Hamidreza Chitsaz, PhD

Staff Software Engineer
AutoX
Remote - Fort Collins, Colorado

Tel: 858-692-3229
Web: http://algorithmicslab.org/chitsaz
Email: hrchitsaz@gmail.com

Employment

2022-	Staff Software Engineer	AutoX	
2020-2022	Senior Software Engineer	Waymo	
2014-2021	Assistant Professor	Computer Science	Colorado State University
2011-2014	Assistant Professor	Computer Science	Wayne State University
2010-2011	Postdoctoral Scholar	Bioinformatics	University of California, San Diego
2008-2009	Postdoctoral Fellow	Computational Biology	Simon Fraser University
2002-2008	Research Assistant	Computer Science	University of Illinois at Urbana-Champaign
1997-2001	Undergrad RA	RoboCup Lab	Sharif University of Technology

Education

Doctor of Philosophy	University of Illinois at Urbana-Champaign *August 2001 - January 2008*	Computer Science
Master of Science	University of Illinois at Urbana-Champaign *December 2006*	Mathematics
Bachelor of Science	Sharif University of Technology *September 1996 - June 2001*	Computer Science Pure Mathematics *double major with honors*

Management Skills

- **Team Building:** Recruitment, advising, and graduation of 2 postdoctoral scholars and 4 graduate students.
- **Collaboration:** Working with multiple stakeholders in different disciplines such as Biology, Medicine, Chemistry, Computer Science, and Electrical Engineering at various organizational levels.
- **Resource Management:** Managed $1M+ federal and institutional research funds.

Technical Skills

- **Machine learning:** DeepNN, CNN, RNN, Autoencoder, Associative Memory, SVM, KNN, PCA and PVA, PyTorch and TensorFlow.
- **Blockchain:** Solidity, DeFi, DApp, ASIC/GPU/CPU PoW Algos, Quantum Resilience.
- **Programming:** C, C++, Java, Python, PC/Microcontroller Assembly, Matlab, HTML, PHP, JavaScript, node.js, Perl, SQL.
- **Robotics:** LQR, RRT*, Optimal control, Nonholonomic motion planning, SLAM.
- **OS:** Linux, Unix, AIX, SunOS.

- **Hardware design:** Microcontrollers, DSP, and FPGA.

SOFTWARE

- **CIC and DeePathology:** Deep neural networks for encoding gene expression data and prediction of cancer subtype. [Torch7]
- **HyDA:** Hybrid *De Novo* Assembler for co-assembly and comparison of multiple datasets, e.g. multiple supposedly related single cells. [C++]
- **Camel:** maximum likelihood error correction for single cell (MDA) Illumina reads. [C++]
- **Velvet-SC:** an adaptation of Velvet for single-cell bacterial genome assembly. [C++]
- **piRNA:** RNA-RNA interaction statistical mechanics package for exact calculation and approximation of partition function, probability, equilibrium concentration, and melting temperature. [C++]
- **biRNA:** RNA-RNA binding sites prediction. [C++]
- **BPPart and BPMax:** RNA-RNA interaction partition function and structure prediction for the base-pair counting model. [C++]

PUBLICATIONS

Books

[1] Hamidreza Chitsaz. *Geodesics for Mobile Robots: A geometric optimal control approach*. VDM, Saarbrücken, Germany, 2009.

Journals

[1] Ali Ebrahimpour Boroojeny, Akash Shrestha, Ali Sharifi-zarchi, Suzanne Renick Gallagher, Süleyman Cenk Sahinalp, and Hamidreza Chitsaz. PyGTED: Python application for computing graph traversal edit distance. *Journal of Computational Biology*, 27(3):436–439, 2020.

[2] Ali Ebrahimpour Boroojeny, Akash Shrestha, Ali Sharifi-Zarchi, Suzanne Renick Gallagher, S. Cenk Sahinalp, and Hamidreza Chitsaz. Graph traversal edit distance and extensions. *Journal of Computational Biology*, 27(3):317–329, 2020.

[3] B. Azarkhalili, A. Saberi, H. Chitsaz, and A. Sharifi-Zarchi. DeePathology: Deep Multi-Task Learning for Inferring Molecular Pathology from Cancer Transcriptome. *Scientific Reports*, 9(1):16526, Nov 2019.

[4] D. A. Murtazina, J. A. Arreguin-Arevalo, J. D. Cantlon, A. E. Boroojeny, A. Shrestha, J. A. Hicks, C. Magee, K. Kirkley, K. Jones, T. M. Nett, H. Chitsaz, and C. M. Clay. Enrichment of ovine gonadotropes via adenovirus gene targeting enhances assessment of transcriptional changes in response to estradiol-17Î². *Biol. Reprod.*, Aug 2019.

[5] Farzad Abdolhosseini, Behrooz Azarkhalili, Abbas Maazallahi, Aryan Kamal, Seyed Abolfazl Motahari, Ali Sharifi-Zarchi, and Hamidreza Chitsaz. Cell Identity Codes: Understanding cell identity from gene expression profiles using deep neural networks. *Scientific Reports*, 9(1):2342, Feb 2019.

[6] Y. An, A. Kawaguchi, C. Zhao, A. Toyoda, A. Sharifi-Zarchi, S. A. Mousavi, R. Bagherzadeh, T. Inoue, H. Ogino, A. Fujiyama, H. Chitsaz, H. Baharvand, and K. Agata. Draft genome of Dugesia japonica provides insights into conserved regulatory elements of the brain restriction gene nou-darake in planarians. *Zoological Letters*, 4:24, 2018.

[7] Ali Sharifi-Zarchi, Daniela Gerovska, Kenjiro Adachi, Mehdi Totonchi, Hamid Pezeshk, Ryan J. Taft, Hans R. Schöler, Hamidreza Chitsaz, Mehdi Sadeghi, Hossein Baharvand, and Marcos J. Araúzo-Bravo. DNA methylation regulates discrimination of enhancers from promoters through a H3K4me1-H3K4me3 seesaw mechanism. *BMC Genomics*, 18(1):964, Dec 2017.

[8] Nadra Alhusini, Ali Sharifi-Zarchi, Seyed Ahmad Mousavi, Hamidreza Chitsaz, and Athar Ansari. Genomewide analysis of Clp1 function in transcription in budding yeast. *Scientific Reports*, 7(1):6894, 2017.

[9] Razieh Karamzadeh, Mohammad Hossein Karimi-Jafari, Ali Sharifi-Zarchi, Hamidreza Chitsaz, and Ghasem Hosseini Salekdeh. Machine learning and network analysis of molecular dynamics trajectories reveal two chains of Red/Ox-specific residue interactions in protein disulfide isomerase. *Scientific Reports*, 7(1):3666, 2017.

[10] Behrouz Bokharaeian, Alberto Diaz, Nasrin Taghizadeh, Hamidreza Chitsaz, and Ramyar Chavoshinejad. SNPPhenA: a corpus for extracting ranked associations of single-nucleotide polymorphisms and phenotypes from literature. *Journal of Biomedical Semantics*, 8(1):14, Apr 2017.

[11] Behrouz Bokharaeian, Alberto Diaz, and Hamidreza Chitsaz. Enhancing Extraction of Drug-Drug Interaction from Literature Using Neutral Candidates, Negation, and Clause Dependency. *PLoS ONE*, 11(10):e0163480, 2016.

[12] Narjes S. Movahedi, Mallory Embree, Harish Nagarajan, Karsten Zengler, and Hamidreza Chitsaz. Efficient synergistic single-cell genome assembly. *Frontiers in Bioengineering and Biotechnology*, 4(42), 2016.

[13] Ali Sharifi-Zarchi, Mehdi Totonchi, Keynoush Khaloughi, Razieh Karamzadeh, Marcos J. Araúzo-Bravo, Hossein Baharvand, Ruzbeh Tusserkani, Hamid Pezeshk, Hamidreza Chitsaz, and Mehdi Sadeghi. Increased robustness of early embryogenesis through collective decision-making by key transcription factors. *BMC Systems Biology*, 9(23), June 2015.

[14] Hamidreza Chitsaz and Mohammad Aminisharifabad. Exact learning of RNA energy parameters from structure. *Journal of Computational Biology*, 22(6):463–473, June 2015.

[15] Seyed Basir Shariat Razavi, Narjes Sadat Movahedi Tabrizi, Hamidreza Chitsaz, and Christina Boucher. HyDA-Vista: Towards optimal guided selection of k-mer size for sequence assembly. *BMC Genomics*, 15(Suppl 10):S9, 2014. Also GIW/ISCB-Asia proceedings.

[16] Milad Gholami, Aryan Arbabi, Ali Sharifi-Zarchi, Hamidreza Chitsaz, and Mehdi Sadeghi. ARYANA: Aligning Reads by Yet Another Approach. *BMC Bioinformatics*, 15(Suppl 9):S12, 2014. Also RECOMB-Seq proceedings.

[17] Mallory Embree, Harish Nagarajan, Narjes Movahedi, Hamidreza Chitsaz, and Karsten Zengler. Single-cell genome and metatranscriptome sequencing reveal metabolic interactions of an alkane-degrading methanogenic community. *The ISME journal*, 8:757–767, 2014.

[18] Z. Taghavi, N. S. Movahedi, S. Draghici, and H. Chitsaz. Distilled single-cell genome sequencing and de novo assembly for sparse microbial communities. *Bioinformatics*, 29(19):2395–2401, Oct 2013.

[19] J. S. McLean, M. J. Lombardo, J. H. Badger, A. Edlund, M. Novotny, J. Yee-Greenbaum, N. Vyahhi, A. P. Hall, Y. Yang, C. L. Dupont, M. G. Ziegler, H. Chitsaz, A. E. Allen, S. Yooseph, G. Tesler, P. A. Pevzner, R. M. Friedman, K. H. Nealson, J. C. Venter, and R. S. Lasken. Candidate phylum TM6 genome recovered from a hospital sink biofilm provides genomic insights into this uncultivated phylum. *Proc. Natl. Acad. Sci. U.S.A.*, 110(26):E2390–2399, Jun 2013.

[20] K. R. Bradnam, J. N. Fass, A. Alexandrov, P. Baranay, M. Bechner, I. Birol, S. Boisvert, J. A. Chapman, G. Chapuis, R. Chikhi, H. Chitsaz, W. C. Chou, J. Corbeil, C. Del Fabbro, T. R. Docking, R. Durbin, D. Earl, S. Emrich, P. Fedotov, N. A. Fonseca, G. Ganapathy, R. A. Gibbs, S. Gnerre, E. Godzaridis, S. Goldstein, M. Haimel,

G. Hall, D. Haussler, J. B. Hiatt, I. Y. Ho, J. Howard, M. Hunt, S. D. Jackman, D. B. Jaffe, E. Jarvis, H. Jiang, S. Kazakov, P. J. Kersey, J. O. Kitzman, J. R. Knight, S. Koren, T. W. Lam, D. Lavenier, F. Laviolette, Y. Li, Z. Li, B. Liu, Y. Liu, R. Luo, I. Maccallum, M. D. Macmanes, N. Maillet, S. Melnikov, D. Naquin, Z. Ning, T. D. Otto, B. Paten, O. S. Paulo, A. M. Phillippy, F. Pina-Martins, M. Place, D. Przybylski, X. Qin, C. Qu, F. J. Ribeiro, S. Richards, D. S. Rokhsar, J. G. Ruby, S. Scalabrin, M. C. Schatz, D. C. Schwartz, A. Sergushichev, T. Sharpe, T. I. Shaw, J. Shendure, Y. Shi, J. T. Simpson, H. Song, F. Tsarev, F. Vezzi, R. Vicedomini, B. M. Vieira, J. Wang, K. C. Worley, S. Yin, S. M. Yiu, J. Yuan, G. Zhang, H. Zhang, S. Zhou, and I. F. Korf. Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. *Gigascience*, 2(1):10, Jul 2013.

[21] Elmirasadat Forouzmand and Hamidreza Chitsaz. The RNA Newton polytope and learnability of energy parameters. *Bioinformatics*, 29(13):i300–i307, 2013. Also ISMB/ECCB proceedings.

[22] Hamidreza Chitsaz, Elmirasadat Forouzmand, and Gholamreza Haffari. An efficient algorithm for upper bound on the partition function of nucleic acids. *Journal of Computational Biology*, 20(7):486–494, 2013.

[23] Roy Ronen, Christina Boucher, Hamidreza Chitsaz, and Pavel Pevzner. SEQuel: improving the accuracy of genome assemblies. *Bioinformatics*, 28(12):i188–i196, 2012. Also ISMB proceedings.

[24] Hamidreza Chitsaz, Joyclyn L. Yee-Greenbaum, Glenn Tesler, Mary-Jane Lombardo, Christopher L. Dupont, Jonathan H. Badger, Mark Novotny, Douglas B. Rusch, Louise J. Fraser, Niall A. Gormley, Ole Schulz-Trieglaff, Geoffrey P. Smith, Dirk J. Evers, Pavel A. Pevzner, and Roger S. Lasken. Efficient de novo assembly of single-cell bacterial genomes from short-read data sets. *Nature Biotech*, 29(10):915–921, Oct 2011.

[25] Hamidreza Chitsaz, Raheleh Salari, S.Cenk Sahinalp, and Rolf Backofen. A partition function algorithm for interacting nucleic acid strands. *Bioinformatics*, 25(12):i365–i373, 2009. Also ISMB/ECCB proceedings.

[26] Hamidreza Chitsaz, Steven M. Lavalle, Devin J. Balkcom, and Matthew T. Mason. Minimum wheel-rotation paths for differential-drive mobile robots. *International Journal of Robotics Research*, 28(1):66–80, 2009.

[27] Manuela M. Veloso, Tucker R. Balch, Peter Stone, Hiroaki Kitano, Fuminori Yamasaki, Ken Endo, Minoru Asada, Mansour Jamzad, Bashir S. Sadjad, Vahab S. Mirrokni, Moslem Kazemi, Hamidreza Chitsaz, Abbas Heydarnoori, MohammadTaghi Hajiaghayi, and Ehsan Chiniforooshan. RoboCup-2001: the fifth robotic soccer world championships. *AI Magazine*, 23(1):55–68, 2002.

[28] Mansour Jamzad, Amirali Foroughnassiraei, Ehsan Chiniforooshan, Reza Ghorbani, Moslem Kazemi, Hamidreza Chitsaz, Farid Mobasser, and Bashir S. Sadjad. ARVAND: a soccer player robot. *AI Magazine*, 21(3):47–51, 2000.

Refereed Conferences

[1] Ali Ebrahimpour-Boroojeny, Sanjay Rajopadhye, and Hamidreza Chitsaz. BPPart: RNA-RNA Interaction Partition Function in the Absence of Entropy. In Alessandra Carbone and Mohammed El-Kebir, editors, *Workshop on Algorithms in Bioinformatics*, volume 201 of *Leibniz International Proceedings in Informatics (LIPIcs)*, pages 14:1–14:24, Dagstuhl, Germany, 2021.

[2] Majdi Khalid, Hamidreza Chitsaz, and Indrakshi Ray. Proximal stochastic AUC maximization. In *International Joint Conference on Neural Networks (IJCNN)*. IEEE, 2020.

[3] Majdi Khalid, Indrakshi Ray, and Hamidreza Chitsaz. Scalable nonlinear AUC maximization methods. In Michele Berlingerio, Francesco Bonchi, Thomas Gärtner, Neil Hurley, and Georgiana Ifrim, editors, *Machine Learning and Knowledge Discovery in Databases*, pages 292–307. Springer, 2019.

[4] Ali Ebrahimpour Boroojeny, Akash Shrestha, Ali Sharifi-Zarchi, Suzanne Gallagher, S. Cenk Sahinalp, and Hamidreza Chitsaz. GTED: Graph traversal edit distance. In *Annual International Conference on Research in Computational Molecular Biology*, volume 10812 of *Lecture Notes in Computer Science*, pages 37–53. Springer, 2018.

[5] Reza Iraji and Hamidreza Chitsaz. Principal variety analysis. In Sergey Levine, Vincent Vanhoucke, and Ken Goldberg, editors, *Proceedings of the 1st Annual Conference on Robot Learning*, volume 78 of *Proceedings of Machine Learning Research*, pages 97–108. PMLR, 13–15 Nov 2017.

[6] Majdi Khalid, Indrakshi Ray, and Hamidreza Chitsaz. Confidence-weighted bipartite ranking. In Jinyan Li, Xue Li, Shuliang Wang, Jianxin Li, and Quan Z. Sheng, editors, *Proceedings of 12th International Conference on Advanced Data Mining and Applications*, pages 35–49. Springer, 2016.

[7] Seyed Basir Shariat Razavi, Narjes Sadat Movahedi Tabrizi, Hamidreza Chitsaz, and Christina Boucher. HyDA-Vista: Towards optimal guided selection of k-mer size for sequence assembly. *BMC Genomics*, 15(Suppl 10):S9, 2014. Also GIW/ISCB-Asia proceedings.

[8] Reza Iraji and Hamidreza Chitsaz. NUROA: A numerical roadmap algorithm. In *IEEE Conference on Decision and Control*, pages 5359–5366, 2014.

[9] Milad Gholami, Aryan Arbabi, Ali Sharifi-Zarchi, Hamidreza Chitsaz, and Mehdi Sadeghi. ARYANA: Aligning Reads by Yet Another Approach. *BMC Bioinformatics*, 15(Suppl 9):S12, 2014. Also RECOMB-Seq proceedings.

[10] Hamidreza Chitsaz and Mohammad Aminisharifabad. Exact learning of RNA energy parameters from structure. In Roded Sharan, editor, *Annual International Conference on Research in Computational Molecular Biology*, volume 8394 of *Lecture Notes in Computer Science*, pages 56–68. Springer, 2014.

[11] Elmirasadat Forouzmand and Hamidreza Chitsaz. The RNA Newton polytope and learnability of energy parameters. *Bioinformatics*, 29(13):i300–i307, 2013. Also ISMB/ECCB proceedings.

[12] Hamidreza Chitsaz. On time-optimal trajectories for a car-like robot with one trailer. In *SIAM Control and Its Applications*, pages 114–120, 2013.

[13] Narjes S. Movahedi, Elmirasadat Forouzmand, and Hamidreza Chitsaz. De novo co-assembly of bacterial genomes from multiple single cells. In *IEEE Conference on Bioinformatics and Biomedicine*, pages 561–565, 2012.

[14] Roy Ronen, Christina Boucher, Hamidreza Chitsaz, and Pavel Pevzner. SEQuel: improving the accuracy of genome assemblies. *Bioinformatics*, 28(12):i188–i196, 2012. Also ISMB proceedings.

[15] Hamidreza Chitsaz, Rolf Backofen, and S.Cenk Sahinalp. biRNA: Fast RNA-RNA binding sites prediction. In S.L. Salzberg and T. Warnow, editors, *Workshop on Algorithms in Bioinformatics (WABI)*, volume 5724 of *LNBI*, pages 25–36, Berlin, Heidelberg, 2009. Springer-Verlag.

[16] Hamidreza Chitsaz, Raheleh Salari, S.Cenk Sahinalp, and Rolf Backofen. A partition function algorithm for interacting nucleic acid strands. *Bioinformatics*, 25(12):i365–i373, 2009. Also ISMB/ECCB proceedings.

[17] Andrei A. Furtuna, Devin J. Balkcom, Hamidreza Chitsaz, and Paritosh A. Kavathekar. Generalizing the dubins and reeds-shepp cars: Fastest paths for bounded-velocity mobile robots. In *IEEE Conference on Robotics and Automation*, pages 2533–2539, 2008.

[18] H. Chitsaz, S.M. LaValle, and J. O'Kane. Exact pareto-optimal coordination of two translating polygonal robots on a cyclic roadmap. In *Proceedings of the 20th Canadian Conference on Computational Geometry (CCCG2008)*, pages 179–182, 2008.

[19] H. Chitsaz and S.M. LaValle. Minimum wheel-rotation paths for differential-drive mobile robots among piecewise smooth obstacles. In *IEEE International Conference on Robotics and Automation*, pages 2718–2723, 2007.

[20] H. Chitsaz and S.M. LaValle. Time-optimal paths for a Dubins airplane. In *IEEE Conference on Decision and Control*, pages 2379–2384, 2007.

[21] H. Chitsaz, S.M. LaValle, D.J. Balkcom, and M.T. Mason. Minimum wheel-rotation paths for differential-drive mobile robots. In *IEEE Conference on Robotics and Automation*, pages 1616–1623, 2006.

[22] H. Chitsaz, S.M. LaValle, D.J. Balkcom, and M.T. Mason. An explicit characterization of minimum wheel-rotation paths for differential-drives. In *Proceedings 12th IEEE International Conference on Methods and Models in Automation and Robotics*, 2006.

[23] H. Chitsaz, J.M. O'Kane, and S.M. LaValle. Exact pareto-optimal coordination of two translating polygonal robots on an acyclic roadmap. In *IEEE Conference on Robotics and Automation*, volume 4, pages 3981–3986, 2004.

[24] Mansour Jamzad, Bashir S. Sadjad, Vahab S. Mirrokni, Moslem Kazemi, Hamidreza Chitsaz, Abbas Heydarnoori, MohammadTaghi Hajiaghai, and Ehsan Chiniforooshan. A fast vision system for middle size robots in RoboCup. In *RoboCup 2001: Robot Soccer World Cup V*, volume 2377 of *Lecture Notes in Computer Science*, pages 71–80. Springer-Verlag, 2002. Won the **Best Engineering Challenge Award** in RoboCup 2001.

[25] Mansour Jamzad, Hamidreza Chitsaz, Amirali Foroughnassirai, Reza Ghorbani, Moslem Kazemi, Vahab S. Mirrokni, and Bashir S. Sadjad. Basic requirements for a teamwork in middle size RoboCup. In *RoboCup 2001: Robot Soccer World Cup V*, pages 621–626. Springer-Verlag, 2002.

[26] Mohammad T. Manzuri, Hamidreza Chitsaz, Reza Ghorbani, Pooya Karimian, Alireza Mirazi, Mehran Motamed, Roozbeh Mottaghi, and Payam Sabzmeydani. Sharif CESR small size RoboCup team. In *RoboCup 2001: Robot Soccer World Cup V*, pages 595–598. Springer-Verlag, 2002.

[27] Mansour Jamzad, Amirali Foroughnassiraei, MohammadTaghi Hajiaghai, Vahab S. Mirrokni, Reza Ghorbani, Abbas Heidarnoori, Moslem Kazemi, Hamidreza Chitsaz, Farid Mobasser, Mohsen EbrahimiMoghaddam, Maziar Gudarzi, and Navid Ghaffarzadegan. A goal keeper for middle size RoboCup. In Peter Stone, Tucker Balch, and Gerhard Kraetzschmar, editors, *RoboCup 2000: Robot Soccer World Cup IV*, volume 2019 of *Lecture Notes in Computer Science*, pages 583–586. Springer Berlin Heidelberg, 2001.

[28] Mansour Jamzad, Amirali Foroughnassiraei, Ehsan Chiniforooshan, Reza Ghorbani, Moslem Kazemi, Hamidreza Chitsaz, Farid Mobasser, and Bashir S. Sadjad. Middle sized soccer robots: ARVAND. In *RoboCup-99: Robot Soccer World Cup III*, pages 61–73. Springer-Verlag, 2000.

[29] Mansour Jamzad, Amirali Foroughnassiraei, Ehsan Chiniforooshan, Reza Ghorbani, Moslem Kazemi, Hamidreza Chitsaz, Farid Mobasser, and Bashir S. Sadjad. Design and construction of a soccer player robot ARVAND. In Manuela Veloso, Enrico Pagello, and Hiroaki Kitano, editors, *RoboCup-99: Robot Soccer World Cup III*, volume 1856 of *Lecture Notes in Computer Science*, pages 745–749. Springer Berlin Heidelberg, 2000.

Abstracts and Non-refereed Publications

[1] Hamidreza Chitsaz, Narjes S. Movahedi, and Elmirasadat Forouzmand. De novo co-assembly of bacterial genomes from multiple single cells. In *Genome Informatics - Wellcome Trust Sanger Institute*, 2012.

[2] R. Backofen, H. Chitsaz, I. Hofacker, S. C. Sahinalp, and P. F. Stadler. Computational studies of non-coding RNAs - Session Introduction. *Pacific Symposium Biocomputing*, 15:54–56, 2010.

Preprints and Submitted

[1] Ali Ebrahimpour Boroojeny, Sanjay Rajopadhye, and Hamidreza Chitsaz. BPPart and BPMax: RNA-RNA interaction partition function and structure prediction for the base pair counting model. *arXiv*, 1904.01235, 2020.

[2] Ali Ebrahimpour Boroojeny and Hamidreza Chitsaz. SARS-CoV-2 orthologs of pathogenesis-involved small viral RNAs of SARS-CoV. *arXiv*, 2007.05859, 2020.

[3] H. Chitsaz. Prediction of RNA-RNA interaction structure by centroids in the Boltzmann ensemble. *ArXiv e-prints 1002.1736, q-bio.BM*, February 2010.

Theses

[1] Hamidreza Chitsaz. *Geodesic Problems for Mobile Robots*. PhD thesis, University of Illinois at Urbana-Champaign, Urbana, IL, 2008.

[2] Hamidreza Chitsaz. Design and implementation of a controller for small size soccer player robot. Bachelor's Thesis (in persian). Sharif University of Technology, 2001.

Awards and Honors

- **Best Highlights Paper Award**, Great Lakes Bioinformatics Conference (GLBio), Pittsburgh, PA 2013.
- Natural Sciences and Engineering Research Council of Canada (NSERC) Industrial Research and Development **Postdoctoral Fellowship**, 2009 (it was declined to accept a postdoctoral position at UCSD).
- **Travel Fellowship**, Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), 2009.
- Winner of **Best Engineering Challenge Award** in RoboCup 2001, Seattle, WA.
- **World Champion** (first rank together with *Sharif CE* team) in RoboCup 1999 Middle Size League, Stockholm, Sweden.
- **World 3rd Place** (together with *Sharif CE* team) in RoboCup 2000 Middle Size League, Melbourne, Australia.
- **Europe Champion** (first rank together with *Sharif CE* team) in European RoboCup Middle Size League, Netherlands, 2000.
- **Bronze Medal** in Iranian Mathematics Olympiad, Fall 1995.
- 1^{st} place among 20,000 in Computer Science and 4^{th} in Computer Engineering Higher Education (MSc) National Universities Entrance Examination, Iran, 2001.
- 31^{st} place among 300,000 in Iranian National Universities Entrance Examination, 1996.
- Diploma with Honors from *Exceptional Talents High School* (Allameh-Helli High School) specialized for gifted and talented students, National Organization for Development of Exceptional Talents, 1996.

Funds

- NSF DBI-1505253 (DBI-1262565), PI: H. Chitsaz, "ABI Innovation: Compressed Single-Cell Sequencing of Bacterial Communities", $507,357, 09/01/2013 - 08/31/2017.

Community Service

Organizer: Robot Learning and Planning Workshop, Robotics: Science and Systems (RSS) 2016; Optimal Motion Planning Minisymposium, SIAM Control and its Applications (CT) 2013; Challenges and Vision Workshop, Robotics: Science and Systems (RSS) 2013; Computational Studies of Non-coding RNAs, Pacific Symposium on Biocomputing (PSB) 2010.

Program Committee Member and Associate Editor: ACM SIGKDD - Medical Informatics and Healthcare Workshop 2017; IEEE/RSJ International Conference on Intelligent Robots and Systems (IROS) 2016, 2017, 2018, 2019; IEEE International Conference on Tools with Artificial Intelligence (ICTAI) 2016, 2017, 2018, 2019; IEEE Data Mining (ICDM) - Data Mining in Biomedical Informatics and Healthcare (DMBIH) Workshop 2013, 2014, 2015, 2016, 2017, 2018, 2019; IEEE International Conference on Artificial Intelligence for Industries 2018, 2019; International Conference on Genome Informatics 2018; IEEE Bioinformatics and Biomedicine (BIBM) 2012; ACM Bioinformatics, Computational biology, and Biomedicine (BCB) 2012; Research in Computational Molecular Biology Next-Generation Sequencing (RECOMB-seq) 2012; IEEE Symposium on Artificial Intelligence and Signal Processing (AISP) 2011; RoboCup Iran Open Symposium (RIOS) 2011, 2012, 2013.

Session Chair: IEEE Bioinformatics and Biomedicine (BIBM) 2012.

Referee for Journals: Acta Astronautica; AIAA Journal of Guidance, Control, and Dynamics; Autonomous Robots; Bioinformatics; Biomedical Informatics; BMC Bioinformatics; BMC Genomics; Cell Systems; Computational Biology and Chemistry; Frontiers in Ecology and Evolution; Genomics; IEEE/ACM Transactions on Computational Biology and Bioinformatics; IEEE Control Systems Letters; IEEE Robotics and Automation Letters; IEEE Transactions on Automatic Control; IEEE Transactions on Control Systems Technology; IEEE Transactions on Robotics; IEEE Transactions on Robotics and Automation; IEEE Transactions on Systems, Man, and Cybernetics; International Journal of Control; International Journal of Molecular Sciences; International Journal of Robotics Research; Journal of Computational Biology; Journal of Optimization Theory and Applications; Journal of Process Control; SIAM Journal on Control and Optimization; Symmetry.

Referee for Conferences: ACM-SIAM Symposium on Discrete Algorithms (SODA); American Control Conference (ACC); Asia Pacific Bioinformatics Conference (APBC); Combinatorial Pattern Matching (CPM); European Conference on Computational Biology (ECCB); IEEE Automation Science and Engineering (CASE); IEEE Bioinformatics and Biomedicine (BIBM); IEEE Conference on Decision and Control (CDC); IEEE Conference on Robotics and Automation (ICRA); IEEE Multiconference on Systems and Control (MSC); IEEE Southeastern Symposium on System Theory (SSST); IEEE/RSJ International Conference on Intelligent Robots and Systems (IROS); Intelligent Systems for Molecular Biology (ISMB); Neural Information Processing Systems (NIPS); Research in Computational Molecular Biology (RECOMB); RoboCup SSL; Robotics: Science and Systems (RSS).

Panelist: NSF IIS, NSF CPS.

Invited Talks

- *Microbial Genome Sequencing at Single-cell Resolution,* Soil and Crop Sciences Seminar, Colorado State University, Fort Collins, CO, October 2017.
- *My Computer Science Career Trajectory: Robotics, Bioinformatics, Machine Learning, and Beyond,* Computer Science Club Meetings, Fort Collins High School, Fort Collins, CO, October 2017.
- *Compressive Single Cell Genomics,* Next Generation Sequencing USA Congress and Single Cell Genomics & Transcriptomics USA Congress, Harvard Medical School, Boston, MA, October 2015.
- *Single cell genomics: progress and prospects,* BME Seminar, Colorado State University, Fort Collins, CO, September 2014.
- *Single-cell genome sequencing and assembly: progress and prospects,* Bioinformatics Seminar, Indiana University, Bloomington, IN, July 2014.
- *Single-cell genome sequencing and assembly: progress and prospects,* CS Colloquium, Colorado State University, Fort Collins, CO, February 2014.

- *De novo co-assembly of bacterial genomes from multiple single cells,* CEA – Institut de Génomique – Genoscope, Évry, Paris, France, June 2013.
- *Genome assembly: one cell at a time,* Next-generation Sequencing Data Congress, London, UK, June 2013.
- *A partition function algorithm for RNA-RNA interaction,* Benasque RNA meeting, Benasque, Spain, July 2012.
- *Prediction of RNA-RNA interaction probability and structure,* Computer Science Graduate Seminar, Wayne State University, Detroit, MI, Fall 2011.
- *De novo assembly of bacterial genomes from single cells,* Dept of Computer Science, Wayne State University, Detroit, MI, March 2011.
- *Prediction of RNA-RNA interaction probability and structure,* Computer Science and Engineering Seminar, University of California, San Diego, CA, September 2009.
- *Prediction of RNA-RNA interaction probability and structure,* Bioinformatics for Combating Infectious Diseases (BCID) meeting, Simon Fraser University, September 2009.
- *Predicting RNA-RNA interaction probability and structure,* MathFest - Annual Meeting of the Mathematical Associaton of America, Portland, OR, August 2009.
- *RNA folding and RNA-RNA interaction prediction,* Advanced CS Seminar, School of Computing Science, Simon Fraser University, March 2009.
- *Geodesics for mobile robots,* Robotics Seminars, Faculty of Applied Sciences, Simon Fraser University, March 2009.
- *Pareto-optimal coordination of multiple robots,* Computer Science Theory Seminar, School of Computing Science, Simon Fraser University, October 2008.
- *Nonlinear optimization in robotics,* Covert Systems Biology Lab, Bio-X Center, Stanford University, July 2007.

Conference Talks

- *GTED: Graph traversal edit distance,* Annual International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, April 2018.
- *Principal Variety Analysis,* Annual Conference on Robot Learning (CoRL), Mountain View, CA, November 2017.
- *The SNPPhenA Corpus: An annotated research abstract corpus for extracting ranked association of single-nucleotide polymorphisms and phenotypes,* Annual Rocky Mountain Bioinformatics Conference, Aspen, CO, December 2016.
- *Exact learning of RNA energy parameters from structure,* Annual International Conference on Research in Computational Molecular Biology (RECOMB), Pittsburgh, PA, April 2014.
- *The RNA Newton polytope and learnability of energy parameters,* Annual International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB), Berlin, Germany, July 2013.
- *On time-optimal trajectories for a car-like robot with one trailer,* SIAM Control and Its Applications, San Diego, CA, June 2013.
- *De novo co-assembly of bacterial genomes from multiple single cells,* Great Lakes Bioinformatics Conference (GLBio), Pittsburgh, PA, May 2013. **Best Highlights Paper Award**.

- *De novo co-assembly of bacterial genomes from multiple single cells,* Genome Informatics - Wellcome Trust Sanger Institute, Cambridge, UK, September 2012.
- *De Bruijn graph based genome assembly for single cells,* SIAM Discrete Math Sequence Analysis Minisymposium, Halifax, Canada, June 2012.
- *Computational studies of non-coding RNAs,* Pacific Symposium on Biocomputing (PSB), Big Island, Hawaii, January 2010.
- *biRNA: fast RNA-RNA binding sites prediction,* Workshop on Algorithms in Bioinformatics (WABI), Philadelphia, PA, September 2009.
- *A partition function algorithm for interacting nucleic acid strands,* Annual International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB), Stockholm, Sweden, July 2009.
- *Minimum wheel-rotation paths for differential-drive mobile robots,* IEEE Conference on Robotics and Automation (ICRA), Orlando, FL, May 2006.

Professional Memberships

- Institute of Electrical and Electronics Engineers (IEEE)
- International Society for Computational Biology (ISCB)
- Society for Industrial and Applied Mathematics (SIAM)