

## Gary Benson Curriculum Vitae

Associate Professor  
Department of Computer Science  
Department of Biology  
Program in Bioinformatics

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### Education

- 1992-1994 Postdoctoral Fellow in Mathematical and Computational Biology  
Advisor: **Dr. Michael S. Waterman**, Department of Mathematics  
University of Southern California, Los Angeles, California
- 1989-1992 **Ph.D., Computer Science**  
Thesis title: "Two Dimensional Periodicity and Matching Algorithms"  
Advisor: **Dr. Amihood Amir**, Department of Computer Science  
University of Maryland, College Park, Maryland
- 1987-1989 **M.S., Computer Science**  
Advisor: **Dr. William Gasarch**, Department of Computer Science  
University of Maryland, College Park, Maryland
- 1978-1979 Science/Math Teacher Certification, University of Illinois at Chicago
- 1977-1978 Graduate School in Neuroscience, Northwestern University, Evanston, Illinois
- 1974-1976 **B.S., Psychology**, University of Maryland, College Park, Maryland
- 1972-1974 Massachusetts Institute of Technology, Cambridge, Massachusetts

### Professional Experience

- 2003- Associate Professor, Department of Computer Science, Department of Biology  
Boston University, Boston, Massachusetts
- 1994-2003 Associate Professor, Assistant Professor, Department of Biomathematical Sciences,  
Department of Human Genetics  
The Mount Sinai School of Medicine, New York, New York
- 1993 Instructor, Departments of Computer Science and Mathematics  
University of Southern California, Los Angeles, California
- 1987-1992 Research Assistant, Summer Instructor, Teaching Assistant  
Department of Computer Science  
University of Maryland, College Park, Maryland

1979-1986 Mathematics and Computer Science High School Teacher  
St. Mary's County (Maryland) Public Schools

1977-1978 Research Assistant, Neuroscience Laboratory  
Northwestern University, Evanston, Illinois

## Awards and Fellowships

2009 Ben-Gurion University of the Negev  
Faculty of Natural Sciences Distinguished Scientist Visitors Program  
Fellowship for collaborative research at:  
Department of Computer Science

2006 University of Montpellier  
"Analysis of Complex Repetitive Features in DNA"  
Fellowship for Collaborative research at:  
Laboratory of Computer Science, Robotics, and Microelectronics  
of Montpellier (LIRMM)

1997 German Academic Exchange Service – DAAD  
"Tandem Repeats and Other Genomic Patterns:  
Detection, Phylogenetic Analysis and Related Problems"  
Fellowship for collaborative research at:  
Department of Computer Science, the Ludwigs Maximilian University, Munich  
Department of Theoretical Bioinformatics, German Cancer Research Center, Heidelberg

## Edited Publications

"Web Server Issue," *Nucleic Acids Research*, Volumes 35–41, July 2007–2013. **G. Benson**, Executive Editor.

"8th Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2008)," Ernst-walter Knapp, **Gary Benson**, Herman-Georg Holzhutter, Minoru Kanehisa, and Satoru Miyano, eds., *Genome Informatics*, vol. 20, Imperial College Press, 2008

"Algorithms in Bioinformatics: Third International Workshop WABI 2003, Proc.," **G. Benson** and R. Page, eds., *Lecture Notes in Bioinformatics*, No. 2812, Springer-Verlag, 2003.

## Journal Publications

"GlycReSoft: A Software Package for Automated Recognition of Glycans from LC/MS Data," E. Maxwell, Y. Tan, Y. Tan, H. Hu, **G. Benson**, K. Aizikov, S. Conley, G. Staples, G. Slys, R. Smith, J. Zaia, *PLoS One*, 7(9):e45474, 2012. (doi: [10.1371/journal.pone.0045474](https://doi.org/10.1371/journal.pone.0045474)).

"Mining Poly-regions in DNA," P. Papapetrou, **G. Benson**, G. Kollios, *International Journal of Data Mining and Bioinformatics*, 6(4):406-428, 2012.

"Whole Genome Sequences of a Male and Female Supercentenarian, ages greater than 114 years," P. Sebastiani, A. Riva, M. Montano, P. Pham, A. Torkamani, E. Scherba, **G. Benson**, J. Milton, C. Baldwin, S. Andersen, N. Schork, M Steinberg, and T. Perls, *Frontiers in Genetics of Aging*, 2:90, 2011. (doi:[10.3389/fgene.2011.00090](https://doi.org/10.3389/fgene.2011.00090)).

"Investigation of the population structure of *Legionella pneumophila* by analysis of tandem repeat copy number and internal sequence variation," P. Visca, S. D'Arezzo, F. Rammis, Y.

- Gelfand, **G. Benson**, G. Vergnaud, N. Fry, and C. Pourcel. *Microbiology*, 157:2582-94, 2011. (doi:[10.1099/mic.0.047258-0](https://doi.org/10.1099/mic.0.047258-0); PMID:[21622529](https://pubmed.ncbi.nlm.nih.gov/21622529/)).
- “Targeted analysis of glycomics liquid chromatography/mass spectrometry data,” J. Dreyfus, C. Jacobs, Y. Gindin, **G. Benson**, G. O. Staples and J. Zaia. *Analytical and Bioanalytical Chemistry*, 399(2):727-35, 2011 (doi:[10.1007/s00216-010-4235-1](https://doi.org/10.1007/s00216-010-4235-1); PMID:[20953780](https://pubmed.ncbi.nlm.nih.gov/20953780/)).
- “The distribution of inverted repeat sequences in the *Saccharomyces cerevisiae* genome,” E. M. Strawbridge, **G. Benson**, Y. Gelfand, and C. J. Benham. *Curr Genet.* 56(4):321-40, 2010 (doi:[10.1007/s00294-010-0302-6](https://doi.org/10.1007/s00294-010-0302-6); PMID:[20446088](https://pubmed.ncbi.nlm.nih.gov/20446088/)).
- “Mutations in the Hepatitis C Virus Core Gene Are Associated with Advanced Liver Disease and Hepatocellular Carcinoma,” S. Fishman, S. Factor, C. Balestrieri, X. Fan, A. DiBisceglie, S. Desai, **G. Benson**, and A. Branch, *Clinical Cancer Research*, 15:3205-3213, 2009 (doi:[10.1158/1078-0432.CCR-08-2418](https://doi.org/10.1158/1078-0432.CCR-08-2418); PMID:[19383824](https://pubmed.ncbi.nlm.nih.gov/19383824/)).
- “All Hits All The Time: Parameter Free Calculation of Spaced Seed Sensitivity,” D.Y.F. Mak and **G. Benson**, *Bioinformatics*, 25(3):302-308, 2009 (doi:[10.1093/bioinformatics/btn643](https://doi.org/10.1093/bioinformatics/btn643); PMID:[19095701](https://pubmed.ncbi.nlm.nih.gov/19095701/)).
- “Pattern matching with address errors: Rearrangement distances,” A. Amir, Y. Aumann, **G. Benson**, A. Levy, O. Lipsky, E. Porat, S. Skiena and U. Vishne, *J. Comput. Syst. Sci.*, 75(6): 359-370 (2009) (doi:[10.1016/j.jcss.2009.03.001](https://doi.org/10.1016/j.jcss.2009.03.001)).
- “3'-UTR SIRF: A Database for Identifying Clusters of Short Interspersed Repeats in 3' Untranslated Regions,” B. Kennedy, I. Lim, **G. Benson**, J. Vincent, M. Ferenc, B. Heinrich, L. Jarzylo, H.-Y. Man, and J. Deshler, *BMC Bioinformatics*, 8:274, 2007 (doi:[10.1186/1471-2105-8-274](https://doi.org/10.1186/1471-2105-8-274); PMID:[17663765](https://pubmed.ncbi.nlm.nih.gov/17663765/); PMCID:[PMC1973087](https://pubmed.ncbi.nlm.nih.gov/PMC1973087/)).
- “Evolutionary History of Mammalian Transposons Determined by Genome-wide Defragmentation,” J. Giordano, Y. Ge, Y. Gelfand, **G. Benson**, and P. Warburton, *PLOS Computational Biology*, 3(7):e137, 2007 (doi: [10.1371/journal.pcbi.0030137](https://doi.org/10.1371/journal.pcbi.0030137)).
- “Elevated Basal Slippage Mutation Rates among the Canidae,” J. Laidlaw, Y. Gelfand, K.-W. Ng, H. Garner, R. Ranganathan, **G. Benson**, and J. Fondon, III, *Journal of Heredity*, 98(5):452-460, 2007 (doi:[10.1093/jhered/esm017](https://doi.org/10.1093/jhered/esm017)).
- “TRDB: the tandem repeats database,” Y. Gelfand, A. Rodriguez, and **G. Benson**, *Nucleic Acids Research*, 35:D80-D87, 2007. (doi:[10.1093/nar/gkl1013](https://doi.org/10.1093/nar/gkl1013))
- “Oligonucleotide Fingerprint Identification for Microarray-Based Pathogen Diagnostic Assays,” W. Tembe, N. Zavaljevski, E. Bode, C. Chase, J. Geyer, L. Wasieloski, **G. Benson** and J. Reifman, *Bioinformatics*, 23(1):5-13, 2007.
- “Tandem Cyclic Alignment,” **G. Benson**, *Discrete Applied Mathematics*, 146:124-133, 2005.
- “Inverted Repeat Structure of the Human Genome: The X-Chromosome Contains a Preponderance of Large, Highly Homologous Inverted Repeats That Contain Testes Genes,” P. Warburton, J. Giordano, F. Cheung, Y. Gelfand and **G. Benson**. *Genome Research*, 14:1861-1869, 2004.
- “Minimal entropy probability paths between genome families,” C. Ahlbrandt, **G. Benson**, W. Casey, *Journal of Mathematical Biology*, 48(5):563-590, 2004.
- “Predicting Human Minisatellite Polymorphism,” F. Denoeud, G. Vergnaud, **G. Benson**, *Genome Research*, 13(5):856-67, 2003.
- “Replication and compartmentalization of HIV-1 in kidney epithelium of patients with HIV-associated nephropathy,” D. Marras, L. Bruggeman, F. Gao, N. Tanji, M. Mansukhani, A. Cara,

M. Ross, G. Gusella, **G. Benson**, V. D'Agati, B. Hahn, M. Klotman, and P. Klotman. *Nature Medicine*, 8(5):522 - 526, 2002.

“Mutation Master: Profiles of Substitutions in Hepatitis C Virus RNA of the Core, Alternate Reading Frame and NS2 Coding Regions,” J. Walewski, J. Gutierrez, W. Branch-Elliman, D. Stump, T. Keller, A. Rodriguez, **G. Benson**, and A. Branch. *RNA*, 8:557-571, 2002.

“A Tandem Repeats Database for Bacterial Genomes: Application to the Genotyping of *Yersinia pestis* and *Bacillus anthracis*,” P. Le Fleche, Y. Hauck, L. Onteniente, A. Prieur, F. Denoed, V. Ramiisse, P. Sylvestre, **G. Benson**, F. Ramiisse, G. Vergnaud, *BioMed Central Microbiology*, 1:2-15, (<http://www.biomedcentral.com/1471-2180/1/2>), 2001.

“Tandem Repeats Finder: A Program to Analyze DNA Sequences,” **G. Benson**, *Nucleic Acids Research*, 27:573-580, 1999.

“On the Distribution of  $k$ -tuple Matches for Sequence Homology: A Constant Time Exact Calculation of the Variance,” **G. Benson** and X. Su, *J. of Computational Biology*, 4:87-100, 1998.

“Two Dimensional Periodicity in Rectangular Arrays,” A. Amir and **G. Benson**, *SIAM Journal of Computing*, 27:90-106, 1998.

“Optimal Parallel Two Dimensional Text Searching on a CREW PRAM,” A. Amir, **G. Benson** and M. Farach, *Information and Computation*, 144:1-17, 1998.

Book Review of D. Gusfield, *Algorithms on Strings, Trees and Sequences: Computer Science and Computational Biology*, **G. Benson**, *Bull. of Mathematical Biology*, 60(3):598-602, 1998.

“Sequence Alignment with Tandem Duplication,” **G. Benson**, *Journal of Computational Biology*, 4:351-367, 1997.

“Pooling Strategies for Establishing Physical Genome Maps Using FISH,” F. Sun, **G. Benson**, N. Arnheim and M. Waterman, *J. of Computational Biology*, 4:467-486, 1997.

“Optimal Two-Dimensional Compressed Matching,” A. Amir, **G. Benson** and M. Farach, *Journal of Algorithms*, 24:354-379, 1997.

“Let Sleeping Files Lie: Pattern Matching in Z-compressed Files,” A. Amir, **G. Benson** and M. Farach, *Journal of Computer and Systems Sciences*, 52:299-307, 1996.

“A Space Efficient Algorithm for Finding Best Scoring Non-overlapping Alignments,” **G. Benson**, *Theoretical Computer Science*, 145:357-369, 1995.

“A Method for Fast Database Search for All  $k$ -Nucleotide Repeats,” **G. Benson** and M. Waterman, *Nucleic Acids Research*, 22:4828-4836, 1994.

“An Alphabet Independent Approach to Two Dimensional Matching,” A. Amir, **G. Benson** and M. Farach, *SIAM Journal of Computing*, 23:313-323, 1994.

## Conference Publications

“Longest Common Subsequence in  $K$  Length Substrings,” **G. Benson**, A. Levy, and B. R. Shalom, *6th International Conference on Similarity Search and Applications (CPM-2013)*, Coruña, Spain, October 2013.

“A Bit-Parallel, General Integer-Scoring Sequence Alignment Algorithm,” **G. Benson**, Y. Hernandez and J. Loving, *24th Annual Symposium on Combinatorial Pattern Matching (CPM-2013), Lecture Notes in Computer Science*, 7922:50-61, Bad Herrenalb, Germany, July 2013. (doi: [10.1007/978-3-642-38905-4\\_7](https://doi.org/10.1007/978-3-642-38905-4_7))

“VNTRseek – A Computational Pipeline to Detect Tandem Repeat Variants in Next-Generation

- Sequencing Data: Analysis of the 454 Watson Genome,” Y. Gelfand, J. Loving, Y. Hernandez and **G. Benson**, *Proceedings of the Third Annual RECOMB Satellite Workshop On Massively Parallel Sequencing (RECOMB-seq 2013)*, Beijing, China, April 2013.
- “Consensus RNA Secondary Structure Prediction by Ranking k-Length Stems,” **G. Benson** and D.Y.F. Mak, *Proceedings of the 2009 International Conference on Bioinformatics and Computational Biology (BIOCOMP’09)*, Las Vegas, Nevada, July 2009.
- “Exact Distribution of a Spaced Seed Statistic for DNA Homology Detection,” **G. Benson** and D.Y.F. Mak, *Proceedings of the 15th String Processing and Information Retrieval Symposium (SPIRE 2008)*, Melbourne, Australia, November 2008.
- “Exact Distribution of a Spaced Seed Statistic for Applications in DNA Repeat Detection,” **G. Benson** and D.Y.F. Mak, *Proceedings of the 2008 International Workshop on Applied Probability (IWAP 2008)*, Compiègne, France, July, 2008.
- “All Hits All the Time: Parameter Free Calculation of Seed Sensitivity,” D. Mak and **G. Benson**, *Proceedings of the Fifth Asia-Pacific Bioinformatics Conference (APBC 2007)*, Hong Kong, China, pp 327-340, January 2007. (10.1142/9781860947995\_0035).
- “Tandem Repeats over the Edit Distance,” D. Sokol, **G. Benson**, and J. Tojeira, *Proceedings of the 5th European Conference on Computational Biology (ECCB 2006)*, Eilat, Israel, *Bioinformatics* 23(2):e30-e35, 2007 (doi:10.1093/bioinformatics/btl309)
- “Discovering Frequent Poly-Regions in DNA Sequences,” P. Papapetrou, G. Kollios, and **G. Benson**, *Proceedings of the IEEE ICDM 2006 Workshop on Data Mining in Bioinformatics (DMB 2006)*, Hong Kong, China, pp 94-98, 2006. (doi.ieeecomputersociety.org/10.1109/ICDMW.2006.63)
- “Indel Seeds for Homology Search,” D. Mak, Y. Gelfand, and **G. Benson**, *Proceedings of the 14th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2006)*, Fortaleza, Brazil, *Bioinformatics* 22(14):e341-e349, 2006. (doi:10.1093/bioinformatics/btl263)
- “Pattern Matching with Address Errors: Rearrangement Distances,” A. Amir, Y. Aumann, **G. Benson**, A. Levy, O. Lipsky, E. Porat, S. Skiena, and U. Vishna, *Proceedings of the 17th Annual ACM-SIAM Symposium on Discrete Algorithms (SODA 2006)*, pp 1221-1226, 2006. (doi.acm.org/10.1145/1109557.1109692)
- “Evaluating distance functions for clustering tandem repeats,” S. Rao, A. Rodriguez, and **G. Benson**, *Proceedings of the 5th International Workshop on Bioinformatics and Systems Biology*, Berlin, August 2005.
- “Composition Alignment,” **G. Benson**, *Proceedings of the Third International Workshop on Algorithms in Bioinformatics (WABI 2003)*, *Lecture Notes in Bioinformatics*, 2812:447-461, September 2003.
- “A New Distance Measure for Comparing Sequence Profiles Based on Path Lengths Along an Entropy Surface,” **G. Benson**, *Proceedings of the European Conference on Computational Biology (ECCB 2002)*, Saarbrücken, Germany, October 2002.
- “Tandem Cyclic Alignment,” **G. Benson**, *Proceedings of the 12th Annual Symposium on Combinatorial Pattern Matching (CPM 2001)*, Jerusalem, July 2001.
- “Reconstructing the Duplication History of a Tandem Repeat,” **G. Benson** and L. Dong, *Proceedings of the Seventh International Conference on Intelligent Systems for Molecular Biology (ISMB-99)*, Heidelberg, Germany, August 1999.
- “An Algorithm for Finding Tandem Repeats of Unspecified Pattern Size,” **G. Benson**, *Proceedings*

of the Second Annual International Conference on Computational Molecular Biology (RECOMB '98), New York City, NY, March 1998.

- “Sequence Alignment with Tandem Duplication,” **G. Benson**, *Proceedings of the First Annual International Conference on Computational Molecular Biology (RECOMB '97)*, Santa Fe, New Mexico, January 1997.
- “Pooling Strategies for Establishing Physical Genome Maps Using FISH,” F. Sun, **G. Benson**, N. Arnhiem and M. Waterman, *Proceedings of the First Annual International Conference on Computational Molecular Biology (RECOMB '97)*, Santa Fe, New Mexico, Jan. 1997.
- “Finding Homologous Regions in a Set of Protein Sequences,” **G. Benson** and M. Waterman, *DI-MACS Special Year on Computational Biology, Workshop on Sequence Alignment*, Princeton, November 1994.
- “Optimal Two-Dimensional Compressed Matching,” A. Amir, **G. Benson** and M. Farach, *21st International Colloquium on Automata, Languages and Programming (ICALP '94)*, Jerusalem, July 1994.
- “A Method for Fast Database Search for All k-nucleotide Repeats,” **G. Benson** and M. Waterman, *IEEE Workshop on Shape and Pattern Matching in Computational Biology*, Seattle, June 1994.
- “A Space Efficient Algorithm for Finding Best Scoring Non-overlapping Alignments,” **G. Benson**, *Computational Pattern Matching '94 (CPM '94)*, Asilomar, California, May 1994.
- “Let Sleeping Files Lie: Pattern Matching in Z-compressed Files,” A. Amir, **G. Benson** and M. Farach, *Proceedings of the Fifth Annual ACM-SIAM Symposium on Discrete Algorithms (SODA '94)*, Washington, D.C., January 1994.
- “Optimal Parallel Two Dimensional Pattern Matching,” A. Amir, **G. Benson** and M. Farach, *Proceedings of the 5th Annual ACM Symposium on Parallel Algorithms and Architectures (SPAA '93)*, Velen, Germany, July 1993.
- “Alphabet Independent Two-Dimensional Matching,” A. Amir, **G. Benson** and M. Farach, *Proceedings of the Twenty-fourth Annual ACM Symposium on Theory of Computing (STOC '92)*, Victoria, British Columbia, May 1992.
- “Efficient Two-Dimensional Compressed Matching,” A. Amir and **G. Benson**, *Data Compression Conference (DCC '92)*, Snowbird, Utah, March 1992.
- “Two-Dimensional Periodicity and its Application,” A. Amir and **G. Benson**, *Proceedings of the Third Annual ACM-SIAM Symposium on Discrete Algorithms (SODA '92)*, Orlando, Florida, January 1992.
- “Two-Dimensional Periodicity in Rectangular Arrays,” A. Amir and **G. Benson**, *Combinatorial Pattern Matching (CPM '91)*, London, April 1991.
- “Recursive Edge Colorings of Recursive Graphs,” **G. Benson**, W. Gasarch and T. Grant, *Twenty-first Southeastern International Conference on Combinatorics, Graph Theory and Computing*, Boca Raton, Florida, February 1990.

## Invited Talks – Symposia

- “Detecting Tandem Repeat Variants in Next-Generation Sequencing Data,” Stringology 2011, Haifa University, Haifa, Israel, April 2011.
- “Innovative Training Methods in the Boston University Bioinformatics IGERT Program,”

National Institute of Biomedical Imaging and Bioengineering and the Howard Hughes Medical Institute 2009 Interdisciplinary Training Workshop, October 2009.  
18th Annual Growth Factor and Signal Transduction Symposium, Systems Biology: Integrative, Comparative, and Multi-Scale Modeling, Iowa State, June 2009.

“Calculating Properties of Spaced Seeds Using a Modified Aho-Corasick Tree,” Stringology 2009, Bar-Ilan University, Israel, March, 2009.

“Exploring Seed Design for Homology Search in DNA Sequences,” 2006 International Workshop on Applied Probability, University of Connecticut, May 2006.

“New Resources for Tandem Repeat Analysis,” Microsatellite Consortium Workshop, London, December 2005.

“Searching for Inverted Repeats in Genomic Sequences,” The Second Annual International Stringology Research Workshop, Haifa University, Haifa, Israel, April 2005.

“Composition Alignment and the Detection of Regions of Similar Composition in Nucleotide Sequences,” Stringology Expert Workshop, Haifa University, Haifa, Israel, May 2004.

“Cluster Analysis and the Development of a Multi-Genome Database of Tandem Repeats,” DIMACS Workshop on Integration of Diverse Biological Data, June 2001.

“Algorithms for Detection and Analysis of Tandem Repeats in DNA Sequences”  
University of Minnesota, Institute for Mathematics and its Applications, “Hot Topics” Workshop: Challenges and opportunities in genomics: production, storage, mining and use, April 1999.

“Heuristic Algorithms for Detecting Tandem Repeats”  
The University of Pennsylvania – DIMACS Conference on Computational Biology, Princeton, May 1996.

## Invited Talks

“Next Generation Sequencing: Technology, Mapping, and Analysis” and “Read Mapping Algorithms.”  
Four lectures given at the Bioinformatics and Comparative Genome Analyses course, Universite de la Reunion, Saint-Denis, Reunion Island, May 2013.

“Next Generation Sequencing: Technology, Mapping, and Analysis” and “Read Mapping Algorithms.”  
Four lectures given at the EMBO Practical Course: Bioinformatics and Comparative Genome Analysis, Stazione Zoologica Anton Dohrn, Naples, Italy, May 2012.

“Detecting Genetic Differences in Next-Generation Sequencing Data,”  
The Puerto Rico Alliance for the Advancement of Biomedical Research Excellence Seminar Tour (PR-AABRE)  
Universidad del Turabo, Puerto Rico  
Universidad de Puerto Rico, Cayey  
Universidad de Puerto Rico, Recinto de Rio Piedras  
February 2012.

“Detecting Tandem Repeat Variants in Next-Generation Sequencing Data,”  
Institute of Genetics and Microbiology Bioinformatics, Genomes and Evolution  
University Paris-Sud 11 Orsay, France, July 2011.  
Department of Computer Science, Ben Gurion University  
Be'er Sheva, Israel, April 2011.

“Next Generation Sequencing: Technology, Mapping, and Analysis” and “Methods for Repeat Detection in Nucleotide Sequences.” Four lectures given at the EMBO Practical Course:

Bioinformatics and Comparative Genome Analysis, Institut Pasteur, Paris, France, June 27 - July 9, 2011.

“Next Generation Sequencing: Read Mapping Algorithms” and “Methods for Repeat Detection in Nucleotide Sequences.” Two lectures given at the EMBO Global Exchange Lecture Course on Bioinformatics and Comparative Genome Analysis, Institut Pasteur Tunis, Tunisia, December 13 - 18, 2010

“Where and How to Get Published,” Panel discussion, Intelligent Systems for Molecular Biology (ISMB 2010), July 2010.

“Next Generation Sequencing: Technology, Mapping, and Analysis” and “Methods for Repeat Detection in Nucleotide Sequences.” Four lectures given at the Bioinformatics and Comparative Genome Analysis Course, Institut Pasteur, Paris, France, July 5 - July 17, 2010.

“Seeded Search Techniques for DNA Homology Detection and Mapping of Next Generation Sequencing Reads,” Department of Computer Science, Ben Gurion University, Be’er Sheva, Israel, October 2009.

“Copy number variation in the human genome based on analysis of whole genome SNP arrays,” Coriell Institute for Medical Research, September 2007.

“Seeds for Homology Search in DNA,”  
Tel Aviv University, Israel, January 2007.  
Bar Ilan University, Israel, January 2007.

“New Resources for Tandem Repeat and Inverted Repeat Analysis,”  
Delaware State University, HBCU-UP, September 2008.  
Clark University, March 2007.  
Dept. of Mol. and Cell Biology, School of Dental Med., Boston Univ., March 2006.  
Seminar Series, Dept of Mol. and Cellular Biology, Univ. of Arizona, May 2006.

“The Human Genome: What’s in it? How do We Know?” DIMACS 2006 High School Student Research Conference, April 2006

“Building DNA models with K’NEX,” DIMACS Bio-Math Connect Institute 2005, DIMACS, Rutgers University, July 2005.

“Biological Sequence Comparison, Mathematics of Homology Detection, Inverted Repeat Detection,” 5th International Summer School on Biocomplexity from System to Gene, Dartmouth University, June 2005

“Waiting Time and Seed Selection for Homology Search; Building DNA models with K’NEX,” DIMACS Conference on Linking Mathematics and Biology in the High Schools, DIMACS, Rutgers University, April 2005.

“Searching for Inverted Repeats in Genomic Sequences,”  
Bioinformatics Seminar, MIT Department of Mathematics, May 2004.

“Finding Similarity in Sequences,”  
Five lectures given at the International Summer School in Computational Biology, Warsaw, Poland, September 2003.

“New Resources for the Study of Tandem Repeats”  
INRIA-Lorraine/LORIA, Nancy, France, Oct. 2002  
LIRMM, Montpellier, France, Oct. 2002  
Biomolecular Seminar Series, Dept. of Biology, Boston University, Oct. 2002



- “Computational Tools for Biological Sequence Analysis”  
Department of Biomedical Engineering, Boston University, April 2002.
- “Cluster Analysis and the Development of a Multi-Genome Database of Tandem Repeats,”  
Mount Sinai School of Medicine, Dept. of Biomathematical Sciences, Seminar Series,  
October 2001.
- “Detection and Analysis of Repetitive Features in Nucleotide Sequences”  
University of Pennsylvania, Center for Bioinformatics, April 2001.  
Pasteur Institute, March 2001.  
Université of Paris-Sud, Institut de Génétique et Microbiologie, March 2001.  
Columbia University, On the Frontiers of Science: Leading Young Investigators and the  
National Science Foundation, December 2000.
- “Algorithms for Detection and Analysis of Tandem Repeats in DNA Sequences”  
Bronx Community College, Dept. of Computer Science, December 2000  
University of Michigan, Depts. of Mathematics and Biology, June 2000  
Iowa State University, Dept. of Computer Science, February 2000  
Virginia Polytechnic Institute, Dept. of Computer Science, January 2000  
NYU Courant Institute, Applied Math Seminar, December 1999
- “Similarity and Biological Sequences”  
National Mathematics Awareness Month – Mathematics and Biology, William Paterson  
University, Dept. of Mathematics, April 1999.
- “Tandem Repeats in the Yeast Genome”  
Mount Sinai School of Medicine, Dept. of Human Genetics Seminar Series, May, 1998.
- “Evolutionary History of Tandem Repeats”  
German Cancer Research Center-DFKZ, Group in Informatics, Heidelberg, Germany,  
October, 1997.
- “Detecting Sequence Homology with  $k$ -tuple Matches: Exploiting a Probabilistic Model of Mutational  
Divergence”  
The University of Pennsylvania, Program in Computational Biology, March 1997.  
Ludwig Maximillians University, Institute for Informatik, Munich, Germany, April 1997.  
German Cancer Research Center-DFKZ, Group in Informatics, Heidelberg, Germany,  
April 1997.  
Rockefeller University, Dept. of Biophysics, May 1997.
- “Detecting Patterns and Functional Sites: Computer analysis of DNA sequences”  
Mount Sinai School of Medicine, Dept. of Microbiology, Seminar Series, September 1996.
- “Approximation Algorithms for the Steiner Tree on a Hypercube with Application to Parsimonious  
Evolutionary Trees”  
University of Southern California, Dept. of Mathematics, Seminar on Mathematical  
Biology, March 1995.
- “Two New Programs for Finding Homologous Regions in DNA and Protein Sequences”  
Mount Sinai School of Medicine, Dept. of Biophysics Seminar Series, January 1995.
- “A Space Efficient Algorithm for Finding Best Scoring Non-overlapping Alignments”  
DIMACS Seminar Series on Mathematics and Computer Science in Molecular Biology,  
Rutgers University, September 1994.
- “Detecting Repeats in Genetic Sequences”  
Mount Sinai School of Medicine, Dept. of Biomathematical Sciences, November 1993.  
DIMACS, Rutgers University, November 1993.

University of Southern California, Dept. of Mathematics, Seminar on Mathematical Biology, September, 1993.

“Two-Dimensional Periodicity and Pattern Matching”

University of Southern California, Dept. of Computer Science, Computer Science Colloquium, April 1993.

University of Maryland Institute for Advanced Computer Studies, Seminar on Algorithms, December 1991.

“Linear-Time, Compressed Two-Dimensional Pattern Matching”

Metropolitan Atlanta Theory Seminar, Georgia Institute of Technology, College of Computing, March 1993.

“Approximating the Shortest Superstring”

University of Southern California, Dept. of Mathematics, Seminar on Mathematical Biology, October 1992.

## Teaching

### Invited Teaching

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| 2013 | Invited Lecturer, Bioinformatics and Comparative Genome Analyses course<br>Université de La Réunion, Saint-Denis, Réunion Island                                   |
| 2012 | Invited Lecturer, EMBO Practical Course: Bioinformatics and Comparative<br>Genome Analysis, Stazione Zoologica Anton Dohrn, Naples, Italy                          |
| 2011 | Invited Lecturer, EMBO Practical Course: Bioinformatics and Comparative<br>Genome Analysis, Institut Pasteur, Paris, France  |
| 2010 | Invited Lecturer, EMBO Global Exchange Lecture Course: Bioinformatics<br>and Comparative Genome Analysis, Institut Pasteur Tunis, Tunisia                          |
| 2010 | Invited Lecturer, Bioinformatics and Comparative Genome Analysis Course<br>Institut Pasteur, Paris, France   |
| 2005 | Invited Lecturer, 5th International Summer School on Biocomplexity:<br>From System to Gene, Dartmouth University   |
| 2003 | Lecturer, Third International Summer School on Computational Biology,<br>Warsaw University, Poland   |
| 1998 | Co-director, Lecturer, Villanova Summer Research Institute in Biology,<br>Computing and Mathematics for High School Teachers and Students,<br>Villanova University |

### Graduate (G) and Undergraduate (U) Courses

- Yeah, there's an app for that: Object oriented programming on the iPhone (U)
- Bioinformatics Challenge Project (G)
- Pattern Matching and Pattern Detection Algorithms with Applications in Biological Sequence  
Analysis (G,U)
- Design of Biological Databases (G)
- Computational Structural Biology (G)
- Advanced Topics in Computational Molecular Biology (G)
- Pattern Detection Techniques for Biological Sequences (G)
- DNA and Protein Sequence Analysis (G)
- Topics in Mathematical Modeling (G)
- Introduction to Design and Analysis of Algorithms (U)
- Computer Science I (Introduction) (U)
- Discrete Mathematics (U)