Hilal Kazan

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Research Area

computatinal biology, regulatory genomics, cancer genomics

Professional Experience

- Department of Computer Engineering, Antalya Bilim University Nov 12-present
  Associate Professor

Education

- **University of Toronto, Canada** Sept 07 – Sep 12
  PhD – Computer Science, Computational Biology Group.
  Thesis: *Inferring binding preferences of RNA-binding proteins*
  Advisor: Prof. Quaid Morris
- **Sabanci University (SU), Turkey** Sept 03 – June 07
  B.Sc. – Computer Science and Engineering
  Graduation Project: *RNA secondary structure prediction using simulated annealing*
  Advisors: Prof. Ugur Sezerman and Prof. Pierre Flener

Journal Publications

- Erten C, Houdjedj A, Kazan H (2021). BetweenNet: Ranking Cancer Driver Genes Using Betweenness Scored Random Walks. **BMC Bioinformatics**, 22(62), 1-16.
- Omranovic A, Kazan H, Oblak P, Curk T (2021). Sparse data embedding and prediction by tropical matrix factorization. **BMC Bioinformatics**, 22, Doi: 10.1186/s12859-021-04023-9
- Baali Ilyes, Erten C, Kazan H (2020). DriveWays: a method for identifying possibly overlapping driver pathways in cancer. **Scientific Reports**, 10(1)
- Yang M,...Kazan H,... (2020). Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. **Cell Systems**, 11(2), 186-1959
- Ahmed R, Baali I, Erten C, Hoxha E, Kazan H. MEXCOwalk: mutual exclusion and coverage based random walk to identify cancer modules. **Bioinformatics**. 2019. 1-8 doi:10.1093/bioinformatics/btz655
- HafezQorani S, Houdjedj A, Arici M, Said A, Kazan H. RBPSponge: genome-wide identification of lncRNAs that sponge RBPs. **Bioinformatics**. 2019. https://doi.org/10.1093/bioinformatics/
- Ozturk DG, Kocak M, Akcay A, Kinoglu K, Kara E, Buyuk Y, Kazan H, Gozuacik D MITF-MIR211 axis is a novel autophagy amplifier system during cellular stress. **Autophagy.** 2018 Oct 5:1-16. doi: 10.1080/15548627.2018.1531197.
- I Baali, DAE Acar, TW Aderinwale, S HafezQorani, H Kazan (2018) Predicting clinical outcomes in neuroblastoma with genomic data integration **Biology Direct** 13 (1), 20
- SK Zahr, G Yang, H Kazan, MJ Borrett, SA Yuzwa, A Voronova, DR Kaplan, FD Miller (2018) A translational repressor complex in developing mammalian neuronal stem cells that regulates neuronal specification. **Neuron,** 97 (1-18)
- H Kazan (2016) Computational Prediction of RNA-protein Interactions **APJES,** 4:3 doi: 10.21541/apjes.92217
- H Kazan (2016) Modeling Gene Regulation in Liver Hepatocellular Carcinoma with Random Forests. **Biomed Research International,** doi:10.1155/2016/1035945
- A Lafzi and H Kazan. (2016) Inferring RBP-Mediated Regulation in Lung Squamous Cell Carcinoma.

PloS One, 11(5): e0155354.

- N Berkowitz, I Silverman, D Childress, H Kazan, L Wang, B Gregory. A comprehensive database of high-throughput sequencing-based RNA secondary structure probing data (Structure Surfer) (2016). **BMC Bioinformatics**,10.1186/s12859-016-1071-0.
- S Chandrasekaran, M Cokol-Cakmak, N Sahin, K Yilancioglu, H Kazan, JJ Collins, M Cokol (2016) Chemogenomics and orthology-based design of antibiotic combination therapies. **Molecular Systems Biology,** 12(5):872.
- S HafezQorani, A Lafzi, RG de Bruin, AJ van Zonneveld, EP van der Veer, YA Son, H Kazan (2016) Modeling the combined effect of RNA-binding proteins and microRNAs in post-transcriptional regulation. **Nucleic Acids Res,** 10.1093/nar/gkw048.
- RG de Bruin ... H Kazan, EAL Biessen, M Ares Jr, AJ van Zonneveld, EP van der Veer (2016) Quaking promotes monocyte differentiation into pro-atherogenic macrophages by controlling pre-mRNA splicing and gene expression. **Nature Communications,** 7:10486.
- R Colak, T Kim, H Kazan, Y Oh, M Cruz, A Valladares-Salgado, J Peralta, J Escobedo, EJ Parra, PM Kim, A Goldenberg (2015) JBASE: Joint Bayesian Analysis of Subphenotypes and Epistasis. **Bioinformatics,** 10.1093/bioinformatics/btv504
- K Yilancioglu, ZB Weinstein, C Meydan, A Akhmetov, I Toprak, A Durmaz, I Iossifov, H Kazan, FP Roth, M Cokol (2014). *Target-independent prediction of drug synergies using only drug lipophilicity.* **J Chemical Information and Modelling** ,54(8):2286-2293
- X Li*, H Kazan*, HD Lipshitz and Q Morris. (2014*) Finding the target sites of RNA-binding proteins.* **WIREs RNA,** doi:10.1002/wrna.1201 *co-first authors
- D Ray*, H Kazan*, KB Cook*, MT Weirauch*, HS Najafabadi* et al., (2013) *A compendium of RNA-binding motifs for decoding gene-regulation.* **Nature,** 499:172-177 *co-first authors
    - featured in ScienceDaily "Scientists decode mystery sequences involved in gene regulation"
    - highlighted in an article as "Learning the language of post-transcriptional gene regulation" published in Genome Biology by Thomas Tuschl's group
- H Kazan* and Q Morris (2013*) RBPmotif: a web server for the discovery of sequence and structure preferences of RNA-binding proteins.* **Nucleic Acids Res.** 41:W180-186 *corresponding author
- ML Wilbert, SC Huelga, K Kapeli, TJ Stark, TY Liang, SX Chen, BY Yan, JL Nathanson, KR Hutt, MT Lovci, H Kazan, AQ Vu, KB Massirer, Q Morris, S Hoon, GW Yeo (2012) *LIN28 binds messenger RNAs at GGAGA motifs and regulates splicing factor abundance.* **Mol Cell**, 48:1-12
- KB Cook, H Kazan, K Zuberi, Q Morris and TR Hughes (2010) *RBPDB: a database of RNA-binding specificities.* **Nucleic Acids Res,** 39 (Database issue) D301-D308.
- H Kazan, D Ray, E Chan, TR Hughes and Q Morris (2010) *RNAcontext: A new method for learning the sequence and structure binding preferences of RNA-binding proteins*. **PLoS Comput Biol,** 6(7): e1000832.
- D Ray*, H Kazan*, E Chan, LP Castillo, S Talukder et. al. (2009) *Rapid and systematic characterization of the RNA recognition specificities of RNA-binding proteins*. **Nature Biotechnology,** 27: 667-670 *co-first authors

Selected Conference Presentations

- H Kazan. Computational challenges in RNA-based gene regulation: protein-RNA recognition, regulation and prediction. Dagstuhl Seminar 17252. (2017)

- S HafezQorani, H Kazan. Genome-wide identification of lncRNAs that sponge RNA-binding proteins. 25th Conference on Intelligent Systems for Molecular Biology (ISMB 2017), Prague, Czech Republic.
- I Baali, T Aderinwale, AE Acar, S HafezQorani, H Kazan. Predicting clinical outcomes in neuroblastoma with genomic data integration. ISMB CAMDA Workshop 2017, Prague, Czech Republic.
- S HafezQorani, A Lafzi, YA Son, H Kazan. Post-transcriptional regulation mediated by the interplay between RNA-binding proteins and miRNAs,
  - RECOMB 2014: ISCB Conference on Regulatory and Systems Genomics, Nov 9-14 in San Diego, California, United States
  - ECCB 2014: The 13th European Conference on Computational Biology, Sep 7-10 in Strasbourg, France.
- S HafezQorani, A Lafzi, YA Son, H Kazan. Identifying the interactions between RNA-binding proteins and miRNAs, MIE 2014: The 25th International Congress of the European Federation for Medical Informatics, Aug 31- Sep 3, Istanbul, Turkey.
- H Kazan et al, A compendium of RNA-binding motifs for decoding gene-regulation. ISMB 2013, 21st Annual International Conference on Intelligent Systems for Molecular Biology, Jul 21-23, Berlin, Germany.
- H Kazan, X Liu, KB Cook, W Jiao, HD Lipsitz, TR Hughes, Q Morris (2010) Learning binding preferences of RNA-binding proteins inferred from large scale binding assays. RECOMB Satellite on Regulatory Genomics, New York City, USA.
- H Kazan, D Ray, E Chan, TR Hughes and Q Morris (2009) Learning the sequence and structure binding preferences of RNA-binding proteins from noisy affinity data. RECOMB Satellite on Regulatory Genomics, Boston, USA.
- H Kosucu*, P Flener, U Sezerman (2008) RNA secondary structure prediction using simulated annealing. Non-coding RNAs: Computational Challenges and Applications, Antalya, Turkey. *maiden surname
- O Bodenreider, Z Coban, MC Doganay, E Erdem and H Kosucu (2008) A preliminary report on answering complex queries related to drug discovery using answer set programming. In Proc. of Applications of Logic Programming to Semantic Web and Web Service, Udine,Italy.

Invited Talks

- RNA-seq data analysis and its use in clinic, TBGK 2015 (XIV. Ulusal Tıbbi Biyoloji ve Genetik Kongresi), Fethiye, Turkey.
- Modeling the combined effect of RNA-binding proteins and microRNAs in post-transcriptional regulation, HİBİT 2015 (International Symposium on Health Informatics and Bioinformatics), Muğla, Turkey.
- Inferring the binding preferences of RNA-binding proteins, Department of Biology, University of Pennsylvania, PA, USA, Nov 2014
- Systematic study of post-transcriptional regulation mediated by RNA-binding proteins and microRNAs, Leiden University Medical Center, Leiden, The Netherlands. Oct 2014

Relevant Experience

Microsoft Research, Cambridge, UK

Research Intern

Supervisor: Dr. John Winn and Prof. Chris Bishop

Memorial Sloan Kettering Institute, New York City, USA.

Summer undergraduate student, worked on prediction of microRNA targets with miRanda

Supervisor: Prof. Chris Sander

Grants

- **TUSEB** Systems Biology and Bioinformatics Grant. (2020-2022) 350.000 TL
- Neuroimmune guidance cues, MicroRNAs & Inflammatory responses: Sex differences in CardioVascular Diseases. **Tübitak ERA-CVD Grant** (2019-2022) 451.800 TL
- Novel methods for cancer gene prioritization and cancer module discovery. **Tübitak 1001** Grant (2018-2021) ~49.301 TL
- Identification of the factors that govern post-transcriptional regulation. **Tübitak 3501** National Young Researchers Career Development Grant (2013-2015) ~163.000 TL
- Systematic study of post-transcriptional regulation mediated by RNA-binding proteins and miRNAs**. EU - FP7 Marie Curie**, Career Integration Grant (2014-2018) 100.000 €

Teaching Experience

- Instructor for the following courses in Antalya Bilim University: CS 101 Introduction to Programming, CS 210 Data Structures, CS 303 Principles of Programming Languages, CS311 Algorithms, CS 441 Artificial Intelligence, CS 445 Machine Learning, MATH 213 Discrete Mathematics, ECE 551 Introduction to Computational Biology, ECE 585 Research Ethics and Scientific Methods

Scholarships and Achievements

- Antalya Bilim University Top Researcher Award 2018
- Grace Hopper Celebration of Women in Computing Scholarship Award, 2008
- SU Certificate of High Honor for 5 semesters, based upon GPA higher than 3.50
- SU Faculty of Engineering Sciences High Honor Scholarship, 2003-2007
  includes full tuition and a monthly stipend
- Nationwide University Entrance Examination of Turkey, 2003
  ranked 21st among 1.7 million applicants

Supervision

1. Atefeh Lafzi (MSc, 2016)

2. Saber HafezQorani (MSc, 2015)
3. Aderinwale Tunde (MSc, 2017)
4. Aissa Houdjedj (MSc, 2021)
5. Ilyes Baali (MSc, 2020)
6. Ahmed Amine Taleb Bahmed (MSc, 2020)
7. Rafsan Ahmed (MSc, 2020)
8. İbrahim Berber(MSc, current)
9. Muhammed Edip Akay (MSc, current)
10. Yacine Marouf (MSc, current)