

Prof. TOLGA CAN

Personal Information

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International Researcher IDs

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Biography

Tolga Can received his BS degree in computer engineering from Middle East Technical University, Turkey, in 1998 and his PhD degree in computer science from the University of California at Santa Barbara in 2004. He is currently a professor in the Computer Engineering Department, Middle East Technical University, Turkey. His main research interests include bioinformatics and scientific visualization. He has worked on protein structure visualization and alignment and on construction and analysis of large-scale protein-protein interaction networks.

Education Information

Doctorate, University of California, Santa Barbara, Bilgisayar Bilimleri, United States Of America 2000 - 2004

Undergraduate, Middle East Technical University, Faculty of Engineering, Department of Computer Engineering, Turkey 1994 - 1998

Research Areas

Computer Sciences, bioinformatics, Engineering and Technology

Academic Titles / Tasks

Professor, Middle East Technical University, Faculty of Engineering, Department of Computer Engineering, 2017 - Continues

Associate Professor, Middle East Technical University, Faculty of Engineering, Department of Computer Engineering, 2011 - 2017

Assistant Professor, Middle East Technical University, Faculty of Engineering, Department of Computer Engineering, 2007 - 2011

Lecturer, Middle East Technical University, Faculty of Engineering, Department of Computer Engineering, 2006 - 2007

Research Assistant, University of California, Santa Barbara, College Of Engineering, Computer Science, 2000 - 2005

Academic and Administrative Experience

Middle East Technical University, Faculty of Engineering, Department of Computer Engineering, 2007 - 2010

Advising Theses

- CAN T., Construction and analysis of tissue/disease specific protein-protein interaction networks by integrating large scale transcriptome data with genome scale protein-protein interaction networks, Doctorate, A.BURÇAK(Student), 2022
- CAN T., Mini autonomous car architecture for urban driving scenarios, Postgraduate, G.Karabulut(Student), 2019
- CAN T., Genome- and tissue-wide analysis of alternative polyadenylation events using clustering and feature learning methods, Postgraduate, P.Yilmazer(Student), 2019
- CAN T., TARI Z. S., Shape models based on elliptic pdes, associated energies, and their applications in 2d and 3d, Doctorate, A.GENÇTAV(Student), 2018
- CAN T., Tools and techniques for assessing functional relevance of genomic loci, Doctorate, B.OTLU(Student), 2017
- CAN T., A layout algorithm for visualization of graph alignments, Postgraduate, A.AKARSU(Student), 2017
- CAN T., A multiplex primer design algorithm for target amplification of continuous genomic regions, Doctorate, A.RAŞIT(Student), 2016
- CAN T., ERSON BENSAN A. E., Alternative polyadenylation dependent 3'-UTR changes in triple negative breast cancers, Doctorate, T.TUNCER(Student), 2015
- CAN T., AYDIN SON Y., A multi-layered graphical model of the relation among SNPs, genes, and pathways based on subgraph search, Postgraduate, G.ERSOY(Student), 2015
- CAN T., ÖZCENGİZ G., Pattern search in pathogenic bacterial proteins for localization and secretory systems, Doctorate, O.ÖZCAN(Student), 2015
- CAN T., Determination of the effect of polyadenylation SLR values on microarray data classification, Postgraduate, Ü.ASLAN(Student), 2014
- CAN T., Identification of interaction sites of G protein-coupled receptors using machine learning techniques, Doctorate, M.EMRE(Student), 2014
- CAN T., A database query based solution for chemical compound and drug name recognition, Postgraduate, Ç.ATA(Student), 2014
- CAN T., Integer linear programming based solutions for construction of biological networks, Doctorate, Ö.EREN(Student), 2014
- CAN T., ŞENER C., Modeling of split step parabolic wave equation using the graphics processing unit, Postgraduate, S.SEKMEK(Student), 2014
- CAN T., ŞENER C., GPU accelerated radio wave propagation modeling using ray tracing, Postgraduate, A.ZUBAROĞLU(Student), 2014
- CAN T., Machine learning methods for using network based information in microRNA target prediction, Doctorate, M.SUALP(Student), 2013
- CAN T., Prediction of polyadenylation sites by probe level analysis of microarray data, Postgraduate, Y.İLGÜNER(Student), 2013
- CAN T., Analysis of 3'UTR shortening events in breast cancer, Postgraduate, O.BALOĞLU(Student), 2013
- CAN T., AYDIN SON Y., A framework for gene co-expression network analysis of lung cancer, Postgraduate, E.AKDEMİR(Student), 2013
- CAN T., Mining fungal effector candidates in biotrophic plant pathogens : rusts and mildews, Postgraduate, S.UĞUR(Student), 2012
- CAN T., SINEC: Large scale signaling network topology reconstruction using protein-protein interactions and RNAi data, Postgraduate, S.HASHEMİKHABİR(Student), 2012
- CAN T., Parallelization of functional flow to predict protein functions, Postgraduate, E.AKKOYUN(Student), 2011
- CAN T., Machine learning methods for promoter region prediction, Postgraduate, H.ARSLAN(Student), 2011
- CAN T., Reconstructing signaling pathways from RNAi data using genetic algorithms, Postgraduate, E.SERDAR(Student), 2011
- CAN T., Identification of functionally orthologous protein groups in different species based on protein network alignment, Postgraduate, Ö.NEBİL(Student), 2010

CAN T., A distributed graph mining framework based on mapreduce, Postgraduate, S.ALKAN(Student), 2010

CAN T., A 3D topological tracking system for augmented reality, Postgraduate, M.ERCAN(Student), 2010

CAN T., A new approach for better load balancing of visibility detection and target acquisition calculations, Postgraduate, A.YİĞİT(Student), 2010

CAN T., A script based modular game engine framework for augmented reality applications, Postgraduate, M.FURKAN(Student), 2009

CAN T., Multi-resolution visualization of large scale protein networks enriched with gene ontology annotations, Postgraduate, S.YAŞAR(Student), 2009

CAN T., Prediction of protein-protein interactions from sequence using evolutionary relations of proteins and species, Postgraduate, T.DOĞACAN(Student), 2009

CAN T., Text classification in Turkish marketing domain and context-sensitive ad distribution, Postgraduate, M.ENGİN(Student), 2009

CAN T., Coevolution based prediction of protein-protein interactions with reduced training data, Postgraduate, B.PAMUK(Student), 2009

CAN T., ATALAY M. V., A classification system for the problem of protein subcellular localization, Postgraduate, G.ALAY(Student), 2007

Published journal articles indexed by SCI, SSCI, and AHCI

- I. **Differential expression of mRNA 3'-end isoforms in cervical and ovarian cancers**
Döken D. N., Özgül İ., Köksal Bıçakçı G., Gol K., Can T., Erson Bensen A. E.
Heliyon, vol.9, no.9, 2023 (SCI-Expanded)
- II. **Targeting HIF1-alpha/miR-326/ITGA5 axis potentiates chemotherapy response in triple-negative breast cancer**
Assidicky R., Tokat U. M., Tarman I. O., Saatci O., Ersan P. G., Raza U., Ogul H., Riazalhosseini Y., CAN T., Sahin O.
BREAST CANCER RESEARCH AND TREATMENT, vol.193, no.2, pp.331-348, 2022 (SCI-Expanded)
- III. **A C-term truncated EIF2B γ protein encoded by an intronically polyadenylated isoform introduces unfavorable EIF2B γ -EIF2 γ interactions.**
Circir A., Bicakci G. K., Savas B., Doken D. N., Henden O., Can T., Karaca E., Erson-Bensen A. E.
Proteins, vol.90, no.3, pp.889-897, 2022 (SCI-Expanded)
- IV. **Identification of an mRNA isoform switch for HNRNPA1 in breast cancers**
Erdem M., Ozgul İ., Dioken D. N., Gurcuoglu I., Guntekin Ergun S., Cetin-Atalay R., Can T., Erson-Bensen A. E.
Scientific Reports, vol.11, no.1, 2021 (SCI-Expanded)
- V. **MotifGenie: A Python Application for Searching Transcription Factor Binding Sequences Using ChIP-Seq Datasets.**
Oguztuzun C., Yasar P., Yavuz K., Muyan M., Can T.
Bioinformatics (Oxford, England), vol.37, pp.4238-4239, 2021 (SCI-Expanded)
- VI. **A prelude to the proximity interaction mapping of CXXC5**
Ayaz G., Turan G., OLGUN Ç. E., Kars G., Karakaya B., Yavuz K., Demiralay O. D., CAN T., MUYAN M., Yasar P.
SCIENTIFIC REPORTS, vol.11, no.1, 2021 (SCI-Expanded)
- VII. **A CpG island promoter drives the CXXC5 gene expression**
Yasar P., Kars G., Yavuz K., Ayaz G., Oguztuzun C., Bilgen E., Suvaci Z., Cetinkol Ö., CAN T., MUYAN M.
SCIENTIFIC REPORTS, vol.11, no.1, 2021 (SCI-Expanded)
- VIII. **JOA: Joint Overlap Analysis of multiple genomic interval sets**
Otlu B., Can T.
BMC BIOINFORMATICS, vol.20, 2019 (SCI-Expanded)
- IX. **Alternative Polyadenylation Patterns for Novel Gene Discovery and Classification in Cancer**
BEGIK O., ÖYKEN M., ALICAN T. C., CAN T., Erson-Bensen A. E.
NEOPLASIA, vol.19, no.7, pp.574-582, 2017 (SCI-Expanded)
- X. **A multiplex primer design algorithm for target amplification of continuous genomic regions**

- OZTURK A. R., CAN T.
BMC BIOINFORMATICS, vol.18, 2017 (SCI-Expanded)
- XI. **Comparison of tissue/disease specific integrated networks using directed graphlet signatures**
Sonmez A. B., Can T.
BMC BIOINFORMATICS, vol.18, 2017 (SCI-Expanded)
- XII. **SUMONA: A supervised method for optimizing network alignment**
TUNCAY E. G., Can T.
COMPUTATIONAL BIOLOGY AND CHEMISTRY, vol.63, pp.41-51, 2016 (SCI-Expanded)
- XIII. **Alternative Polyadenylation: Another Foe in Cancer**
Erson-Bensan A. E., CAN T.
MOLECULAR CANCER RESEARCH, vol.14, no.6, pp.507-517, 2016 (SCI-Expanded)
- XIV. **3' UTR shortening and EGF signaling: implications for breast cancer**
AKMAN H. B., ÖYKEN M., TUNCER T., CAN T., Erson-Bensan A. E.
HUMAN MOLECULAR GENETICS, vol.24, no.24, pp.6910-6920, 2015 (SCI-Expanded)
- XV. **Reconstruction of the temporal signaling network in Salmonella-infected human cells**
Budak G., Ozsoy O. E., Son Y., Can T., Tunçbağ N.
FRONTIERS IN MICROBIOLOGY, vol.6, 2015 (SCI-Expanded)
- XVI. **The ChEMBL corpus of chemicals and drugs and its annotation principles**
Krallinger M., Rabal O., Leitner F., Vazquez M., Salgado D., Lu Z., Leaman R., Lu Y., Ji D., Lowe D. M., et al.
JOURNAL OF CHEMINFORMATICS, vol.7, 2015 (SCI-Expanded)
- XVII. **Div-BLAST: Diversification of Sequence Search Results**
Eser E., CAN T., Ferhatosmanoglu H.
PLOS ONE, vol.9, no.12, 2014 (SCI-Expanded)
- XVIII. **GPCRsort-Responding to the Next Generation Sequencing Data Challenge: Prediction of G Protein-Coupled Receptor Classes Using Only Structural Region Lengths**
Sahin M. E., Can T., Son Ç. D.
OMICS-A JOURNAL OF INTEGRATIVE BIOLOGY, vol.18, pp.636-644, 2014 (SCI-Expanded)
- XIX. **Identification of Novel Reference Genes Based on MeSH Categories**
Ersahin T., ÇARKACIOĞLU L., CAN T., Konu O., Atalay V., Cetin-Atalay R.
PLOS ONE, vol.9, no.3, 2014 (SCI-Expanded)
- XX. **A Divide and Conquer Approach for Construction of Large-Scale Signaling Networks from PPI and RNAi Data Using Linear Programming**
Ozsoy O. E., Can T.
IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS, vol.10, pp.869-883, 2013 (SCI-Expanded)
- XXI. **Estrogen-induced upregulation and 3'-UTR shortening of CDC6**
AKMAN B. H., CAN T., Erson-Bensan A. E.
NUCLEIC ACIDS RESEARCH, vol.40, no.21, pp.10679-10688, 2012 (SCI-Expanded)
- XXII. **Large-Scale Signaling Network Reconstruction**
Hashemikhabir S., Ayaz E. S., Kavurucu Y., Can T., Kahveci T.
IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS, vol.9, pp.1696-1708, 2012 (SCI-Expanded)
- XXIII. **Using network context as a filter for miRNA target prediction**
Sualp M., Can T.
BIOSYSTEMS, vol.105, pp.201-209, 2011 (SCI-Expanded)
- XXIV. **METADATA MANAGEMENT AND SEMANTICS IN MICROARRAY REPOSITORIES**
Kocabas F., CAN T., BAYKAL N.
BALKAN JOURNAL OF MEDICAL GENETICS, vol.14, no.2, pp.49-63, 2011 (SCI-Expanded)
- XXV. **Bi-k-bi clustering: mining large scale gene expression data using two-level biclustering**
Carkacioglu L., Atalay R. C., KONU KARAKAYALI Ö., Atalay V., CAN T.
INTERNATIONAL JOURNAL OF DATA MINING AND BIOINFORMATICS, vol.4, no.6, pp.701-721, 2010 (SCI-

- Expanded)
- XXVI. **RRW: repeated random walks on genome-scale protein networks for local cluster discovery**
MACROPOL K., Can T., Singh A. K.
BMC BIOINFORMATICS, vol.10, 2009 (SCI-Expanded)
- XXVII. **Integration of topological measures for eliminating non-specific interactions in protein interaction networks**
BAYIR M. A., GUNAY T. D., Can T.
DISCRETE APPLIED MATHEMATICS, vol.157, no.10, pp.2416-2424, 2009 (SCI-Expanded)
- XXVIII. **Discovering functional interaction patterns in protein-protein interaction networks**
Turanalp M. E., Can T.
BMC BIOINFORMATICS, vol.9, 2008 (SCI-Expanded)
- XXIX. **Efficient molecular surface generation using level-set methods**
Can T., Chen C., Wang Y.
JOURNAL OF MOLECULAR GRAPHICS & MODELLING, vol.25, no.4, pp.442-454, 2006 (SCI-Expanded)
- XXX. **Integrating multi-attribute similarity networks for robust representation of the protein space**
Camoglu O., Can T., Singh A. K.
BIOINFORMATICS, vol.22, no.13, pp.1585-1592, 2006 (SCI-Expanded)

Articles Published in Other Journals

- I. **Informatics Olympiads in Turkey Team Selection and Training**
CAN T., SIĞIRCI İ. O., ABUL O., DEMİRCİ M. F.
OLYMPIADS IN INFORMATICS, vol.9, pp.225-232, 2015 (Peer-Reviewed Journal)

Books & Book Chapters

- I. **Introduction to Bioinformatics**
CAN T.
in: miRNomics MicroRNA Biology and Computational Analysis, Yousef Malik, Allmer Jens, Editor, Springer Protocols, pp.51-71, 2013

Refereed Congress / Symposium Publications in Proceedings

- I. **Transcription Elongation in Connection to 3'UTR Ends**
ÖZGÜL İ., CAN T., ERSON BENSAN A. E.
Moleküler Biyoloji Kongresi MolBiyokON18, İzmir, Turkey, 5 - 08 September 2018, pp.20
- II. **Deregulated APA and cancer specific APA isoforms**
Begik O., Ercan M., Cingoz H., CAN T., ÖYKEN M., Erson-Bensan A. E.
Annual Meeting of the American-Association-for-Cancer-Research (AACR), Illinois, United States Of America, 14 - 18 April 2018, vol.78
- III. **Alternative Polyadenylation patterns for cancer classification**
BEGİK O., ÖYKEN M., ÇINKILLI t., CAN T., ERSON BENSAN A. E.
HIBIT 2017, 28 - 30 June 2017
- IV. **Alternative Polyadenylation patterns for novel gene discovery and classification in cancer**
BEĞİK O., ÖYKEN M., CAN T., ERSON BENSAN A. E.
Annual Meeting of the RNA Society, 30 May - 03 June 2017
- V. **APA isoform diversity in triple negative breast cancers**
AKMAN TUNCER H. B., ÖYKEN M., AĞUŞ H. H., ERDEM M., YAVUZ E., CAN T., ERSON BENSAN A. E.

AACR Annual Meeting, USA, Washington, United States Of America, 1 - 05 April 2017, vol.77, pp.3374

- VI. **Identification of a potential cancer related lncRNA**
BEĞİK O., cinkilli t., ÖYKEN M., CAN T., ERSON BENSAN A. E.
Functional Genomics to Systems Biology-EMBO, 12 - 15 November 2016
- VII. **Comparison of tissue disease specific integrated networks using directed graphlet signatures**
SÖNMEZ A. B., CAN T.
Proceedings of the 7th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics - BCB '16, Seattle, WA, USA, United States Of America, 2 - 05 October 2016
- VIII. **3 UTR Length Changes In Connection With Estrogen Receptor Alpha In Breast Cancer**
ÖYKEN M., CAN T., ERSON BENSAN A. E.
FEBS 2016, KUSADASI, Turkey, 3 - 08 September 2016
- IX. **3 ' UTR lengths change in connection with estrogen receptor-alpha in breast cancer**
ÖYKEN M., CAN T., Erson-Bensan A. E.
41st FEBS Congress on Molecular and Systems Biology for a Better Life, Kusadasi, Turkey, 3 - 08 September 2016, vol.283, pp.207
- X. **Unsupervised identification of redundant domain entries in InterPro database using clustering techniques**
RİFAİOĞLU A. S., DOĞAN T., CAN T.
6th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics, BCB 2015, Georgia, United States Of America, 9 - 12 September 2015, pp.505-506
- XI. **Reconstruction of the Temporal Signaling Network in Salmonella Infected Human Cells**
güngör b., EREN ÖZSOY Ö., AYDIN SON Y., CAN T., nurcan t.
23rd Annual International Conference on Intelligent Systems for Molecular Biology and the 14th European Conference on Computational Biology (ISMBECCB'2015), Dublin, Ireland, 10 - 14 July 2015
- XII. **Dbchem A database query based solution for the chemical compound and drug name recognition task**
ATA Ç., CAN T.
Proceedings of the Fourth BioCreative Challenge Evaluation Workshop, BioCreative IV,, 1 - 03 October 2013, vol.2, pp.42-46
- XIII. **M4B: A novel method for designing and ordering of the genetic devices**
Hashemikhabir S., Ersoy G., Oguz G., Yaldiz B., Tuncel Y., Budak G., Karaaslan S., AYDIN SON Y., CAN T.
2012 7th International Symposium on Health Informatics and Bioinformatics, HIBIT 2012, Cappadocia, Turkey, 19 - 22 April 2012, pp.123-127
- XIV. **Parallel SPiCi**
Hashemikhabir S., CAN T.
6th International Symposium on Health Informatics and Bioinformatics (HIBIT), İzmir, Turkey, 2 - 05 May 2011, pp.86-90
- XV. **CONSTRUCTING SIGNALING PATHWAYS FROM RNAI DATA USING GENETIC ALGORITHMS**
Ayaz E. S., CAN T.
6th International Symposium on Health Informatics and Bioinformatics (HIBIT), İzmir, Turkey, 2 - 05 May 2011, pp.95-98
- XVI. **The effect of representative training dataset selection on the classification performance of the promoter sequences**
YAMAN A. G., CAN T.
6th International Symposium on Health Informatics and Bioinformatics, HIBIT 2011, İzmir, Turkey, 2 - 05 May 2011, pp.55-58
- XVII. **Coevolution based prediction of protein-protein interactions with reduced training data**
Pamuk B., CAN T.
2010 5th International Symposium on Health Informatics and Bioinformatics, HIBIT 2010, Antalya, Turkey, 20 - 22 April 2010, pp.187-193
- XVIII. **Text Classification in the Turkish Marketing Domain for Context Sensitive Ad Distribution**

Engin M., Can T.

24th International Symposium on Computer and Information Sciences, Güzelyurt, Cyprus (Kktc), 14 - 16 September 2009, pp.105-110

XIX. Human Skeletal and Muscle Deformation Animation Using Motion Capture Data

Bayer A. O., Sevinc A. M., CAN T.

16th International Conference in Central Europe on Computer Graphics, Visualization and Computer Vision, Plzen, Czech Republic, 4 - 07 February 2008, pp.167-168

XX. Analysis of protein-protein interaction networks using random walks

Can T., Orhan Ç., Singh A. K.

5th International Workshop on Bioinformatics, BIOKDD 2005 - In Conjunction with 11th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining, KDD 2005, Chicago, IL, United States Of America, 21 August 2005, pp.61-68

XXI. CTSS: A robust and efficient method for protein structure alignment based on local geometrical and biological features

Can T., WANG Y.

2nd International Computational Systems Bioinformatics Conference, California, United States Of America, 11 - 14 August 2003, pp.169-179

Supported Projects

MUYAN M., DEMİRALAY Ö. D., CAN T., Project Supported by Higher Education Institutions, Genom Düzeyindeki Protein Bağlanma Verilerinin Biyoinformatik ve Deneysel Yöntemlerle Analizi, 2021 - 2022

ERSON BENSAN A. E., GÜLEZ B., BANERJEE S., ÖZKAN S., CAN T., Project Supported by Higher Education Institutions, Yaygın kanser tiplerinde transkriptom 3'UTR isoform çeşitliliğinin incelenmesi, 2017 - 2019

CAN T., Project Supported by Higher Education Institutions, G-Proteini Kenetli Reseptörlerin Etkileşimleri:hesaplamalı Yöntemlerin Ve Deneysel Çalışmaların Sentezlenmesi, 2010 - 2019

SON Ç. D., ÇELEBİ M., CAN T., Project Supported by Higher Education Institutions, G-proteine kenetli reseptörlerin etkileşim bölgelerinin işlemsel olarak 3D modellenmesi, 2017 - 2017

MUYAN M., ERSON BENSAN A. E., CAN T., Project Supported by Higher Education Institutions, Meme Kanseri Model Hücrelerinde Tüm Genom Düzeyinde RNA Ekspresyon Analizleri, 2015 - 2016

ERSON BENSAN A. E., ozdemir n., CAN T., Project Supported by Higher Education Institutions, CDC6 alternatif poliadenilasyonunun meme kanseri hücrelerinde incelenmesi, 2013 - 2015

Patent

CAN T., APADetect: Alternatif Poliadenilasyon Tespiti, Patent, CHAPTER G Physics, Standard Registration, 2016

Metrics

Publication: 53

Citation (WoS): 654

Citation (Scopus): 694

H-Index (WoS): 12

H-Index (Scopus): 14

Non Academic Experience

METU

METU

University of California, Santa Barbara

University of California, Santa Barbara

METU