterion for selection.

Current projects include a new algorithm to compute biologically meaningful distances between RNA foldings on the same molecule, with applications to clustering a large number of foldings into a few distinct groups. Another project is investigating the relationship between the entropy of the Boltzmann distribution of RNA foldings and the ability to predict a reliable secondary structure for a group of homologous sequences.

Applications:

Dr. Zuker’s well-known RNA folding software has proved useful in computing a number of secondary structures that can experimentally tested for validity. Predicted foldings can be constrained by the incorporation of (experimentally determined) constraints. Such computations have been used to identify functionally important regions of single-stranded RNA viruses or conserved structures in 3’UTR regions of mRNAs that function as controls for the spacial and temporal expression of certain genes.

The database searching, hybridization and melting profile computations have important applications in biotechnology, where they can be used to design, for example, efficient gene specific probes, PCR primers or molecular beacons. Molecular beacons are used to identify SNPs (Single Nucleotide Polymorphisms) in DNA.

Dr. Zuker’s software is widely used around the world and is also available to the scientific community on a web server that is maintained by RPI and that runs on a computer cluster donated

by IBM Research.

Invited and Plenary Lectures

1. **May 1984:** “RNA folding prediction: The continued need for interaction between biologists and mathematicians.” DNA Sequence Analysis – Symposium on Some Mathematical Questions in Biology, Annual Meeting of the American Association for the Advancement of Science, New York City, NY
2. **May 1984:** “Folding single-stranded RNAs by computer.” Department of Microbiology, SUNY at Stony Brook, NY
3. **May 1984:** “Computer predictions of RNA secondary structures.” The Rockefeller University, New York City, NY
4. **June 1984:** “Computer analysis of DNA and amino acid sequences.” Canadian Society of Microbiologists – annual meeting, Queen’s University, Kingston, Ont.
5. **July 1984:** “Analysis of secondary structure in nucleic acids.” Gordon Research Conference on Theoretical Biology and Biomathematics, Colby-Sawyer College, NH
6. **August 1984:** “Computer Prediction of RNA Secondary Structure.” Symposium on Mathematics and Computers in Biomedical Applications, National Institutes of Health, Bethesda, MD
7. **September 1984:** “Predicting RNA secondary structure by computer analysis.” Département de Biologie Moléculaire, Université de Genève, Switzerland
8. **September 1984:** “Computer prediction of RNA secondary structure.” Istituto Internazionale di Genetica e Biofisica, Naples, Italy
9. **October 1984:** “Computer prediction of RNA secondary structure.” The Institute for Virology, University of Rome, Italy
10. **February 1985:** “Computer prediction of RNA secondary structure.” Département de Biochimie, Université de Montréal, Que.
11. **February 1985:** “Computer predictions of RNA secondary structure.” Lilly Research Laboratories, Indianapolis, IN
12. **June 1985:** “What can mathematics contribute to the analysis of molecular sequences?” Canadian Society of Theoretical Biology, Montréal, Que.
13. **July 1985:** “Computer prediction of RNA secondary structures.” Hayashibara Forum ’85, International Symposium on Computer Analysis for Life Science, Okayama, Japan
14. **July 1985:** “Computer prediction of RNA secondary structures.” Research Laboratory for Genetic Information, Kyushu University School of Medicine, Fukuoka, Japan
15. **November 1985:** “The Sensitivity of Eigenvalues Under Elementary Matrix Perturbations.” Operator Theory seminar, Department of Mathematics, University of Toronto, Ont.
16. **November 1985:** “Computer modeling in molecular biology.” Department of Biology, University of Ottawa, Ont.
17. **December 1985:** “Predictions of RNA secondary structure.” Biotechnology Research Institute, National Research Council, Montréal, Que.
18. **February 1986:** “RNA secondary structure prediction.” Departments of Molecular Biology and Department of Computer Science, Princeton University, NJ
19. **May 1986:** “A new strategy for finding suboptimal solutions using dynamic programming algorithms.” Special Session on Mathematics of Molecular Sequence Analysis, 827th Meeting of the American Mathematical Society, Johns Hopkins University, Baltimore, MD
20. **October 1986:** “A new algorithm for finding suboptimal solutions to problems in sequence alignment and RNA folding.” University of Wisconsin Biotechnology Center, Madison, WI
21. **January 1987:** “A strategy for finding suboptimal solutions using dynamic programming algorithms with applications to problems in molecular biology.” Department of Combinatorics and Optimisation, University of Waterloo, Ont.
22. **March 1987:** “Computer prediction of RNA secondary structure.” Department of Chemistry, University of Rochester, NY
23. **May 1987:** “Calculation of RNA secondary structures using the VAX and IBM-PC computer.” Computers in Biology - a Genetics Cluster workshop, University of Rochester, NY
24. **June 1987:** “Suboptimal solutions to problems of RNA secondary structure prediction, molecular sequence alignment, and 3-D comparisons of protein structure.” Symposium on the Computer Analysis of DNA/Protein Sequences, American Society of Biological Chemists 78th annual meeting, Philadelphia, PA
25. **September 1987:** “Approaches to protein structure.” CIAR annual meeting, White Point Beach Lodge, NS

26. **March 1988:** “Molecular Sequence Alignment.” Atlantic Research Laboratory, National Research Council, Halifax, NS
27. **March 1988:** “Alignment of Proteins in Three Dimensions.” Workshop on Algorithms for Molecular Genetics, Lister Hill National Center for Biomedical Communications of the National Library of Medicine, Bethesda, MD
28. **June 1988:** “An Overview of Molecular Biology Database Activities.” Third Chemical Congress of North America, Herman Skolnik Award Symposium, Toronto, Ont.
29. **July 1988:** “Computer Applications in Molecular Genetics: Database systems, mathematical algorithms and modeling.” Short Course on Molecular Genetics Applied to Animal Breeding and Production, University of Guelph, Ont.
30. **September 1988:** “Biomolecular Sequence Comparisons.” Informatics Seminar, Division of Informatics, NRC
31. **October 1988:** “Protein comparisons: sequence alignment versus structural superposition.” CIAR annual meeting, Ste. Marguerite St. , Que.
32. **October 1988:** “Computer Prediction of RNA Secondary Structure.” Bolt, Beranek and Newman Laboratories, Cambridge, MA
33. **December 1988:** “Computer Prediction of RNA Structure.” Departments of Genetics and Cell Biology, Biochemistry, Microbiology and the Institute of Human Genetics, University of Minnesota, St. Paul, MN
34. **April 1989:** “Protein Comparisons: Sequence Alignment versus Structural superposition.” AMOCO Technology Company, Biotechnology Division, Naperville, IL
35. **July 1989:** “Protein Comparisons: Sequence Alignment versus Structural superposition.” First Canadian Workshop on Bioinformatics, Ottawa, Ont.
36. **July 1989:** “Computer Applications in Molecular Genetics.” CIAR Evolution Group Meeting for Graduate Students, Université de Montréal, Que.
37. **September 1989:** “RNA Secondary Structure Computations: energy minimization versus phylogeny.” CIAR Annual Meeting, Dunsmuir Lodge, Victoria, BC
38. **October 1989:** “Molecular sequence and structure comparisons by alignment.” Département de Biologie Moléculaire, Université de Genève, Switzerland
39. **August 1990:** “Suboptimal Sequence Alignment in Molecular Biology: Alignment with Error Bars.” CIAR Annual Meeting, Chaffey’s Locks, Elgin, Ont.
40. **September 1990:** “Automatic Comparisons of Proteins in Three Dimensions.” Département de Biochimie, Université de Montréal, Que.
41. **October 1990:** “Computer Prediction of RNA secondary structure.” International Conference on “Catalytic RNA as an Anti-HIV Agent: Design and Delivery to Cells,” San Diego, CA
42. **January 1991:** “Sequence Comparison in Molecular Biology.” Department of Microbiology, University of Guelph, Ont.
43. **May 1991:** “Algorithms for Comparing Protein Sequences and Structures.” Department of Microbiology and Immunology, Department of Biochemistry, University of Western Ontario, London, Ont.
44. **May 1991:** “Algorithms for Comparing Protein Sequences and Structures.” Department of Microbiology, SUNY at Stony Brook, NY
45. **June 1991:** “Extracting Quantitative Information from Protein Sequences and Structures.” Conference on “Open Problems of Computational Biology”, Telluride, CO
46. **August 1991:** “Inferring Evolutionary Relationships for DNA and RNA Polymerases from Mitochondrial Plasmids.” CIAR Annual Meeting - Evolutionary Biology Program, Lac Délage, Que.
47. **November 1991:** “Computer Predictions of RNA Secondary Structures.” Joint Labs RNA Meeting, University of California, San Francisco, CA.
48. **November 1991:** “Algorithms for Comparing Protein Sequences and Structures.” Structural Biology Seminar, UC Berkeley, CA
49. **December 1991:** “Algorithms for Comparing Protein Sequences and Structures.” Department of Microbiology and Molecular Genetics, UC Los Angeles, CA
50. **February 1992:** “Prediction of RNA Secondary Structure.” Department of Pharmaceutical Chemistry, UC San Francisco, CA
51. **March 1992:** “Structural Analysis by Energy Dot Plot of a Large Messenger RNA.” Linus Pauling Institute, Palo Alto, CA
52. **March 1992:** “Structural Analysis by Energy Dot Plot of a Large Messenger RNA.” Biotechnology Center, University of Wisconsin, Madison, WI
53. **April 1992:** “Structural Analysis by Energy Dot Plot of a Large Messenger RNA.” Biology and Computer & Information Science Departments, Sinsheimer Labs, UC Santa Cruz, CA

54. **May 1992:** “Structural Analysis by Energy Dot Plot of a Large Messenger RNA.” Department of Pharmaceutical Chemistry, UC San Francisco, CA
55. **September 1992:** “RNA Secondary Structure Modeling” Conference on “Molecular Bioinformatics”, Schloss Dagstuhl, Wadern, Germany
56. **October 1992:** “Structural Analysis by Energy Dot Plot of a Large Messenger RNA.” Second Albany Conference on computational biology: “Patterns of Biological Organization”, Rensselaerville, NY
57. **October 1992:** “Structural Analysis by Energy Dot Plot of a Large Messenger RNA.” Symposium on “Sequence and Analysis of Nucleic Acids and Proteins” Department of Biochemistry (Medical School), University of Rochester, Rochester, NY
58. **November 1992:** “Structural Analysis by Energy Dot Plot of a Large Messenger RNA.” Mathematics and Molecular Biology III – “Computational Approaches to Nucleic Acid Structure and Function”, Santa Fe, NM
59. **November 1992:** “Structural Analysis by Energy Dot Plot of a Large Messenger RNA.” Department of Molecular and Cellular Biology, University of Colorado, Boulder, CO
60. **November 1992:** “RNA Folding Prediction” (lecture in a course on sequence analysis) Institute for Molecular Virology, Department of Animal Health and Biomedical Sciences, University of Wisconsin, Madison, WI
61. **March 1993:** “Reliability of RNA secondary structure prediction by energy minimization. Application to *rRNA* and coliphage *Q β* .” Affymetrix (subsidiary of Affymax Corp.) Santa Clara, CA
62. **May 1993:** “Reliability of RNA secondary structure prediction by energy minimization. Application to *rRNA* and coliphage *Q β* .” Keck Center for Computational Biology, Carnegie Mellon University, Pittsburgh, PA
63. **October 1993:** “Reliability of RNA secondary structure prediction. Application to *rRNA* and coliphage *Q β* .” CIAR Annual Meeting - Evolutionary Biology Program, Banff, Alberta
64. **November 4, 1994:** “Algorithms and Unsolved Problems in RNA Secondary Structure Prediction” Symposium on Combinatorial Structures in Molecular Biology, DIMACS, Rutgers University, New Brunswick, NJ
65. **November 30, 1994:** “Computing Optimally Compact Domains in Protein Structures.” Informatique et biologie moléculaire. Septièmes Entretiens du Centre Jacques Cartier, Lyons, France
66. **February 6, 1995:** “Reliable Predictions of RNA Secondary Structure: Applications to rRNA and *Q β* .” Department of Biochemistry, University of Missouri, Columbia, MO
67. **August 1995:** “Computing optimally compact domains in protein structures.” CIAR Annual Meeting - Evolutionary Biology Program, Val Morin, Québec
68. **September 30, 1995:** Untitled talk on the thermodynamic approach to RNA folding. Workshop on “Sequence Structure Relations in Biopolymers”, Santa Fe Institute, Santa Fe, NM
69. **August 30, 1996:** “WWW servers in computational biology/genomics.” CIAR Annual Meeting - Evolutionary Biology Program, Dunsmuir Lodge, Sidney, British Columbia
70. **September 24, 1996:** “Assigning confidence to RNA/DNA secondary structure predictions.” GMD - German National Research Center for Information Technology, Sankt Augustin, Germany
71. **September 26, 1996:** “Assigning confidence to RNA/DNA secondary structure predictions.” Bielefeld Workshop on RNA Structure Exploration, Universität Bielefeld, Germany
72. **January 10, 1997:** “Assigning confidence to RNA/DNA secondary structure predictions.” Biological Chemistry Seminar, Wayne State University, Detroit, MI
73. **June 28, 1997:** “Assigning relative confidence to different regions of predicted RNA secondary structures.” RNA Structure Symposium, University of California, Santa Cruz, CA
74. **January 22, 1998:** “RNA secondary structure helps to explain the biological phenotype of mutant coliphages.”, Department of Biochemistry, Case Western Reserve University, Cleveland, OH.
75. **April 3, 1998:** “Assigning Confidence to RNA Secondary Structure Predictions, with an application to explaining the biological phenotype of mutant coliphages.”, Department of Chemistry, Brown University, Providence, RI.
76. **July 28, 1998:** “Assigning Confidence to RNA Secondary Structure Predictions, with an application to explaining the biological phenotype of mutant coliphages.”, CIAR Annual Meeting - Evolutionary Biology Program, Mont Gabriel, Québec.
77. **October 5, 1998:** “Comparing RNA Secondary Structures using the Prokhorov Metric.”, Universität Bielefeld, Germany.
78. **October 10, 1998:** “The other folding problem: Algorithms and thermodynamics for nucleic acid secondary structure.”, GCG98 (German Conference on Bioinformatics), Köln, Germany.
79. **October 12 & 15, 1998:** “RNA secondary structure prediction.”, RNA Biochemistry and Biotechnology, NATO Advanced Study Institute, Poznań, Poland.
80. **November 12, 1998:** “RNA secondary structure prediction”, Institute for Marine Biosciences, National Research Council of Canada, Halifax, NS.

81. **December 9, 1998:** “The RNA folding web server; current state and future plans.”, Emerging Sources of RNA Information, NSF, Arlington, VA.
82. **April 29, 1999:** “RNA secondary structure prediction.” Genetics Seminar, Stanford University, Stanford, CA.
83. **May 19, 1999:** “Assigning Confidence to RNA Secondary Structure Predictions, with an application to explaining the biological phenotype of mutant coliphages.”, Department of Biology, University of Calgary, Calgary, AB.
84. **October 8, 1999:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Predictions”, North Carolina State University, Raleigh, NC.
85. **October 23, 1999:** “Analyzing the Frequencies of Structural Motifs in RNA.”, CIAR Annual Meeting - Evolutionary Biology Program, Banff, AB.
86. **November 29, 1999:** “Assigning Confidence to RNA Secondary Structure Predictions, with an Application to Explaining the Biological Phenotype of Mutant Coliphages.”, Wadsworth Center, Albany, NY.
87. **November 30, 1999:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Prediction”, Rensselaer Polytechnic Institute (RPI), Troy, NY.
88. **November 30, 1999:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Prediction”, Rensselaer Polytechnic Institute (RPI), Troy, NY.
89. **March 15, 2000:** “Algorithms and Confidence in Nucleic Acid Secondary Structure Prediction”, Amgen, Thousand Oaks, CA.
90. **June 19, 2000:** (invited speaker) “Statistical analysis of base pair stacking frequencies in RNA secondary structures.”, Gordon Research Conference, Newport, RI
91. **October 2, 2001:** Chemistry Department, Syracuse University, NY.
92. **October 13, 2001:** “Statistically derived base pair stacking free energies for RNA folding”, 15th Annual CIAR Evolutionary Biology Program meeting, Val-David, Québec.
93. **February 1, 2002:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Prediction”, Williams College, MA.
94. **March 11, 2002:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Prediction”, Nanogen, San Diego, CA.
95. **May 21, 2002:** Pels seminar - “Statistically Derived Base Pair Stacking Free Energies for RNA Folding”, The Rockefeller University, NY, NY.
96. **September 20, 2002:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Prediction.”, Courant Institute of Mathematical Sciences, NY, New York, NY.
97. **October 15, 2002:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Prediction.”, University of Vermont, Burlington, VT.
98. **December 30, 2002:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Prediction.”, Weizmann Institute of Science, Rehovot, Israel
99. **January 2, 2003:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Prediction.”, Hebrew University Medical School, Jerusalem, Israel
100. **January 8, 2003:** “Algorithms and Statistics for Nucleic Acid Secondary Structure Prediction.”, University of Haifa, Israel
101. **January 9, 2003:** “Energy Minimization and Partition Function Computations for Nucleic Acid Secondary Structures.”, Technion, Haifa, Israel
102. **July 31, 2003:** “Algorithms for RNA folding and partition function computation”, invited lecture at the “Regulatory and functional RNAs: computational, genomic, and structural approaches” meeting in Benasque, Spain.
103. **December 16, 2003:** “Predicting nucleic acid hybridization and melting profiles.”, Keynote invited speaker at the 14th International Conference on Genome Informatics (GIW 2003), Yokohama, Japan,
104. **December 18, 2003:** “Predicting nucleic acid hybridization and melting profiles.”, Tokyo University, Japan.
105. **December 19, 2003:** “Predicting nucleic acid hybridization and melting profiles.”, Keio University, Yokohama, Japan
106. **January 2, 2004:** “Predicting nucleic acid hybridization and melting profiles.”, Jawaharlal Nehru University, New Delhi, India.
107. **January 7, 2004:** “Predicting nucleic acid hybridization and melting profiles.”, invited speaker at the NCBS Symposium on Molecules, Machines and Networks; National Centre of Biological Sciences, Bangalore, India
108. **March 24, 2004:** “Predicting nucleic acid hybridization and melting profiles.”, L. H. Baker Center for Bioinformatics and Biological Statistics, Iowa State University, Ames, IA
109. **May 14, 2004:** “Quick and dirty database searching for nucleic acid hybridization targets and intricate methods for melting profile prediction.”, Cleveland Clinic Foundation, Cleveland, OH

110. **June 3, 2004:** “Predicting nucleic acid hybridization and melting profiles.”, Bioinformatics 2004 (annual meeting of SocBIN, Society for Bioinformatics in the Nordic Countries), Linköping, Sweden
111. **June 21, 2004:** “Predicting nucleic acid hybridization and melting profiles.”, Keynote presentation, Profiling PCR and Beyond “In Celebration of Twenty Years of PCR”, Cambridge Healthtech Institute’s 12th Annual NUCLEIC ACID-BASED TECHNOLOGIES meeting, McLean, VA
112. **September 14(?), 2004:** “New computational methods for predicting nucleic acid hybridization.”, opening session of the Ribo-Club, a Quebec RNA research consortium based at the University of Sherbrooke, QC.
113. **October 16, 2004:** “FASTH: Searching nucleic acid sequences databases with nucleic acid sequence queries.”, 18th Annual CIAR Evolutionary Biology Program meeting, Carling Lake Resort, North Brownsburg, Québec.
114. **October 22, 2004:** “FASTH: Searching nucleic acid sequences databases with nucleic acid sequence queries.”, RNA retreat at SUNY Albany, organized by Marlene Belfort at Wadsworth.
115. **April 3, 2006:** Invited bioinformatics lecture, “Predicting nucleic acid hybridization and melting profiles”, Massachusetts Institute of Technology, Cambridge, MA.
116. **April 4, 2006:** Invited bioinformatics lecture at Boston College, “Computational Methods for RNA Secondary Structure”
117. **November 3, 2006:** visiting scientist lecture: HHMI, Janelia Farm Research Campus, “Computational Methods for RNA Secondary Structure”
118. **January 9, 2007:** “Predicting nucleic acid hybridization and melting profiles”, University of Rochester Medical School, Rochester, NY.
119. **June 28, 2007:** Visiting investigator lecture: “Structural RNAs from a mathematicians perspective: The good, the bad and the ugly.”
120. **October 17, 2007:** “Structural RNAs from a mathematicians perspective: The good, the bad and the ugly.”, Hudson Valley RNA Club (HVRC) monthly seminar, Bruggeman Conference Center, RPI
121. **October 29 – November 2, 2007:** Invited participant, workshop on “RNA in Biology, Bioengineering and Nanotechnology”, Institute for Mathematics and its Applications (IMA), University of Minnesota; first speaker: “Computational Methods for RNA Secondary Structure”
122. **November 8, 2007:** “Computational Methods for RNA Secondary Structure”, Union College, Schenectady, NY
123. **January 1, 2008:** Distinguished visiting scientist lecture: “Computational methods for RNA secondary structure”, Ben Gurion University of the Negev, Be’er Sheva, Israel

Publications

1. S. M. Tanny & M. Zuker. On a Unimodal Sequence of Binomial Coefficients. *Discrete Mathematics* **9**, 79–89, 1974.
2. S. M. Tanny & M. Zuker. On a Unimodal Sequence of Binomial Coefficients II. *J. Combinat. Info. & Sys. Sci.* **1**, 81–91, 1976.
3. G. E. Willick & M. Zuker. Equivalency of Linear Least Squares Curve Fitting and Reciprocal Functions in Protein Circular Dichroic Spectra Analysis. *Biophys. Chem.* **7**, 223–227, 1977.
4. N. T. Gridgeman & M. Zuker. Mercator, the Antigudermannian, and a Fluke. *The Canadian Cartographer* **15**, 50–57, 1978.
5. S. M. Tanny & M. Zuker. Analytic Methods Applied to a Sequence of Binomial Coefficients. *Discrete Mathematics* **24**, 299–310, 1978.
6. G. B. Calleja, B. F. Johnson, M. Zuker & A. P. James. The Mating System of a Homothallic Fission Yeast. *Molec. Gen. Genet.* **172**, 1–6, 1979.
7. G. B. Calleja, M. Zuker & B. F. Johnson. Estimation of meiosis and sporulation efficiencies in the fission yeast by ascus analysis. *Genet. Res. Camb.* **33**, 109–119, 1979.
8. M. Zuker, J. M. Ridgeway & D. R. Miller. A Study of Atmospheric Radionuclide Transport and Exposure Using Trajectory Analysis. (IAEA-SM-237/26) Biological Implications of Radionuclides Released from Nuclear Industries. Vienna, Vol. II, 381–398, 1979.
9. M. Yaguchi, A. T. Matheson, L. P. Visentin & M. Zuker. Molecular Evolution of the Alanine-Rich Acidic Ribosomal A Protein. In *Genetics and Evolution of RNA Polymerase, tRNA and Ribosomes*, S. Osawa, H. Ozeki, H. Uchida and T. Yura eds. University of Tokyo Press, 585–599, 1980.
10. A. B. Cairnie, L. F. Prud’homme-Lalonde, R. K. Harding & M. Zuker. The measurement of rectal and testis temperature in conscious mice, with observations on the effect of direct heating. *Physics in Medicine and Biology* **25**, 317–322, 1980.
11. M. Zuker, G. Mihailov & M. Romanowski. Systematic Search for Orthogonal Systems in the Calibrations of Submultiples and Multiples of the Unit of Mass. *Metrologia* **16**, 51–54, 1980.

12. D. Rose, C. M. Pearson, M. Zuker & J. R. Roberts. Ethylenethiorea: Criteria for the Assessment of its Effects on Man. Associate Committee on Scientific Criteria for Environmental Quality ISSN 0316-0114 NRCC No. 18469, 1980.
13. G. B. Calleja, M. Zuker, B. F. Johnson & B. Y. Yoo. Analysis of Fission Scars as Permanent Records of Cell Division in *Schizosaccharomyces pombe*. *J. Theoretical Biology* **84**, 523–544, 1980.
14. R. Watson, M. Zuker, S. M. Martin & L. P. Visentin. A New Site-specific Endonuclease from *Neisseria cinerea*. *FEBS Letters* **118**, 47–50, 1980.
15. P. Stiegler, P. Carbon, M. Zuker, J-P. Ebel & C. Ehresmann. Structure secondaire et topographie du RNA ribosomique 16S d'*Escherichia coli*. *C. R. Acad. Sc. Paris*, t. **291**, Serie D 937–940, 1980.
16. M. Zuker & P. Stiegler. Optimal computer folding of large RNA sequences using thermodynamics and auxiliary information. *Nucleic Acids Res.* **9**, 133–148, 1981.
17. P. Stiegler, P. Carbon, M. Zuker, J-P. Ebel & C. Ehresmann. Structural organization of the 16S ribosomal RNA from *E. coli*. Topography and secondary structure. *Nucleic Acids Res.* **9**, 2153–2172, 1981.
18. G. B. Calleja, M. Zuker & B. F. Johnson. Temporal Asymmetry of Sex Interconversion in a Strain of the Homothallic Fission Yeast *Schizosaccharomyces pombe*. *Current Microbiology* **6**, 225–227, 1981.
19. M. Yaguchi, L. P. Visentin, M. Zuker, A. T. Matheson, C. Roy & A. R. Strom. Amino-Terminal Sequences of Ribosomal Proteins from the 30S Subunit of Archaeobacterium *Halobacterium cutirubrum*. *Zentralblatt für Bakteriologie*, I. Abt. Orig. C3, 200–208, 1982.
20. B. F. Johnson, G. B. Calleja, B. Y. Yoo, M. Zuker & I. J. McDonald. Cell Division: Key to Cellular Morphogenesis in the Fission Yeast, *Schizosaccharomyces*. In *International Review of Cytology*, G. H. Bourne and J. F. Danielli eds. , Volume 75, Academic Press, 1982.
21. D. O. Foster, F. Depocas & M. Zuker. Heterogeneity of the sympathetic innervation of rat interscapular brown adipose tissue via intercostal nerves. *Can. J. Physiology and Pharmacology* **60**, 747–754, 1982.
22. J-L. Darlix, M. Zuker & P-F. Spahr. Structure-function relationship of Rous sarcoma virus leader RNA. *Nucleic Acids Res.* **10**, 5183–5196, 1982.
23. N. C. Fournier, M. Zuker, R. E. Williams & I. C. P. Smith. Self-Association of the Cardiac Fatty Acid Binding Protein. Influence on Membrane-Bound, Fatty Acid Dependent Enzymes. *Biochemistry* **22**, 1863–1872, 1983.
24. T. R. Cech, N. K. Tanner, I. Tinoco Jr. , B. R. Weir, M. Zuker & P. S. Perlman. Secondary structure of the *Tetrahymena* ribosomal RNA intervening sequence : Structural homology with fungal mitochondrial intervening sequences. *Proc. Natl. Acad. Sci. USA* **80**, 3903–3907, 1983.
25. S. M. Tanny & M. Zuker. Signs of Terms in a Combinatorial Recursion. *Siam J. Alg. Disc. Meth.* **4**, 437–441, 1983.
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