Gary Benson
Curriculum Vitae

January 2024

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

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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

2022	Expert Witness, Quinn Emanuel Urquhart & Sullivan, LLP Bioinformatics False Advertising Lawsuit
2019-2021	Expert Witness, Choate Hall & Stewart, LLP Bioinformatics Patent Dispute Lawsuits Expert reports, Deposition.
2019 (Jan–Jul)	Acting Director, Program in Bioinformatics, Boston University
2015-Present	Director of Graduate Studies, Program in Bioinformatics, Boston University
2003-Present	Associate Professor, Program in Bioinformatics, Department of Computer Science, Department of Biology, Boston University

1994-2003	Associate Professor, Assistant Professor, Department of Biomathematical Sciences, Department of Human Genetics, The Mount Sinai School of Medicine, 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

Grants

2023-2028	NIH 1T32GM150533-01 “Predoctoral Training in Bioinformatics and Computational Biology“ **Co-Principal Investigator**
2021-2022	NIH 3T32GM100842-08 Supplement, NIH T32 Institutional Training Grant “Collaborations to Improve the AI/ML-Readiness of NIH-Supported Data” **Senior (Lead) Personnel**
2020-2024	NSF BIO DBI-1949968 “REU Site: Bioinformatics Research and Interdisciplinary Training Experience in Analysis and Interpretation of Information-Rich Biological Data Sets (REU-BRITE)” **Principal Investigator**
2018-2022	NSF EHR DRL-1812982 “Integrating Computational Thinking in Mathematics and Science High School Teacher Professional Development” **Co-investigator**
2018	Boston University Hariri Institute Research Incubation Award #2017-10-001 “Tools for Detection of DNA Genomic Structural Variants and Application to the Analysis of Human Whole Genome Sequencing Datasets” **Principal Investigator**
2016-2019	NSF DBI-1559829 “REU Site: Bioinformatics Research and Interdisciplinary Training Experience in Analysis and Interpretation of Information-Rich Biological Data Sets (REU-BRITE)” **Principal Investigator**
2014-2019	NSF IIS-1423022 “III:Small:Bit-Parallel Algorithms for Sequence Alignment and Applications in Detecting Human Genetic Variation and Bacterial Strain Typing” **Principal Investigator**
2010-2014	NSF DRL-1020166

“The Challenge of Interdisciplinary Education: Math-Bio”
Co-Principal Investigator

2010-2015 NSF IIS-1017621
“III:Small:Algorithms for Tandem Repeat Variant Discovery Using Next Generation Sequencing Data”
Principal Investigator

2008-2013 NCRR/NIH 1UL1 RR025771
“Boston University Clinical and Translational Science Award Program”
Co-investigator, Translational Bioinformatics Core

2007-2014 NSF DGE-0654108
“IGERT: Integrating Computational Science into Research in Biological Networks”
Principal Investigator

2007-2009 NSF CNS-0709115
“CRI: Acquisition of a Linux Cluster for Bioinformatics Research and Education”
Co-Principal Investigator

2006-2009 NSF CISE-SEIII IIS-0612153
“SEI(BIO): DNA Inverted Repeats: Sensitive Detection Methods and Research Database”
Principle Investigator

2006-2010 NIH-NIGMS 1 R01 GM072084
“The repetitive DNA structure of the human genome”
Co-investigator

2004-2009 NIH-NIDDK R01 DK066939-01
“Modulation of HCV Gene Expression”
Co-investigator

2003-2008 NIH-NIGMS
“Analysis of Human Chromosome 13q Neocentromere Formation”
Co-investigator

2001-2005 NSF DBI-0413462 (DBI-0090789)
“TRDB: A multi-genome database of tandem repeats”
Principle Investigator

2000-2003 NSF CCF-0073081
“Composition Patterns in Nucleotide Sequences”
Principle Investigator

1999-2004 NIH-NIDDK
“Pathogenesis of HIV-Associated Nephropathy Project 2: Viral Pathogenesis of HIVAN”
Co-investigator

1998-2001 NSF Teacher Enhancement Program
“Villanova Teacher and Student Development Through Research Experience
Project in Biology, Mathematics and Computing”
Co-Principle Investigator

1996-2000 NSF Faculty Early Career Development Program (**CAREER**) CCR-9623532
“Tandem Repeats: Sequence Comparison and Search Algorithms”

Principle Investigator

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 Maximillian University, Munich Department of Theoretical Bioinformatics, German Cancer Research Center, Heidelberg
1990-1991	Graduate School Retention Fellowship University of Maryland, College Park, Maryland
1990	Samuel N. Alexander Award Washington, D.C. Chapter of the Association for Computing Machinery
1989-1990	General Electric Information Systems Graduate Scholarship University of Maryland, College Park, Maryland
1989-1990	Teaching Assistant Award of Excellence, Department of Computer Science University of Maryland, College Park, Maryland
1986	Creative Teaching Award, St. Mary’s County (Maryland) Public Schools

Edited Publications

“Web Server Issue,” *Nucleic Acids Research*, **G. Benson**, Executive Editor.
Volume 47, July 2019. 331 proposals, 122 submitted papers, 94 accepted papers.
(https://academic.oup.com/nar/issue/47/W1)
Volume 46, July 2018. 273 proposals, 99 submitted papers, 85 accepted papers.
(https://academic.oup.com/nar/issue/46/W1)
Volume 45, July 2017. 284 proposals, 102 submitted papers, 86 accepted papers.
(http://nar.oxfordjournals.org/content/45/W1.toc)
Volume 44, July 2016. 296 proposals, 115 submitted papers, 94 accepted papers.
(http://nar.oxfordjournals.org/content/44/W1.toc)
Volume 43, July 2015. 295 proposals, 118 submitted papers, 97 accepted papers.
(http://nar.oxfordjournals.org/content/43/W1.toc)
Volume 42, July 2014. 269 proposals, 106 submitted papers, 80 accepted papers.
(http://nar.oxfordjournals.org/content/42/W1.toc)
Volume 41, July 2013. 293 proposals, 129 submitted papers, 95 accepted papers.

(http://nar.oxfordjournals.org/content/41/W1.toc)
Volume 40, July 2012. 289 proposals, 141 submitted papers, 102 accepted papers.
(http://nar.oxfordjournals.org/content/40/W1.toc)
Volume 39, July 2011. 297 proposals, 135 submitted papers, 92 accepted papers.
(http://nar.oxfordjournals.org/content/39/suppl_2.toc)
Volume 38, July 2010. 344 proposals, 162 submitted papers, 122 accepted papers.
(http://nar.oxfordjournals.org/content/38/suppl_2.toc)
Volume 37, July 2009. 282 proposals, 141 submitted papers, 112 accepted papers.
(http://nar.oxfordjournals.org/content/37/suppl_2.toc)
Volume 36, July 2008. 265 proposals, 123 submitted papers, 94 accepted papers.
(http://nar.oxfordjournals.org/content/36/suppl_2.toc)
Volume 35, July 2007. 309 proposals, 206 submitted papers, 130 accepted papers.
(http://nar.oxfordjournals.org/content/35/suppl_2.toc)

"Pattern Matching, Text Data Structures and Compression Issue, in Honor of the 60th Birthday of Amihood Amir," Guest Editors: **G. Benson**, M. Farach-Colton, M Lowenstein, E. Porat, *Theoretical Computer Science*, Vol. 638, July 2016. (http://www.sciencedirect.com/science/journal/03043975/638)

"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. (http://www.jsbi.org/journal1/gi20/)

"Third International Workshop on Algorithms in Bioinformatics (WABI 2003)," **G. Benson** and R. Page, eds., *Lecture Notes in Bioinformatics*, No. 2812, Springer-Verlag, 2003. (http://link.springer.com/book/10.1007%2Fb13243)

Journal Publications

"Genome-wide characterization of human minisatellite VNTRs: population-specific alleles and gene expression differences," M. Rasekh, Y. Hernandez, S. Drinan, J. Fuxman-Bass, and **G. Benson**, *Nucleic Acids Research*, 2021 (doi:10.1093/nar/gkab224)

"Sleep-wake disorders in Alzheimer's disease: Further genetic analyses in relation to objective sleep measures," J. Yesavage, A. Noda, A. Heath, M. McNerney, B. Domingue, Y. Hernandez, **G. Benson**, J. Hallmayer, R. O'Hara, L. Williams, A. Goldstein-Piekarski, J. Zeitzer, and J. Fairchild, *International Psychogeriatrics*, 1-7, 2019. (doi:10.1017/S1041610219001777)

"LCSk: A Refined Similarity Measure," **G. Benson**, A. Levy, S. Maimoni, D. Noifeld and B. R. Shalom, *Theoretical Computer Science*, 638:11-26, 2016. (doi:10.1016/j.tcs.2015.11.026)

"VNTRseek – A Computational Tool to Detect Tandem Repeat Variants in High-Throughput Sequencing Data," Y. Gelfand, Y. Hernandez, J. Loving, and **G. Benson**, *Nucleic Acids Research*, 42(14):8884-8894, 2014. (doi:10.1093/nar/gku642)

"BitPAl: A Bit-Parallel, General Integer-Scoring Sequence Alignment Algorithm," J. Loving, Y. Hernandez, and **G. Benson**, *Bioinformatics*, 30(22):3166-3173, 2014. (doi:10.1093/bioinformatics/btu507)

"Clinical PathoScope: Rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data," A. Byrd, J. Perez-Rogers, C. Hong, S. Manimaran, E. Nallar, I. Toma, T McCaffrey, **G. Benson**, K. Crandall, W. E. Johnson, *BioMed Central*, 15:262, 2014. (doi:10.1186/1471-2105-15-262)

"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. Slysz, R. Smith, J. Zaia, *PLoS One*, 7(9):e45474, 2012. (doi: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)

“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)

“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. Ramisse, Y. Gelfand, **G. Benson**, G. Vergnaud, N. Fry, and C. Pourcel. *Microbiology,* 157:2582-94, 2011. (doi:10.1099/mic.0.047258-0)

“The distribution of inverted repeat sequences in the Saccharomyces cerevisiae genome,” E. M. Strawbridge, **G. Benson**, Y. Gelfand, and C. J. Benham. *Current Genetics,* 56(4):321-40, 2010. (doi:10.1007/s00294-010-0302-6)

“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)

“Pattern matching with address errors: Rearrangement distances,” A. Amir, Y. Aumann, **G. Benson**, A. Levy, O. Lipsky, E. Porat, S. Skiena and U. Vishne, *Journal of Computer and Systems Sciences*, 75(6): 359-370. 2009. (doi:10.1016/j.jcss.2009.03.001)

“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)

“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)

“TRDB: the tandem repeats database,” Y. Gelfand, A. Rodriguez, and **G. Benson**, *Nucleic Acids Research*, 35:D80-D87, 2007. (doi:10.1093/nar/gkl1013)

“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)

“$3'$-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)

“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. (doi:10.1093/bioinformatics/btl549)

“Tandem Cyclic Alignment,” **G. Benson**, *Discrete Applied Mathematics*, 146(2):124-133, 2005. (doi:10.1016/j.dam.2004.04.009)

"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. (doi:10.1101/gr.2542904)

"Minimal entropy probability paths between genome families," C. Ahlbrandt, **G. Benson**, W. Casey, *Journal of Mathematical Biology*, 48(5):563-590, 2004. (doi:10.1007/s00285-003-0248-0)

"Predicting Human Minisatellite Polymorphism," F. Denoeud, G. Vergnaud, **G. Benson**, *Genome Research*, 13(5):856-67, 2003. (doi:10.1101/gr.574403)

"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. (doi:10.1038/nm0502-522)

"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. (http://rnajournal.cshlp.org/content/8/5/557.abstract)

"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. Denoeud, V. Ramisse, P. Sylvestre, **G. Benson**, F. Ramisse, G. Vergnaud, *BioMed Central Microbiology*, 1:2-15, 2001. (doi:10.1186/1471-2180-1-2)

"Tandem Repeats Finder: A Program to Analyze DNA Sequences," **G. Benson**, *Nucleic Acids Research*, 27:573-580, 1999. (doi:10.1093/nar/27.2.573)

"On the Distribution of k-tuple Matches for Sequence Homology: A Constant Time Exact Calculation of the Variance," **G. Benson** and X. Su, *Journal of Computational Biology*, 4:87-100, 1998. (doi:10.1089/cmb.1998.5.87)

"Two Dimensional Periodicity in Rectangular Arrays," A. Amir and **G. Benson**, *SIAM Journal of Computing*, 27:90-106, 1998. (doi:10.1137/S0097539795298321)

"Optimal Parallel Two Dimensional Text Searching on a CREW PRAM," A. Amir, **G. Benson** and M. Farach, *Information and Computation*, 144:1-17, 1998. (doi:10.1006/inco.1998.2705)

"Pooling Strategies for Establishing Physical Genome Maps Using FISH," F. Sun, **G. Benson**, N. Arnheim and M. Waterman, *Journal of Computational Biology*, 4:467-486, 1997. (doi:10.1089/cmb.1997.4.467)

"Sequence Alignment with Tandem Duplication," **G. Benson**, *Journal of Computational Biology*, 4:351-367, 1997. (doi:10.1089/cmb.1997.4.351)

"Optimal Two-Dimensional Compressed Matching," A. Amir, **G. Benson** and M. Farach, *Journal of Algorithms*, 24:354-379, 1997. (doi:10.1006/jagm.1997.0860)

"Let Sleeping Files Lie: Pattern Matching in Z-compressed Files," A. Amir, **G. Benson** and M. Farach, *Journal of Computer and Systems Sciences*, 52(2):299-307, 1996. (doi:10.1006/jcss.1996.0023)

"A Space Efficient Algorithm for Finding Best Scoring, Non-overlapping Alignments," **G. Benson**, *Theoretical Computer Science*, 145:357-369, 1995. (doi:10.1016/0304-3975(95)92848-R)

"A Method for Fast Database Search for All k-Nucleotide Repeats," **G. Benson** and M. Waterman, *Nucleic Acids Research*, 22:4828-4836, 1994. (doi:10.1093/nar/22.22.4828)

"An Alphabet Independent Approach to Two Dimensional Matching," A. Amir, **G. Benson** and M. Farach, *SIAM Journal of Computing*, 23:313-323, 1994. (doi:10.1137/S0097539792226321)

Conference Publications

"An SIMD Algorithm for Wraparound Tandem Alignment," J. Loving, J. Scaduto and **G. Benson**, *Proceedings of the 13th International Symposium on Bioinformatics Research and Applications (ISBRA 2017)*, *Lecture Notes in Computer Science*, 10330:140-149, Honolulu, Hawaii, May 2017. (doi:10.1007/978-3-319-59575-7_13)

"Bit-Parallel Alignment with Substitution Scoring," J. Loving, E. Becker and **G. Benson**, *Proceedings of the 8th International Conference on Bioinformatics and Computational Biology (BICoB-2016)*, Las Vegas, Nevada, April 2016. (**Received Best Paper Award**).

"Longest Common Subsequence in k Length Substrings," **G. Benson**, A. Levy, and B. R. Shalom, *6th International Conference on Similarity Search and Applications (SISAP-2013)*, *Lecture Notes in Computer Science*, 8199:257-265, Coruña, Spain, October 2013. (doi:10.1007/978-3-642-41062-8_26)

"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.

"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)

"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)*, *Lecture Notes in Computer Science*, 5280:282-293, Melbourne, Australia, November 2008. (doi:10.1007/978-3-540-89097-3_27)

"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. (doi: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)*, *Bioinformatics* 23(2):e30-e35, Eilat, Israel, January 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: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)*, *Bioinformatics* 22(14):e341-e349, Fortaleza, Brazil, 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. Vishne, *Proceedings of the 17th Annual ACM-SIAM Symposium on Discrete Algorithms (SODA 2006)*, pp 1221-1226, 2006. (doi: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, Genome Informatics*, 16(1):3-12, Berlin, August 2005.

"Composition Alignment," **G. Benson**, *Proceedings of the Third International Workshop on Algorithms in Bioinformatics (WABI 2003), Lecture Notes in Computer Science*, 2812:447-461, September 2003. (doi:10.1007/978-3-540-39763-2_32)

"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), Bioinformatics* 18(suppl 2): S44-S53, Saarbrucken, Germany, October 2002. (doi:10.1093/bioinformatics/18.suppl_2.S44)

"Tandem Cyclic Alignment," **G. Benson**, *Proceedings of the 12th Annual Symposium on Combinatorial Pattern Matching (CPM 2001), Lecture Notes in Computer Science*, 2089:118-130, Jerusalem, July 2001. (doi:10.1007/3-540-48194-X_10)

"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. (doi:10.1145/279069.279079)

"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, January 1997. (doi:10.1145/267521.267888)

"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. (doi:10.1145/267521.267526)

"Finding Homologous Regions in a Set of Protein Sequences," **G. Benson** and M. Waterman, *DIMACS 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), Lecture Notes in Computer Science*, 820:215-226, Jerusalem, July 1994. (doi:10.1007%2F3-540-58201-0_70)

"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), Lecture Notes in Computer Science*, 807:1-14, Asilomar, California, May 1994. (doi:10.1007%2F3-540-58094-8_1#)

"Let Sleeping Files Lie: Pattern Matching in Z-compressed Files," A. Amir, **G. Ben-**

son and M. Farach, *Proceedings of the Fifth Annual ACM-SIAM Symposium on Discrete Algorithms (SODA '94)*, Washington, D.C., January 1994. (http://dl.acm.org/citation.cfm?id=314464.314678)

"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. (doi:10.1145/165231.165242)

"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. (doi:10.1145/129712.129719)

"Efficient Two-Dimensional Compressed Matching," A. Amir and **G. Benson**, *Data Compression Conference (DCC '92)*, Snowbird, Utah, March 1992. (doi:10.1109/DCC.1992.227453)

"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. (http://dl.acm.org/citation.cfm?id=139404.139489)

"Two-Dimensional Periodicity in Rectangular Arrays," A. Amir and **G. Benson**, *Combinatorial Pattern Matching (CPM '91)*, London, April 1991. (doi:10.1137/S0097539795298321)

"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.

Conference Posters

"Finding *de novo* tandem repeats using VNTRseek, G. Hidalgo, **G. Benson**, *Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS 2022)*, Anaheim, CA, November 2022.

"Compressing DNA Read Sequences to Reduce Database Size," J. Schulte, **G. Benson**, *Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS 2022)*, Anaheim, CA, November 2022.

"Testing the accuracy and speed of VNTRseek, a genetic variation detector, using a restricted read dataset," S. Filler, **G. Benson**, *Annual Biomedical Research Conference for Minority Students (ABRCMS 2021)*, Online, November 2021.

"Identifying Possible Variable Number of Tandem Repeats (VNTRs) Using Read Mapping Coverage," N. Fields, **G. Benson**, *Annual Biomedical Research Conference for Minority Students (ABRCMS 2021)*, Online, November 2021.

"Population-specific VNTR Alleles in the Human Genome," M. Rasekh*, Y. Hernandez, **G. Benson**, *Intelligent Systems for Molecular Biology (ISMB-2020), July 2020.* ***Selected for oral presentation.**

"Using Machine Learning to Classify Tandem Repeats Within the Human Genome," M. Korovkin, M. Rasekh, **G. Benson**, *Annual Biomedical Research Conference for Minority Students (ABRCMS 2018)*, Anaheim, November, 2019.

"Single Copy VNTR Identification," K. Duchinski, M. Rasekh, **G. Benson**, *Annual Biomedical Research Conference for Minority Students (ABRCMS 2018)*, Indianapolis, November, 2018.

"Do Some Science Authors Game Their Citation Count Statistics? Creating a Platform for Examining Biomedical Publications Using Author Self-Citation Rate," M. Korovkin, **G. Benson**, *Annual Biomedical Research Conference for Minority Students (ABRCMS 2018)*, Indianapolis, November, 2018.

"Tandem Repeats Annotation and Enrichment Analysis," A. Ferrell, Y. Hernandez, M. Rasekh, **G. Benson**, *Annual Biomedical Research Conference for Minority Students (ABRCMS 2017)*, Phoenix, November, 2017.

"Investigation of the performance of a genetic variation detection program, VNTRseek," A. Okundaye, Y. Hernandez, M. Rasekh, **G. Benson**, *Annual Biomedical Research Conference for Minority Students (ABRCMS 2017)*, Phoenix, November, 2017.

"Hidden Variability in the Human Genome: a Computational Analysis of the Variability of Polymorphic Minisatellite Loci," Y. Hernandez*, Y. Gelfand, **G. Benson**, *Human Genome Meeting 2017* (HGM-2017), Barcelona, Spain, February 2017. ***Selected for oral presentation.**

"Bit-Parallel Methods in a GPU Setting to Improve Longest Common Subsequence and Edit-Distance Alignment Algorithms," H. Dedhiya, Y. Hernandez, **G Benson**, *Annual Biomedical Research Conference for Minority Students (ABRCMS 2016)*, November, 2016.

"SIMD Bit-Parallel Tandem Alignment," J.P. Scaduto, J. Loving, **G. Benson**, *Annual Biomedical Research Conference for Minority Students (ABRCMS 2016)*, November, 2016.

Invited Talks – Symposia

"Bit-Parallel Sequence Alignment with Substitution Scoring and Affine Gap," AmiFest, a workshop on Pattern Matching, Data Structures and Compression, Bar-Ilan University, Israel, June 2016.

"Tandem Repeat Variants in the Human genome," International Conference on Genomics and Bioinformatics, Izmir International Biomedicine and Genome Institute, Izmir, Turkey, May 2016.

"Bit Parallel Alignment with Substitution Scoring," StringMasters, Murdoch University, Perth, Australia, October 2015.

"Bit Parallel Sequence Alignment Algorithms," Stringology 2015, Dead Sea, Israel, January 2015.

"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

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

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

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

"Seeded Search Techniques for DNA Homology Detection and Mapping of Next Generation Sequencing Reads,"
Ben Gurion University, Department of Computer Science,
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, School of Computer Science, Israel, January 2007.
Bar Ilan University, Department of Computer Science, Israel, January 2007.

"New Resources for Tandem Repeat and Inverted Repeat Analysis,"
Delaware State University, HBCU-UP, September 2008.
Clark University, March 2007.
Boston Univ. School of Dental Med., Dept. of Mol. and Cell Biology, March 2006.
Univ. of Arizona, Dept of Mol. and Cellular Biology, Seminar Series, 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" and "Waiting Time and Seed Selection for Homology Search"
DIMACS Bio-Math Connect Institute 2005, DIMACS, Rutgers University, July 2005.
DIMACS Conference on Linking Mathematics and Biology in the High Schools, DIMACS, Rutgers University, April 2005.

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

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

"Computational Tools for Biological Sequence Analysis"
Boston University, Department of Biomedical Engineering, 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"
William Paterson University, Dept. of Mathematics, National Mathematics Awareness Month – Mathematics and Biology, 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"
Georgia Institute of Technology, College of Computing, Metropolitan Atlanta Theory Seminar, March 1993.

"Approximating the Shortest Superstring"
University of Southern California, Dept. of Mathematics, Seminar on Mathematical Biology, October 1992.

Online Software

Tandem Repeats Finder (TRF)	https://tandem.bu.edu/trf
Inverted Repeats Finder (IRF)	https://tandem.bu.edu/irf
VNTRseek	https://github.com/Benson-Genomics-Lab/VNTRseek
VNTRview	https://bioinfoppc.bu.edu/VNTRview
Tandem Repeats Database (TRDB)	http://tandem-test.bu.edu/cgi-bin/trdb/trdby.exe
Inverted Repeats Database (IRDB)	http://tandem.bu.edu/cgi-bin/irdb/irdb.exe
BitPAl: Bit-Parallel Alignment	http://lobstah.bu.edu/BitPAl/BitPAl.html
Composition Alignment	http://tandem.bu.edu/align.comp.tool.html
RNA Fold Support	http://tandem.bu.edu/foldsupport/foldsupport.html
Mutation Master	http://tandem.bu.edu/cgi-bin/mutationmaster/mutmast.exe
Tandem Repeat History Reconstruction	http://tandem.bu.edu/cgi-bin/history/history.exe
BUtheBus shuttle schedule, iPhone app (no longer available)	http://itunes.apple.com/us/app/buthebus/id401746377?mt=8

Service

2020-present	Study Section Member, NIH Training and Workplace Development-B T-32 Predoctoral Training Grant Review Panel
2023	Judge, Student Poster Session, Computational and Systems Biology 2023 ABRCMS National Conference, Phoenix, Arizona
2022	Judge, Student Poster Session, Computational and Systems Biology 2022 ABRCMS National Conference, Anaheim, California
2019	Judge, Student Poster Session, Computational and Systems Biology 2019 ABRCMS National Conference, Anaheim, California
2019	Ad hoc Study Section Reviewer, NIH Training and Workplace Development-B T32 Predoctoral Training Grant Review Panel
2018	Judge, Student Poster Session, Computational and Systems Biology 2018 ABRCMS National Conference, Indianapolis, Indiana
2017	Judge, Student Poster Session, Molecular and Computational Biology

	2017 ABRCMS National Conference, Phoenix, Arizona
2016	Judge, Student Poster Session, Molecular and Computational Biology 2016 ABRCMS National Conference, Tampa, Florida
2016	Ad hoc Reviewer, Proposals for New Junior Research Group Leaders, Institut Pasteur, Inception Program (Institut Convergence for the study of Emergence of Pathology Through Individuals and Populations)
2016	Member, Internal Review Panel, Genetics and Genomics Graduate Program Division of Graduate Medical Studies, Boston University School of Medicine
2016	Ad hoc Reviewer, NSF III Informatics Small Grant Review Panel Information & Intelligent Systems
2015	Member, NSF III Informatics Small Grant Review Panel, Information & Intelligent Systems Division (IIS), CISE
2014	Panel Member, Compelling Applications for Graduate School, Broad Institute
2013	National Judge, Siemens Competition in Math, Science, and Technology
2013	BU Representative, NEAGEP-Five Colleges Research Fair, U. Massachusetts, Amherst (a recruiting event for minority undergraduates from STEM disciplines)
2012	Member, NSF III Medium Informatics Grant Review Panel, Information & Intelligent Systems Division (IIS), CISE
2012	Judge, Student Poster Session, Computer Science, 2012 SACNAS National Conference, Seattle, Washington
2012	Member, NSF Biogenome Informatics SM12-SS Grant Review Panel
2011	Judge, Student Poster Session, Molecular and Computational Biology, 2011 ABRCMS National Conference, St. Louis, Missouri
2010	Judge, Student Poster Session, Bioinformatics and Computer Science, 2010 SACNAS National Conference, Anaheim, California
2010	Member, NSF SS Bio CAREER Grant Review Panel
2010	Program Comm., 10th Annual International Workshop on Bioinformatics and Systems Biology
2009	Program Comm., 9th Annual International Workshop on Bioinformatics and Systems Biology
2008	Program Comm., 15th Annual String Processing and Information Retrieval Symposium (SPRIRE 2008)
2009	Program Comm., 8th Annual International Workshop on Bioinformatics and Systems Biology
2007	National Judge, Siemens Competition in Math, Science, and Technology
2007	Program Comm., 7th Annual International Workshop on Bioinformatics and Systems Biology
2006	National Judge, Siemens Competition in Math, Science, and Technology
2006	Program Comm., 6th Annual International Workshop on Bioinformatics and Systems Biology
2005	Program Comm., Tenth Ann. Intl. Conf. on Comp. Molecular Biology (RECOMB 2006)
2005	Organizing Comm., Ninth Ann. Intl. Conf. on Comp. Molecular Biology (RECOMB 2005)
2005	Program Comm., Fifth International Workshop on Algorithms in Bioinformatics (WABI 2005)
2004	Program Comm., Fourth International Workshop on Algorithms in Bioinformatics (WABI 2004)
2002-2003	Co-chair, Program Comm, Third International Workshop on Algorithms in Bioinformatics (WABI 2003)
2001	Program Comm., 2nd IEEE Symp. on Bioinformatics and Bioengineering (BIBE 2001)
2000	Program Comm., 12th Ann. Symp. on Combinatorial Pattern Matching (CPM 2001)
1999	Participant, NSF CAREER PI Program Evaluation Conference
1999	Member, NSF Grant Review Committee, Theory of Computing
1998	Program Comm., Third Ann. Intl. Conf. on Comp. Molecular Biology (RECOMB 99)
1997-1998	Conference Chair, Program Comm., Second Ann. Intl. Conf. on Comp. Molecular Biology (RECOMB 98)
1997	Program Comm., 9th Ann. Symp. on Combinatorial Pattern Matching (CPM 98)
1996	Member, NSF Advisory Comm. on DNA/Biomolecular Computing
1996	Program Comm., University of Pennsylvania – DIMACS Conference on Comp. Biology, Princeton, May 1996.
1992-present	Referee for various conferences, journals and federal grant applications

Teaching and Other Educational Activities

PhD Student Training

2017-2021	**Marzie Rasekh**, Boston University, “VNTRs in the Human Population.” **Current Position:** Bioinformatics Scientist, Illumina.
2012-2019	**Yozen Hernandez**, PhD in Bioinformatics, Boston University, 2019, “A Study of the Variability of Minisatellite Tandem Repeat Loci in the Human Genome Based on High-Throughput Sequencing Data.” **Current Position:** Bioinformatics Specialist, Laboratory of Genetically Encoded Small Molecules, Rockefeller University.
2012-2016	**Joshua Loving**, PhD in Bioinformatics, Boston University, 2016, “Bit-Parallel and SIMD Alignment Algorithms for Biological Sequence Analysis.” **Current Position:** Senior Clinical Data Scientist, Syapse Inc. (field: Real World Evidence for Oncology).
2003-2008	**Denise Mak**, PhD in Bioinformatics, Boston University, 2009. “Seed Modeling, Inverted Repeat Detection and Consensus RNA Secondary Structure Prediction.” **Postdoctoral Fellow:** Krembil Family Epigenetics Laboratory, Centre for Addiction and Mental Health, Toronto, Canada. **Current Position:** Program Advisor, Healthcare, Cystic Fibrosis, Canada.

Invited Teaching – Graduate Level Short Courses in Bioinformatics

Sponsorship through the **Institut Pasteur**, **EMBO**, and the **Universite de Tunis El Manar** (Students are primarily second and third world graduate students and postdocs).
Invited Lectures: “Next Generation Sequencing: Technology, Mapping, and Analysis,” “Read Mapping Algorithms,” and “Methods for Repeat Detection in Nucleotide Sequences.”

2018	Bioinformatics and Genome Analyses course Institut Pasteur Tunis, Tunisia
2017	Bioinformatics and Genome Analyses course Institut Pasteur Tunis, Tunisia
2017	EMBO Bioinformatics and Genome Analyses course Aristotle University of Thessaloniki, Thessaloniki, Greece
2016	EMBO Bioinformatics and Genome Analyses Course Izmir International Biomedicine and Genome Institute, Izmir, Turkey
2014	EMBO-Global Exchange Lecture Course on High-throughput/NGS Applied To Infectious Diseases, Institut Pasteur Tunis, Tunisia
2014	EMBO Practical Course: Bioinformatics and Genomes Analyses The Hellenic Pasteur Institute, Athens, Greece
2013	Bioinformatics and Comparative Genome Analyses course Université de La Réunion, Saint-Denis, Réunion Island
2012	EMBO Practical Course: Bioinformatics and Comparative Genome Analysis, Stazione Zoologica Anton Dohrn, Naples, Italy
2011	EMBO Practical Course: Bioinformatics and Comparative Genome Analysis, Institut Pasteur, Paris, France
2010	EMBO Global Exchange Lecture Course: Bioinformatics and Comparative Genome Analysis, Institut Pasteur Tunis, Tunisia
2010	Bioinformatics and Comparative Genome Analysis Course Institut Pasteur, Paris, France

Other Sponsors

2005	5th International Summer School on Biocomplexity: From System to Gene,

Dartmouth University. Invited Lectures: “Biological Sequence Comparison,” “Mathematics of Homology Detection,” “Inverted Repeat Detection.”

2003 Third International Summer School on Computational Biology, Warsaw University, Poland. Five Invited Lectures: “Finding Similarity in Sequences,”

Master’s Student Training

2022	Kyler Anderson. BU. ”An improved pipeline for Variable Number Tandem Repeats Detection.”
2008-2009	Harshith Chennamaneni. BU. “A multi-threaded program for tree-to-tree alignment.”
2003-2005	Suyog Rao. BU. “Evaluating distance functions for clustering tandem repeats.”

Research Experience for Undergraduates

2023 **BU BRITE REU.** Bioinformatics Research and Interdisciplinary Training Experience (BRITE). Directed summer program for twelve students. Evaluated applications, arranged faculty sponsors, taught sessions on scientific communication/posters, coordinated programming workshop sessions, taught session on SQL programming, monitored mentor-student interaction and student progress. **All students were accepted to present posters at ABRCMS 2023.**

- Habeebu Adenuga (mentor: Josh Campbell)
- Rebecca Anderson (mentor: Pawel Przytycki)
- Sasha Bacot⋆ (mentor: Xiaoling Zhang)
- Malachy Guzman (mentors: Ilija Dukovski, Daniel Segre)
- Emily Kim (mentor: Chao Zhang)
- Ruby Krasnow (mentor: Ethan Deyle)
- Emmanuel Mekasha¶# (mentor: Julia TCW)
- Cressida Michaloski (mentor: Brian Cleary)
- Josue Navarrete¶ (mentor: Ethan Deyle)
- Joshua Ploshay†+ (mentor: Michael Dietze)
- Emilee Walden (mentor: Ana Fiszbein)
- Amelia Zug (mentor: Rubin Dries)

¶ABRCMS Presentation Award
† NSF Bio REU travel award
⋆ABRCMS travel award
+American Geophysical Union Fall Meeting 2023
#Festival of Genomics and Biodata 2023

2022 **BU BRITE REU.** Bioinformatics Research and Interdisciplinary Training Experience (BRITE). Directed summer program for ten students. Evaluated applications, arranged faculty sponsors, taught sessions on scientific communication/posters, coordinated programming workshop sessions, taught session on SQL programming, monitored mentor-student interaction and student progress. **All students were accepted to present posters at ABRCMS 2022.**

- Payton Bock¶ (mentor: Xiaoling Zhang)
- Joshua Bowers+ (mentor: Michael Deitze)
- Ashley Eng (mentor: Jennifer Bhatnagar)
- Gisselle Hidalgo⋆ (mentor: Gary Benson)
- Angela Jiang (mentor: Sarah Davies)
- Cecilia McCormick (mentor: Rubin Dries)
- Laila Norford† (mentor: Rubin Dries)
- Hannah O'Grady+ (mentor: Ethan Deyle)
- Julia Schulte (mentor: Gary Benson)
- My My Tran⋆ (mentor: Andrew Emili)

¶ABRCMS Presentation Award
+American Geophysical Union Fall Meeting 2022
† NSF Bio REU travel award
⋆ABRCMS travel award

2021 **BU BRITE REU.** Bioinformatics Research and Interdisciplinary Training Experience (BRITE). Directed remote (online) summer program for ten students. Evaluated applications, arranged faculty sponsors, taught sessions on scientific communication/posters, coordinated programming workshop sessions, taught session on SQL programming, monitored mentor-student interaction and student progress. **Nine of ten students sent posters to ABRCMS 2021. All nine gave presentations and one was selected for a Lightening Talk. Four received Presentation Awards.**

- Zoe Barinaga¶⋆ (mentor: Cynthia Bradham)
- Sara Filler¶⋆ (mentor: Gary Benson)
- Ryan Hernandez-Cancela¶⋆ (mentor: Josee Dupuis)
- Jorge Lopez-Nava⋆ (mentor: Jennifer Bhatnagar)
- Madeline Hughes⋆ (mentor: Cynthia Bradham)
- Anika Rueppell¶⋆ (mentor: Evan Johnson)
- Katie Tyrrell (mentor: Ethan Deyle)
- Miguel Yanez⋆ (mentor: Ana Fiszbein)
- Victor Feagins†⋆ (mentor: Michael Dietze)
- Noah Fields⋆ (mentor: Gary Benson)

¶ABRCMS Presentation Award
†ABRCMS Lightening Talk
⋆ABRCMS Poster presentation

2019 **BU BRITE REU.** Bioinformatics Research and Interdisciplinary Training Experience (BRITE). Directed summer program for eight students. Evaluated applications, arranged faculty sponsors, teaching sessions on scientific communication/posters, coordinating programming workshop sessions, teaching session on SQL programming, monitoring mentor-student interaction and student progress. **All students were accepted to present posters at ABRCMS 2019. Seven attended. Two received ABRCMS travel awards and two received NSF Bio REU travel awards.**

- Durdona Gaibova (mentor: Josh Campbell)
- Briana Hackos⋆ (mentor: Jennifer Bhatnagar)
- Blessing Ibe†(mentor: Paola Sebastiani)
- Nebiyou Kebede⋆ (mentor: Evan Johnson)
- Aubrey Odom† (mentor: Evan Johnson)
- Nofal Ouardaoui (mentor: Andrew Emili)
- Corinna Pilcher (mentor: Sarah Davies)
- Eric Sinton (mentor: Josh Campbell)

† NSF Bio REU travel award
⋆ABRCMS travel award

2018 **BU BRITE REU.** Bioinformatics Research and Interdisciplinary Training Experience (BRITE). Directed summer program for ten students. Evaluated applications, arranged faculty sponsors, taught sessions on scientific communication/posters, coordinated programming workshop sessions, monitored mentor-student interaction and student progress. **All students were accepted to present posters at ABRCMS 2018 and eight attended.**

- Kathryn Atherton (mentor: Jenny Bhatnagar)
- Michelle Patino Calero (mentor: Kirill Korolev)
- Luke Dramko (mentor: Michael Dietze)
- Katherine Duchinski (mentor: Gary Benson)
- Adam Lewis (mentor: Josh Campbell)
- Olivia Marx (mentor: Joe Zaia)
- Mia Price (mentor: Cyndi Bradham)
- Rahul Ramesh (mentor: Gary Benson)
- Spencer Richman (mentor: Andrew Emili)
- Alyssa Taylor (mentor: Paola Sebastiani)

2018 – 2019 Michael Korovkin. BU. NSF Research Experience for Undergraduates. “Using Machine Learning to Classify Tandem Repeats Within the Human Genome,” and “Do Some Science Authors Game Their Citation Count Statistics? Creating a Platform for Examining Biomedical Publications Using Author Self-Citation Rate.”

2017 **BU BRITE REU.** Bioinformatics Research and Interdisciplinary Training Experience (BRITE). Directed summer program for ten students. Evaluated applications, arranged faculty sponsors, taught sessions on scientific communication/posters, coordinated programming workshop sessions, monitored mentor-student interaction and student progress. **All students attended ABRCMS 2017. Two received Certificates of Achievement, three received ABRCMS travel awards, and one received an NSF travel award.**

- Edel Aron (mentor: Josee Dupuis,)
- Andrew Ferrell⋆ (mentor: Gary Benson,)
- Maddy Griswold (mentor: Tom Tullius,)
- Alan Herbert (mentor: Daniel Segre)
- Rowan Ogilvie¶ (mentors: David Waxman, Gracia Bonilla)
- Albert Okundaye⋆ (mentor: Gary Benson,)
- Brianna Richardson (mentor: Kirill Korolev)
- Christopher Rodriguez¶⋆ (mentor: Doug Densmore,)
- Jacquelyn Turcinovic† (mentors: Joseph Zaia, Joshua Klein)
- Kyndall Tyler (mentor: Paola Sebastiani)

¶ABRCMS Certificate of Achievement
† NSF travel award
⋆ABRCMS travel award

2016 **BU BRITE REU.** Bioinformatics Research and Interdisciplinary Training Experience (BRITE). Directed summer program for nine students. Evaluated applications, arranged faculty sponsors, taught sessions on scientific communication/posters, monitored mentor-student interaction and student progress. **All students attended ABRCMS 2016.**

- Anna Cates (mentors: Jenny Talbot, Colin Averill)
- Harsh Dedhiya (mentors: Gary Benson, Yozen Hernandez)
- Elsa Fecke (mentors Mark Kon, Mia Li)
- Michael Hasson (mentors: Daniel Segre, Ilija Dukovski)
- Graham Kulig (mentor: Daniel Segre)
- Sunny Mahesh (mentors: Doug Densmore, Yury Ivanov)
- Seth McDonald (mentors: Karen Allen)
- Vivek Ramanan (mentors: Kirill Korolev, Rajita Menon)
- John Scaduto (mentors: Gary Benson, Josh Loving)

2016 Harsh Dedhiya. BU. Undergraduate Research Opportunities Program, Summer 2016; NSF Research Experience for Undergraduates. “Bit-Parallel Methods in a GPU Setting to Improve DNA Alignment Algorithms.”

2015 BU Bioinformatics Research and Interdisciplinary Training Experience (BRITE). Directed summer program for three students: Grace Barkhuff, Andria Ellis, Xiangxi Gao. Evaluated applications, arranged faculty sponsors, taught sessions on scientific communication/posters, monitored student progress.

- Andria Ellis awarded a **Best Poster Award** in the area of **Molecular and Computational Biology** (one of 14 awarded) at the Annual Biomedical Research Conference for Minority Students (ABRCMS 2015).
- Xiangxi Gao presentation a poster at the Southeastern Medical Scientist Symposium (SEMSS) in Nashville. He received a **Travel Award** to attend (one of 20 awarded).
- Grace Barkhuff gave a poster and oral presentation at Women In Mathematics In New England (WIMIN) at Smith College.

2014-2015 Beth Becker. BU. Undergraduate Research Opportunities Program, 2014 Mark W. Riemen Summer Research Prize; NSF Research Experience for Undergraduates. “Bit-parallel Methods Using SIMD Instructions To Improve DNA Alignment Algorithms.” Beth was awarded a SACNAS travel fellowship to present her research at the SACNAS 2014 National Undergraduate Research Conference (Society for the Advancement of Chicanos and Native Americans). **Beth received a PhD in Bioinformatics at Boston University in Summer 2020.**

2009 Daniel Negron. BU. “Analysis of the Likely Ancestral Relationship Between Junction Repeats (Different Tandem Repeats in Close Proximity) in the Human And Other Genomes.” Daniel entered an MS program in Bioinformatics at Johns Hopkins University in 2010 and a PhD program in Bioinformatics at George Mason University in 2014. **Daniel received a PhD in Bioinformatics and Computational Biology at George Mason University in Spring 2021.**

2007 – 2008 Brandon Mensing. BU. “A statistic for multiple hits with spaced seeds and application to clustering homologous tandem repeat families.”

2004 Brian Patton. BU. “A Simulation Program to Determine the Distribution of Composition Alignment Scores in Random Sequences.” Brian joined Google after graduating and is now working for them as a software engineer in London.

2004 Naomi Levin. BU. “Comparison of sequence composition in sequences flanking tandem repeats.”

2003 Esther Richler. Touro College. “Using the Inverted Repeats Finder to Search for Small RNA Stem Loops and Applications to Neurological Diseases.” **Esther received a PhD in Cellular and Molecular Physiology at UCLA in 2011.**

2003 Madhu Achalla. NYU. NSF Research Experience for Undergraduates. “Study of Alignment Parameters for Composition Alignment.”

2002 – 2003 Igor Daysudov. NYU. NSF Research Experience for Undergraduates. “Transcription Factor Binding Sites In Tandem Repeats”. Igor developed tools for the Tandem Repeats Database.

2000 – 2001 Craig Stevenson. Bronx Community College. New York City Alliance for Minority Participation in Science, Engineering and Mathematics; NSF Research Experience for Undergraduates. “Explorations of a Divergence Measure for Comparing Repeat Profiles”

1996-1998 Astrid Jervis. Hunter College. Louis and Rachel Rudin Foundation – Sigma Xi Undergraduate Summer Research Fellow; NSF Research Experience for Undergraduates. “Statistical Issues for an Algorithm in the Search for Tandem Repeats.” Astrid assisted on the initial validation of the Tandem Repeats Finder program.

1995	Michael Dwyer. Oberlin College. Louis and Rachel Rudin Foundation – Sigma Xi Undergraduate Summer Research Fellow, “Immune System Selection of HIV Quasispecies as an Agent of AIDS Pathogenesis”

Research Experience for High School Students

2002	Payal Bassi, Bayside High School. “Cyclic Permutations and Reverse Complements.”
2001	Benjamin Klein, The Yeshiva of Flatbush, “Constructing a Connected Graph of Random Points on a Three-Dimensional Entropy Surface.”
1999	Malini Sur, Hunter College High School, “Effects of the Variation of Alignment Match and Mismatch Parameter Values on Alignments of Tandem Repeats.”
1999	Madhurima Anne, Brooklyn Technical High School, Secondary Education Through Health Program, “Analysis of Variation in Nucleotide Composition in DNA Sequences.”
1997	David Slifka, The Dalton School. DIMACS/Mount Sinai Computational Biology Program. “A Program to Guide Experimental Combinatorics for Genome Mapping with Fluorescent *in-situ* Hybridization (FISH).”

Graduate (G) and Undergraduate (U) Courses Taught

Boston University
- Bioinformatics Challenge Project (G)
- Design of Biological Databases (G)
- Pattern Matching and Pattern Detection Algorithms with Applications in Biological Sequence Analysis (G,U)
- Yeah, there’s an app for that: Object oriented programming on the iPhone (U)

Mount Sinai School of Medicine
- 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)

University of Maryland
- Introduction to Design and Analysis of Algorithms (U)
- Computer Science I (Introduction) (U)
- Discrete Mathematics (U)

High School Programs

Integrating Computational Thinking in Mathematics and Science High School Teacher Professional Development, 2018-2021. I participatied in the development and teaching of an online course for high school mathematics and biology teachers which covers topics in *computational thinking* which can be integrated into their curricula. I taught two versions of the course, in June 2020 and October 2020. This project was funded by the National Science Foundation through the Center for Discrete Mathematics and Theoretical Computer Science (DIMACS) at Rutgers University.

The Challenge of Interdisciplinary Education: Math-Bio, 2011–2014. I wrote a high school level instructional module on sequencing and sorting, which develops ideas and concepts concerning the use of next-generation sequencing to detect mutational variation in human DNA sequences. Activities include classroom simulations to 1) map ”reads” to a segment of the human genome 2) detect SNPs and deletions in the mapped reads, and 3) sort DNA sequences, specifically using radix sort, to speed up mapping. This project was a joint collaboration with Rutgers University DIMACS and COMAP of Bedford, Massachusetts.

National Judge, Siemens Competition in Math, Science, and Technology for high school research related to bioinformatics, 2013, 2007, 2006. In 2013, I was the lead judge for the first place winner ($100,000 prize) with a project entitled: “Discovery of Novel Influenza Endonuclease Inhibitors to Fight Flu Pandemic.” In 2007, I was the lead judge for the second place team winners ($50,000 prize) with a project entitled: “A computational model for translational efficiency and frameshifts in *E. coli* using genetic signal processing approach.” In 2006, I was the lead judge for the first place team winners ($100,000 prize) with a project entitled: “Linking Supercomputing and Systems Biology for Efficient Bioethanol Production.” A lead judge interprets the project for the other judges and leads the questioning of the students by the judges.

Boston University Mathematics Field Day, 2007. I gave an invited lecture, “The Mathematics and Biology of Genetics and Disease,” to an audience of 500 high school students from schools in the Boston area. The talk described crossing-over of chromosomes during meiosis and how that facilitates the use of Single Nucleotide Polymorphisms (SNPs) as markers to locate the site of disease genes.

Wentworth Institute of Technology (Boston) SLAM, 2007. I gave an invited lecture on DNA structure and models for 10 students participating in the SLAM (Students Loving Adventures in Mathematics) Saturday morning enrichment program sponsored by the Mathematical Association of America and directed by Mathematics Professor Amanda Hattaway at Wentworth. Students were primarily from underrepresented groups at three Boston public schools, the Urban Science Academy, the Parkway Academy of Health and Technology, and O’Bryant School of Math and Science.

Rutgers University (DIMACS) Bio-Math Connection, 2006-2007. I participated in the development of a curriculum module on protein and DNA sequence homology for an interdisciplinary high school mathematics and biology course.

Gateway to Higher Education, 2001-2001. (Inner City and Minority Students in New York City). I collaborated with high school mathematics teacher, Mark Saul, to develop curriculum modules related to biological sequence comparison, pattern searching methods and internet access to biological sequence databases.

Villanova University Summer Research Institute in Biology, Computing and Mathematics, for High School Teachers and Students, 1998. I was the co-director and a lecturer for this summer research experience program for high school teachers and high school students.

Villanova University Young Scholars Program in Biology and Mathematics 1997.
Guest lecturer.

DIMACS Young Scholars Program in Discrete Mathematics, 1996.
Guest lecturer.

Miscellaneous

KNE’X DNA Models (http://tandem.bu.edu/knex/dna.models.knex.html), 1997