Amir Manzour

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EXPERIENCE AND	Assistant Professor SUNY Polytechnic Institute, Dept. of Computer Science	Sep 2024 - now	
RESEARCH	Visiting Assistant Professor Colgate University, Dept. of Computer Science	Jul 2022 - Jun 2024	
	• Taught Algorithms and Introduction to Computing I		
	 Visiting Assistant Professor Aug 2021 - Jun 2022 Indiana University–Purdue University Indianapolis (IUPUI), Indianapolis, IN School of Informatics and Computing, Department of BioHealth Informatics Taught undergraduate and graduate bioinformatics courses including Introduc- tion to bioinformatics and computational methods to biomedical informatics. 		
	Postdoctoral and Research Fellow	Jul 2014 - Jul 2021	
	 National Institutes of Health, Bethesda, MD National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS) Designed and launched RNA-binding-protein (RBP) mRNA target analysis. The pipeline intersects RNA-seq data with in-vivo RBP-mRNA binding experiment (PAR-CLIP). Significantly improved target identification using probabilistic mod- eling. The pipeline was developed in R and is deployed on a Shiny web-server. 		
	• National Center for Biotechnology Information (NCBI) Designed an approach for efficient prediction of RNA molecule's alternative struc- ture (CondAlt in Java and Perl). Significantly improved prediction speed. Conducted evolutionary study on HIV-1 Nef RNA structure. Identified regions with high RNA plasticity.		
	Ph.D. Student, Research Assistantship	Jan 2009 - May 2014	
	 Led and completed original interdisciplinary research in RNA secondary structure. Designed and implemented a recursive algorithm using stochastic context-free grammar (SCFG) modeling of RNA. The SCFGEntropy software package was developed in C++ and is generalized to handle ambiguous SCFGs. 		
	• Worked under the direction of Jonathan Arnold to find putative riboswitches in <i>Bacillus subtilis, Escherichia coli,</i> and <i>Synechococcus elongatus.</i> Predictions were based on binomial logistic regression model training using SPSS.		
	Database and Reporting Manager Mobile Company of Iran (IR-MCI), Tehran, Iran	Sep 2007 - Oct 2008	
	• Imported, cleaned, validated, and stored daily performance reports from multiple telecommunications vendors. Maintained and updated the nationwide database and performed SQL-based scheduled reports needed for critical decision making.		
	Masters Student, Research Assistantship Isfahan University of Technology, Isfahan, Iran • Performed GWAS on Age-related Macular Degeneration	Sep 2003 - May 2006 disease for epistatic in-	
	teractions. C#, recursive SQL, and CLR function implementation.		
	• Implemented 802.11a Physical Layer, OFDM, viterbi, B	Berlekamp's BCH, adap-	

tive neural networks, classification, clustering, and 16QAM in Matlab.

EDUCATION	<i>Ph.D. in Bioinformatics</i> University of Georgia, Athens, GA	Jan 2009 - May 2014
	Masters in Telecommunications Engineering Isfahan University of Technology, Isfahan, Iran	Aug 2004 - May 2007
	Bachelors in Electrical Engineering University of Guilan, Rasht, Iran	Jan 1999 - Feb 2004

PUBLICATIONS Manzourolajdad A. Analysis of nucleotide position and orientation in 3D space reveals RNAs tendency for A and U unpaired nucleotides in close distance [version 1; not peer reviewed]. F1000Research 2024, 13:1159 (poster) (doi: 10.7490/f1000research.1119909.1)

> Dhesi, T. S., Bannister, A. W., Manzourolajdad, A., Deep Learning of Ligandbound RNA Tertiary Structures Diverges from Learning Unbound Ones: A Case Study Using The gRNAde Software, bioRxiv, September, 2023

> Fallatah, A., Anastasakis D. G., Manzourolajdad A., Sharma P., Wang X., Jacob A., Alsharif S., Elgerbi A., Coulombe P. A., Hafner M., Chung B. M., Keratin 19 binds and regulates cytoplasmic HNRNPK mRNA targets in triple-negative breast cancer, BMC Molecular and Cell Biology, August, 2023

Genzor P., Konstantinidou, P., Stoyko, D., Manzourolajdad, A., Andrews, C. M., Elchert, A. R., Stathopoulos, C., Haase, A. D. Cellular abundance shapes function in piRNA-guided genome defense. Genome Research, October 19, 2021.

Srivastava, M., Dukeshire, M. R., Mir, Q., Omoru, Q., B., Manzourolajdad, A., Janga, S. C., Experimental and computational methods for studying the dynamics of RNA-RNA interactions in SARS-COV2 genomes, Briefings in Functional Genomics, February 7, 2023

Dukeshire, M., Schaeper, D., Venkatesan, P., Manzourolajdad, A. Variant-Specific Analysis Reveals a Novel Long-Range RNA-RNA Interaction in SARS-CoV-2 Orf1a, International Journal of Molecular Sciences, 23(19), September 21, 2022.

Omoru, O. B., Pereira, F., Janga, S. C., Manzourolajdad, A. A Putative long-range RNA-RNA interaction between ORF8 and Spike of SARS-CoV-2. PLoS ONE, 17(9), September 1, 2022.

Fallatah, A., Anastasakis D. G., Manzourolajdad A., Sharma P., Wang X., Jacob A., Alsharif S., Elgerbi A., Coulombe P. A., Hafner M., Chung B. M., **HNRNPK is re-**tained in the cytoplasm by Keratin 19 to stabilize target mRNAs, BioRxiv, January, 1, 2022.

Genzor P., Konstantinidou, P., Stoyko, D., Manzourolajdad, A., Andrews, C. M., Elchert, A. R., Stathopoulos, C., Haase, A. D. Cellular abundance shapes function in piRNA-guided genome defense. Genome Research, October 19, 2021.

Manzourolajdad, A., Spouge, J.L. Structural prediction of RNA switches using conditional base pair probabilities. PLoS ONE, 14(6), June 12, 2019.

Manzourolajdad, A., Gonzalez, M., Spouge, J.L. Changes in the Plasticity of HIV-1 Nef RNA during the Evolution of the North American Epidemic, PLoS ONE 11(9), Sept. 29, 2016.

Manzourolajdad, A., Arnold, J. Secondary Structural Entropy in RNA Switch (Riboswitch) Identification, BMC Bioinformatics, 2015, 16:133.

Manzourolajdad A., Wang, Y., Shaw, T.I., Malmberg, R.L. Information-theoretic uncertainty of SCFG modeled folding space of the non-coding RNA, Journal of Theoretical Biology, 2013, Vol. 318, 140-163.

Wang, Y., Manzour, A., Shareghi, P., Shaw, T.I., Li, Y.W., Malmberg, R.L., Cai, L. Stable stem enabled shannon entropies distinguish non-coding RNAs from random backgrounds, BMC Bioinformatics,2012, 13 Suppl 5, S1. Shaw, T.I., Manzour, A., Wang, Y., Malmberg, R.L., Cai, L. Analyzing modular RNA structure reveals low global structural entropy in microRNA sequences, Journal of Bioinformatics and Computational Biology, 2011, 9, 283-98. Manzourolajdad, A., Saraee, M., Mirlohi, A., Javan, A., Genome-wide efficient Attribute Selection for Purely Epistatic Models via Shannon Entropy, The international journal of Business Intelligence and Data Mining, 2008. Vol. 3, No. 4,

BOOKManzourolajdad, A. (2016). The application of grammar space entropy in RNACHAPTERSsecondary structure modeling. In Emerging trends in applications and infrastructures for computational biology, bioinformatics, and systems biology, 2nd Edition. Elsevier.

390-408.

 CONFERENCES Manzourolajdad A, Do Empirical and Abstract Shannon Entropies Converge in Value? A Case in RNA Molecular Structure, 2020 Intermountain Engineering, Technology and Computing (IETC), Oct 2-3, 2020, Orem, UT, USA, IEEE Manzourolajdad A, Shannon's Entropy of The Stochastic Context-Free Grammar and an Application to RNA Secondary Structure Modeling, Int'l Conf. Bioinformatics and Computational Biology (BIOCOMP'15), July 27-30, 2015. Las Vegas, USA, pp. 3-7 Wang Y, Manzour A, Shareghi P, Shaw TI, Li YW, Malmberg RL, Cai L. Stable stem

enabled shannon entropies distinguish non-coding RNAs from random backgrounds, Computational Advances in Bio and Medical Sciences, 2011, 184-189.

Shaw TI, Manzour A, Wang Y, Malmberg RL, Cai L. Analyzing modular RNA structure through shannon entropy reveals low global structural entropy in miRNAs, Computational Systems Bioinformatics Conference, Proceedings, 2010. 9, 146-155.

Saraee M, Nikoofar H, Manzour A. Epistasy Search in Population-Based Gene Mapping Using Mutual Information, The IEEE Symposium on Signal Processing and Information Technology, 2007. 621-625.

Manzour A, Saraee M. Entropy-based epistasy search in SNP case-control studies, In Fourth International Conference on Fuzzy Systems and Knowledge Discovery, 2007. Haikou, China, pp. 21-26

COURSESIntroduction to BioinformaticsTAUGHTData Structures and Algorithms
Computational Methods in Biomedical Informatics
Machine Learning in Bioinformatics
Database Management
Introduction to Computing

TALKS AND
SEMINARSPredicted spike-ORF8 RNA-RNA interaction unique to SARS-CoV-2 may
impact N-gene sub-genomic RNA synthesis, NIH/FDA COVID-19 Research
Symposium/Workshop, October 29-30th, 2020, Bethesda, MD, USA
Exploring the sequence diversity of piRNAs, 84th Symposium: RNA Control &
Regulation, Cold Spring Harbor Laboratory, Laurel Hollow, 2019, NY, USA

Synonymous mutations allow structural plasticity of HIV-1 Nef RNA while maintaining selective pressure, 2018, RNA Club Interest Group, National Institutes of Health

Entropy, SCFG, and RNA Switches, Laboratoire d'Informatique de l'Ecole Polytechnique (LIX), Ecole Polytechnique, August 2018, Palaiseau, France

Structural Prediction of RNA Switches using Conditional Base-Pair Probabilities, Computational Biology Branch (CBB) Seminars, National Center for Biotechnology Information (NCBI), September 26, 2017, Bethesda, MD, USA

The tendency of HIV-1 Nef to accommodate for high RNA conformational plasticity, Cold Spring Harbor Laboratory Retroviruses Meeting, May 22–May 27, 2017, NY, USA

Thermodynamic analyses suggest selective pressure on HIV-1 nef RNA's conformational plasticity, Computational Biology Branch (CBB) Seminars, National Center for Biotechnology Information (NCBI), January 17, 2017, Bethesda, MD, USA

RNA Secondary Structure Modeling, The 2015 International Conference on Bioinformatics and Computational Biology (BIOCOMP 2015: Las Vegas, USA)

RNA Secondary Structural Dynamics and HIV, Howard University Cancer Center, May 26, 2015, Washington DC, USA

AWARDSProject EPIC, DEI Program, IUPUI, Indianapolis, INNovember 2021Achievement Award, BIOCOMP'15 Conference, Las Vegas, NVJul 2015Graduate Assistantship, University of Georgia, Athens, GADec 2008Ranked Top 7% amongst 10000, Elec. Eng. National Masters Exam., IranJun 2004Received Financial Aids and Awards, Concordia University, Montréal, Canada 1998

DESIGNATIONS Chair/Coordinator, International Conference on Bioinformatics and Computational Biology (BIOCOMP'15). Reviewer, Bioinformatics, The Journal of Theoretical Biology, Scientific Reports. Lead Judge, Postbac Poster Day, NIH. Secretary, Visiting Postdoctoral Fellows Committee, NIH.