Can Alkan

CONTACT INFORMATION

Department of Computer Engineering
Bilkent University
Engineering Building, EA 509
Bilkent, Ankara 06800
Turkey

Fax: (+90) 312-266-4047
E-mail: calkan@cs.bilkent.edu.tr
Web: http://www.alkanlab.org
ORCID: 0000-0002-5443-0706
ResearcherID: D-2982-2009

RESEARCH INTERESTS

Combinatorial algorithms for the analysis of next-generation sequencing data, genomic structural variation, human and primate segmental duplications.

EXPERIENCE

Department of Computer Engineering, Bilkent University, Bilkent, Ankara, Turkey
Assistant Professor **January 2012 - present**

Seven Bridges Genomics, Cambridge, MA, United States
Visiting Scholar **September 2018 - February 2019**

Department of Computer Science, ETH Zürich, Zürich, Switzerland
Visiting Professor (on sabbatical) **February - July 2018**

Department of Genome Sciences, University of Washington, Seattle, Washington, USA
Acting Assistant Professor **June 2011 - December 2011**
Senior Fellow **October 2005 - May 2011**

School of Computing Science, Simon Fraser University, Burnaby, British Columbia, Canada
Visiting Researcher **January, 2004 - September 2005**

EDUCATION

University of Washington, Seattle, Washington, USA
Department of Genome Sciences and Howard Hughes Medical Institute

Postdoctoral Fellow, Genomics, October 2005 - December 2011

- Worked on computational methods to reconstruct the evolutionary history of alpha-satellite DNA, *de novo* alphoid sequence prediction from whole-genome shotgun sequence data, and detection of human structural variation and segmental duplications using next-generation sequencing technologies.
- Advisor: Evan E. Eichler

Case Western Reserve University, Cleveland, Ohio, USA
Department of EECS

Ph.D., Computer Science, August 2005

- Dissertation Topic: "Computational Studies on Evolution and Functionality of Genomic Repeats"
- Advisor: S. Cenk Şahinalp

Bilkent University, Ankara, Turkey
Department of Computer Engineering

B.Sc., Computer Science, May, 2000

Honors and Awards

- TÜBİTAK Incentive Award, 2015.
- Thomson Reuters Highly Cited Researcher, 2014, 2018.
- Young Investigator Award (BAGEP), Science Academy of Turkey, 2013.
- AAAS Newcomb Cleveland Prize for the Most Outstanding Paper Published in Science, American Association for the Advancement of Science, USA, 2010.

Professional Memberships

- International Society for Computational Biology
- Association for Computing Machinery and SIGBio
- IEEE Computer Society and TCuArch

Research Grants

Previous

- Scientific and Technical Research Council of Turkey (TÜBİTAK-2546-115E596), 2017-2019
  Title: BacGenTrack – an integrated system for bacterial genome tracking using high throughput sequencing technology: from identification to visualization.
  Goal: Developing a user-friendly web system and novel analysis algorithms needed to facilitate the analysis and provide the essential data sharing tools necessary for its effective use in the field of molecular epidemiology
  PI: Can Alkan and Joao Andre Carriço
- European Molecular Biology Organization Installation Grant (IG-2521), 2013-2018
  Title: Development and application of computational methods to analyze next generation sequence data to characterize both normal and disease causing variation, and build de novo genome assemblies.
  Goal: Analysis of biological sequences generated with the next-gen sequencing platforms.
  PI: Can Alkan
- Scientific and Technical Research Council of Turkey (TÜBİTAK-1001-215E172), 2016-2018
  Title: Algorithms for structural variation discovery using hybrid sequencing technologies and library preparation protocols.
  Goal: Discovery and characterization of structural variants using multiple sequencing platforms, linked-reads, and read clouds.
  PI: Can Alkan
- Scientific and Technical Research Council of Turkey (TÜBİTAK-1001-214Z130), 2015-2018
  Elucidating the mechanisms of sequential trastuzumab/T-DM1 resistance in in vitro and in vivo models of HER-2 overexpressing breast cancer.
  Goal: Unraveling molecular mechanisms of acquired T-DM1 resistance in trastuzumab resistant breast cancer models and to regain T-DM1 sensitivity. I served as a researcher for the bioinformatics components of this project.
  PI: Özgür Şahin
- Scientific and Technical Research Council of Turkey (TÜBİTAK-1001-115O391), 2015-2018
  Title: *de novo* genome sequencing and identification of genes involved in biotic-abiotic stress of wild beet species (Beta Corolliflora and Beta Procumbens), and cloning several genes activated in drought.
  Goal: Analysis of beet genomes. I served as a consultant for this project for the *de novo* assembly work package.
  PI: Ali Ergül
- Scientific and Technical Research Council of Turkey (TÜBİTAK-1001-114Z927), 2015-2017
  Title: Characterization of Central Anatolian Neolithic populations by ancient DNA extraction and genome sequencing of individuals from Tepecik-Çiftlik (Niğde) and Çatalhöyük (Konya).
  Goal: Ancient DNA analysis of Neolithic populations. I served as a bioinformatics consultant for this project.
  PI: Mehmet Somel

- Scientific and Technical Research Council of Turkey (TÜBİTAK-1001-215S364), 2015-2017
  Title: Identifying and targeting sponge long non-coding RNAs to inhibit metastasis in triple negative breast cancer using a systems biology approach.
  Goal: Delineating the mRNA-miRNA-lncRNA regulatory network controlling metastatic progression in TNBC. I served as a researcher for the bioinformatics components of this project.
  PI: Özgür Şahin
- National Institutes of Health (R01 HG006004), 2011-2016
  Title: Novel algorithms and hardware designs for ultra-fast next-gen sequence analysis.
  Goal: Developing specialized hardware architectures to accelerate mapping reads generated with the high throughput sequencing platforms.
  PI: Onur Mutlu
  Co-PI: Can Alkan
- European Union Marie Curie Actions Career Integration Grant (PCIG10-GA-2011-303772), 2012-2016
  Title: Integrated approaches for genomic variation discovery using high throughput sequencing.
  Goal: Developing novel combinatorial algorithms to comprehensively and quickly discover genomic variation.
  PI: Can Alkan
- Scientific and Technical Research Council of Turkey (TÜBİTAK-1001-112E135), 2012-2016
  Title: Development and application of novel genome assembly algorithms that use multiple data sources.
  Goal: Developing assembly algorithms to more reliably construct de novo genome assemblies using data from multiple sources.
  PI: Can Alkan
- National Institutes of Health (U01 HG0052209), 2009-2012
  Title: Structural Genomic Variation Analysis for the 1000 Genomes Project.
  Goal: Develop computational methods to mine structural variation data from the 1000 Genomes. As part of the consortium, I was involved in testing paired-end read approaches to detect insertions and deletions as a postdoctoral fellow at the Eichler Lab.
  PI: Charles Lee

Students and Interns (Current)

Ph.D.

- **Fatma Kahveci:** Ph.D. student, Computer Engineering, Fall 2014 - present. Bilkent University.

M.Sc.

- **Alim Şükrü Gökkaya:** M.Sc. student, Computer Engineering, Spring 2017 - present. Bilkent University.
- **Ezgi Ebren:** M.Sc. student, Computer Engineering, Summer 2017 - present. Bilkent University.
- **Zülal Bingöl:** M.Sc. student, Computer Engineering, Fall 2017 - present. Co-supervisor: Özcan Öztürk. Bilkent University.
- **Mete Han Kahraman:** M.Sc. student, Computer Engineering, Fall 2019 - present. Bilkent University.

Undergraduate Volunteers

- **Aldo Tali:** B.Sc. student in Computer Engineering, Bilkent University. Since Fall 2019.
- **Banu Cavlak:** B.Sc. student in Computer Engineering, Bilkent University. Since Summer 2019.
- **Naisila Puka:** B.Sc. student in Computer Engineering, Bilkent University. Since Spring 2019.

Students and Interns (Alumni)

Ph.D.

- **Arda Söylev:** Ph.D., Computer Engineering, Fall 2018. Bilkent University.
  "Algorithms for structural variation discovery using multiple sequence signatures"
  now: Assistant professor at Konya Food and Agriculture University.
- **Mohammed Alser:** Ph.D., Computer Engineering, Summer 2018. Bilkent University.
  Co-supervisor: Onur Mutlu.
  "Accelerating the understanding of life's code through better algorithms and hardware design"
  now: Postdoctoral Fellow at ETH Zürich.
- **Pınar Kavak:** Ph.D., Computer Engineering, Spring 2017. Boğaziçi University. Co-supervised with Tunga Güngör.
  "Developing new approaches for multi-platform and multi-individual genomic sequence assembly"
  now: Software engineer at Splunk Inc., Vancouver, BC, Canada

M.Sc.

- **Emre Doğru:** M.Sc. student, Computer Engineering, Summer 2019. Bilkent University. *started the program in Spring 2016 under the supervision of Prof. Cevdet Aykanat.*
  "Paralog specific gene copy number discovery within segmental duplications"
  now: Researcher at TÜBİTAK BİLGEM.
- **Halil İbrahim Özercan:** M.Sc., Computer Engineering, Summer 2019. Bilkent University.
  "A cryptocurrency incentivized voluntary grid computing platform for DNA read alignment"
  now: Software Engineer, Opsgenie at Atlassian.
- **Balanur İçen:** M.Sc., Computer Engineering, Summer 2019. Bilkent University. *started the program in Fall 2016 under the supervision of Assoc. Prof. Selim Aksoy.*
  "Breakpoint refinement of genomic structural variation using split read analysis"
- **Fatih Karaoğlanoğlu:** M.Sc., Computer Engineering, Summer 2018. Bilkent University.
  "Characterization of large structural variation using Linked-Reads"
  now: Ph.D. student at Simon Fraser University.
- **F. Tuğba Doğan:** M.Sc., Computer Engineering, Spring 2018. Bilkent University.
  "High Throughput UDP-based Peer-to-Peer Secure Data Transfer"
- **Can Fırtına:** M.Sc., Computer Engineering, Fall 2017. Bilkent University.
  "Assessment and correction of errors in DNA sequencing technologies"
  now: Ph.D. student at ETH Zürich.
- **Gülfem Demir:** M.Sc., Computer Engineering, Spring 2017. Bilkent University.
  "Characterization of short tandem repeats using local assembly"
  now: software engineer at Facebook.
- **Azita Nouri:** M.Sc., Computer Engineering, Spring 2016. Bilkent University.
  "Read mapping methods optimized for multiple GPGPUs"
  now: Ph.D. student at Rutgers University.
- **Marzieh Eslami Rasekh:** M.Sc., Computer Engineering, Spring 2015. Bilkent University.
  "Algorithms for the discovery of large genomic inversions using pooled clone sequencing"
  now: Ph.D. student at Boston University.
- **Elif Dal:** M.Sc., Computer Engineering, Fall 2014. Bilkent University.
  "Genome scaffolding using pooled clone sequencing"
  now: software engineer at HAVELSAN.
- **Fatma Kahveci (née Balcı):** M.Sc., Computer Engineering, Spring 2014. Bilkent University.
  "Bias correction in finding copy number variation using read depth based methods in exome sequencing data"
  now: Ph.D. student at Bilkent University.
- **Mustafa Korkmaz:** M.Sc., Computer Engineering, Fall 2012. Bilkent University.
  Co-supervised with Cevdet Aykanat.
  "Massively parallel mapping of next generation sequence reads using GPU"
  last seen: Ph.D. student at University of Waterloo.

Undergraduate volunteers

- **Figali Taho:** B.Sc. student in Computer Engineering, Bilkent University. Fall 2017 - Spring 2018. *now: M.Sc. student at Simon Fraser University.*
- **Baraa Orabi:** B.Sc. student in Computer Engineering, Bilkent University. Spring 2016 - Summer 2017. *now: M.Sc. student at Simon Fraser University.*
- **Ezgi Ebren:** B.Sc. student in Computer Engineering, Bilkent University. Summer 2016 - 2017.
- **Abdullah Alperen:** B.Sc. student in Computer Engineering, Bilkent University. Spring 2015 - 2017. *now: Ph.D. student at Michigan State University.*
- **Halil İbrahim Özercan:** B.Sc. student in Computer Engineering, Bilkent University. Fall 2015 - Spring 2016.
- **Ayhun Tekat:** B.Sc. student in Computer Engineering, Bilkent University. Summer 2015.
- **Damla Şenol:** B.Sc. student in Computer Engineering, Bilkent University. Spring 2015. *now: Ph.D. student at Carnegie Mellon University.*
- **Can Fırtına:** B.Sc. student in Computer Engineering, Bilkent University. Spring 2015.
- **Atalay Mert İleri:** B.Sc. student in Computer Engineering, Bilkent University. 2014. *now: Ph.D. student at MIT.*
- **Gülfem Demir:** B.Sc. student in Computer Engineering, Middle East Technical University. 2013-2014. *now: software engineer at Facebook.*
- **Can Koçkan:** B.Sc. student in Computer Engineering, Bilkent University. 2012-2014. *last seen: Ph.D. student at Indiana University.*
- **Yiğit Küçük:** B.Sc. student in Computer Engineering, Bilkent University. 2012-2014. *last seen: Ph.D. student at Case Western Reserve University.*
- **Serhat Kıyak:** B.Sc. student in Computer Engineering, Bilkent University. 2013-2014. *last seen: software engineer at Microsoft.*

Undergraduate Students in the Introduction to Research course

- **Ayşe Berceste Dinçer:** Discovery of large inversions using hybrid sequencing technologies, Fall 2016.
- **Can Fırtına:** Fast filters for pairwise comparison of short and long NGS reads, Spring 2015.
- **Damla Şenol:** Transmission patterns discovery of genome structural variations among generations of a family, Spring 2015.
- **Atalay Mert İleri:** ScienceCoin: a cryptocurrency with DNA sequence alignment as proof-of-work, Spring 2014.

Others

- **Shatlyk Asyralyyev:** Ph.D. student, Computer Engineering, Fall 2013 - 2016. Bilkent University. Co-supervised with Cevdet Aykanat. Left the program in Fall 2016.
- **Dilek Genç:** M.Sc. student, Computer Engineering, Fall 2015. Bilkent University. Left the program in Spring 2016.
- **Farnush Farhadi:** Intern between July to September 2014 at Bilkent.
- **Vineet Bhakhar:** Intern between May to July 2014 at Bilkent.
- **Farhad Hormozdiari:** Research Scientist at the Eichler Lab between February to September 2010. *last seen: Postdoctoral fellow at Harvard University.*
- **Sònia Casillas:** Visiting scientist at the Eichler Lab between February to July 2011.
- **Michael Duyzend:** Rotation student at the Eichler Lab between June to August 2010. *last seen: Resident Physician at Boston Children's Hospital.*
- **Pietro D'Addabbo:** Visiting scientist at the Eichler Lab between August to November 2009. *last seen: Staff scientist at University of Bari.*

- **Peter H. Sudmant:** Ph.D. student at the Eichler Lab between May 2009 to December 2011. *last seen: Postdoctoral Fellow at Massachusetts Institute of Technology.*
- **Jacob O. Kitzman:** Rotation student at the Eichler Lab between January to April 2009. *last seen: Assistant Professor at University of Michigan.*
- **Iman Hajirasouliha:** Intern UW between February to July 2009 at UW. *now: Assistant Professor at Weill Cornell Graduate School of Medical Sciences.*
- **Fereydoun Hormozdiari:** Intern between February to July 2008 at UW. *now: Assistant Professor at University of California, Davis.*
- **Kerry Hall:** Intern at UW in 2006.

Thesis Committees (Current)

Ph.D.

- **Dilek Koptekin**: Ph.D., Molecular Biology and Genetics, Since Spring 2019. Advisor: Mehmet Somel. Middle East Technical University.

Thesis Committees (Past)

Ph.D.

- **Gülden Olgun:** Ph.D., Computer Engineering, Summer 2019. Advisor: Öznur Taştan Okan, Ercüment Çiçek. Bilkent University.
- **Fahrettin Can Koyuncu:** Ph.D., Computer Engineering, Fall 2018. Advisor: Çiğdem Gündüz Demir. Bilkent University.
- **Abdullah Atmaca:** Ph.D., Computer Engineering, Summer 2018. Advisors: Yavuz Oruç and Cevdet Aykanat. Bilkent University.
- **Arif Yılmaz:** Ph.D., Bioinformatics, Spring 2018. Advisor: Yeşim Aydın Son. Middle East Technical University.
- **Burçak Otlu:** Ph.D., Computer Engineering, Spring 2017. Advisor: Tolga Can. Middle East Technical University.
- **Evrim Tekeli:** Ph.D., Anthropology, Spring 2017. Advisor: Timur Gültekin. Ankara University.
- **Onur Baloğlu:** Ph.D. candidate, Biology, since Fall 2015 - Spring 2018. I left the committee in Spring 2018. Advisor: Mehmet Somel. Middle East Technical University.
- **Daria Iakovishina:** Ph.D., Bioinformatics, November 2015. Advisor: Valentina Boeva. École Polytechnique, Palaiseau, France. *last seen: CEO at Ksivalue, Moscow, Russia*
- **Yogesh Paudel:** Ph.D., Biostatistics and Informatics, January 2015. Advisor: Martien A.M. Groenen. Institut für Biostatistik und Informatik in Medizin und Alternsforschung, Wageningen University, Wageningen, The Netherlands. *last seen: Postdoc at Roche Pharmaceuticals, Basel, Switzerland.*
- **Gülşah Merve Dal:** Ph.D., Molecular Biology and Genetics, Fall 2014. Advisor: Tayfun Özçelik. Bilkent University. *last seen: Postdoctoral fellow at Department of Biology, Middle East Technical University.*
- **Özlem Tufanlı:** Ph.D. candidate, Molecular Biology and Genetics, since Fall 2013 - Spring 2015. I left the committee in Spring 2015. Advisor: Ebru Erbay. Bilkent University.

M.Sc.

- **Zahit Saygın Doğu:** M.Sc., Computer Engineering, Summer 2019. Advisor: Cevdet Aykanat. Bilkent University. **Gizem Çaylak:** M.Sc., Computer Engineering, Summer 2019. Advisor: Ercüment Çiçek. Bilkent University.
- **Halil İbrahim Kuru:** M.Sc., Computer Engineering, Spring 2019. Advisor: Öznur Taştan Okan, Ercüment Çiçek. Bilkent University.
- **Simge Yücel:** M.Sc., Computer Engineering, Fall 2018. Advisor: Çiğdem Gündüz Demir. Bilkent University.
- **M. Yağmur Şahin:** M.Sc. Computer Engineering, Fall 2016. Advisor: Buğra Gedik. Bilkent University.

- **Mona Shojaei:** M.Sc. Bioinformatics, Summer 2016. Advisor: Rengül Çetin Atalay. Middle East Technical University Informatics Institute.
- **Melike Dönertaş:** M.Sc. Biology, Spring 2016. Advisor: Mehmet Somel. Middle East Technical University.
- **Doğukan Çağatay:** M.Sc. Computer Engineering, Fall 2015. Advisor: Buğra Gedik. Bilkent University.
- **Gülsüm Ece Ekşi:** M.Sc. Computer Engineering, Fall 2015. Advisor: Bedir Tekinerdoğan. Bilkent University.
- **Onur Özdemir:** M.Sc. Computer Engineering, Fall 2015. Advisor: Bedir Tekinerdoğan. Bilkent University.
- **Havva Gülay Gürbüz:** M.Sc. Computer Engineering, Summer 2014. Advisor: Bedir Tekinerdoğan. Bilkent University. *last seen: Software Development Engineer at Microsoft, Redmond, WA, USA.*
- **Mehmet Başaran:** M.Sc. Computer Engineering, Fall 2014. Advisor: Cevdet Aykanat. Bilkent University. *last seen: Ph.D. student at Bilkent University.*
- **Merve Çakır:** M.Sc. Computer Engineering, Spring 2013. Advisor: Uğur Doğrusöz. Bilkent University. *last seen: Ph.D. student at Duke University, Durham, NC, USA.*
- **Fahrettin Can Koyuncu:** M.Sc. Computer Engineering, Fall 2012. Advisor: Çiğdem Gündüz Demir. Bilkent University.

Academic Service

University Duties

- Academic Coordinator for Erasmus+ and International Exchange Programs, Department of Computer Engineering, Bilkent University, since Summer 2014.

Editorial & Program Committees

- **Steering Committee Member**, RECOMB Workshop on Massively Parallel Sequencing (RECOMB-Seq), 2017-*present*.
- **Organization Committee Member**, ISCB COSI for High Throughput Sequencing and Applications (HiTSeq), 2016-*present*.
- **Associate Editor**, BMC Bioinformatics, 2010-*present*.
- **Track and Area co-chair**, Annual International Conference on Intelligent Systems for Molecular Biology and the European Conference on Computational Biology (ISMB-ECCB)
  - ISMB-ECCB 2019 (Basel, Switzerland), ISMB 2018 (Chicago, IL, USA), ISMB-ECCB 2017 (Prague, Czech Republic), ISMB 2016 (Orlando, FL, USA)
- **Chair**, First Annual RECOMB Workshop on Massively Parallel Sequencing (RECOMB-seq), March 26-27, 2011, Vancouver, BC, Canada.
- **PC Member**, Annual International Conference on Research in Computational Molecular Biology (RECOMB)
  - RECOMB 2020 (Padova Italy), RECOMB 2019 (Washington, DC, USA), RECOMB 2016 (Santa Monica, CA, USA), RECOMB 2011 (Vancouver, Canada)
- **PC Member**, Annual RECOMB Workshop on Massively Parallel Sequencing (RECOMB-Seq)
  - RECOMB-Seq 2018 (Paris, France), RECOMB-Seq 2017 (Hong Kong), RECOMB-Seq 2013 (Beijing, China), RECOMB-Seq 2012 (Barcelona, Spain)
- **PC Member**, Annual International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB-ECCB)
  - ISMB-ECCB 2015 (Dublin, Ireland), ISMB 2014 (Boston, MA, USA), ISMB 2013 (Berlin, Germany), ISMB 2012 (Long Beach, CA, USA), ISMB-ECCB 2011 (Vienna, Austria), ISMB 2010 (Boston, MA, USA)

- **PC Member**, Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq)
  - ◇ HiTSeq 2015 (Dublin, Ireland)
- **PC Member**, HPCA Workshop on Accelerator Architecture in Computational Biology and Bioinformatics (AACBB)
  - ◇ AACBB 2018 (Vienna, Austria)
- **PC Member**, ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)
  - ◇ ACM-BCB 2019 (Niagara Falls, NY, USA), ACM-BCB 2017 (Boston, MA, USA).
- **PC Member**, International Symposium on Health Informatics and Bioinformatics (HIBIT)
  - ◇ HIBIT 2017 (Güzelyurt, Northern Cyprus), HIBIT 2013 (Ankara, Turkey)
- **PC Member**, Next Generation Sequencing Conference (NGS)
  - ◇ NGS 2017 (Barcelona, Spain)
- **PC Member**, International Conference on Algorithms for Computational Biology (AlCoB)
  - ◇ AlCoB 2019 (Berkeley, CA, USA), AlCob 2017 (Aveiro, Portugal), AlCoB 2016 (Trujillo, Spain)
- **Session Chair**, 12^{th} National Medical Genetics Congress, Çeşme, Turkey, October 7, 2016.
- **Co-Chair**, Bertinoro Computational Biology Meeting, June 14-17, 2015, Bertinoro, Italy.
- **Session Co-Chair**, Session on Personal Genomics at the Pacific Symposium for Biocomputing (PSB)
  - ◇ PSB 2011 (Big Island of Hawaii, USA), PSB 2010 (Big Island of Hawaii, USA)
- **PC Member**, The IEEE International Conference on Advanced Information Networking and Applications (AINA)
  - ◇ AINA 2008 (Okinawa, Japan), AINA 2007 (Niagara Falls, Canada)

Scientific Advisory Boards

- Prototype Capital, Los Angeles, CA, United States. 2018 - *present*.
- Turkish Institutes of Health (TÜSEB), Ankara, Turkey. 2016 -2019.
- Center for Advanced Genomics and Bioinformatics (İGBAM) in TÜBİTAK Marmara Research Center, Gebze, Turkey. 2012 - 2014.

Consortium Memberships

- 1000 Genomes Project Structural Variation Analysis Group, 2008-2015, 2019-*present*.
- Bonobo Genome Consortium, 2008-2012.
- Orangutan Genome Consortium, 2008-2011.
- Neandertal Genome Consortium, 2009-2012.
- Gorilla Genome Consortium, 2009-2013.
- Denisovan Genome Consortium, 2010-2012.
- Great Ape Diversity Project, 2011-2014.
- Genome in a Bottle Consortium, 2015-*present*

Ad-hoc Reviewer

- Nature Genetics, Nucleic Acids Research, Nature Reviews Genetics, Genome Research, PLoS Genetics, PLoS Computational Biology, Nature Biotechnology, BMC Genomics, Genome Biology, Methods, Transactions of Computational Biology and Bioinformatics, Bioinformatics, Briefings in Bioinformatics, RECOMB, RECOMB-seq, SODA, FOCS, ICDE, CPM, AINA, PSB, ISMB, HiTSeq.

Teaching

- CS 476 Automata Theory and Formal Languages, Fall 2014, 2015, 2016, 2017; Spring 2014, 2015, 2016, 2017, 2019.
- CS 481 Bioinformatics Algorithms, Fall 2012, 2013, 2016, 2017, 2019.
- CS 319 Object Oriented Software Engineering, Summer 2012; Spring 2013; Fall 2013, 2014, 2015.
- CS 681 Advanced Topics in Computational Biology, Spring 2012, 2013, 2019.
- CS 202 Fundamental Structures of Computer Science II, Spring 2013.
- CS 590/690 Research Topics (coordinator), Spring 2012, 2014, 2019.

Senior Project Supervision

- LIBRA: Integrated web-based system to aid diagnosis using clinical sequencing, 2019-*present*.
- Pengout: Mobile application to find events and organize group outings, 2019-*present*.
- CryptDist: Content distribution network using the blockchain technology, 2016-2017.
- Espionage Game: Stealth game with adaptive artificial intelligence, 2015-2016.
- BioPeer: Secure research data sharing platform, 2014-2015.
- Coinami: Cryptocurrency mining system for scientific computation, 2014-2015.
- Anotice: Anonymized social network platform, 2014-2015.
- Touravel: Travel logging application, 2014-2015.
- SUN (Social University Network): Study group game application, 2014-2015.
- SmartVote: Electronic Voting System for Mobile Devices, 2013-2014.
  Recipient of the Best Senior Project Award in 2014.
- Daycept: Concept-based idea sharing platform, 2013-2014.
- Betcha: Social platform that enables betting among friends, 2013-2014.
  Recipient of the Usability Award in 2014.
- SocioDiary: Digital diary system, 2013-2014.
- CMPS101: Activity planning for university students, 2013-2014.
- chkDNA: Genomic variant analysis tool, 2012-2013.

Other

- Individual Member, Global Alliance for Genomic Health. November 2014 - *present.*
- Observer to ELIXIR for Turkey. 2013 - 2015.

Selected Conference and Invited Talks

Total of 64 invited talks, seminars, lectures, and keynotes.

- Lecture, **Characterization of genomic structural variation using various sequencing technologies.** Computational Genomics Summer Institute, University of California, Los Angeles, CA, United States, July 19, 2019.
- Invited Speaker, **Population reference graphs – a primer to computational pan-genomics.** Clinical genomics and NGS hybrid course, European School of Genetic Medicine and Acıbadem University, İstanbul, Turkey, April 30, 2019.
- Invited Speaker, **Addressing computational burden for low-priority genome analyses.** HPCA 2018 Workshop On Accelerator Architecture in Computational Biology and Bioinformatics, Vienna, Austria, February 24, 2018.
- Invited Speaker, **Kodlamayan genomu anlamlandırmak.** *(in Turkish)* 12^{th} National Medical Genetics Congress, Çeşme, Turkey, October 6, 2016.
- Invited Speaker, **High throughput sequencing and bioinformatics for characterization of diseases of genomic origin.** 24^{th} Conference of the Asian Pacific Association for the Study of the Liver (APASL 2015), İstanbul, Turkey, March 11, 2015.

- Instructor, **EMBO Practical Course: Computational biology: from genomes to cells and systems.** Cappadocia, Nevşehir, Turkey. September 29 - October 4, 2013.
- Invited Speaker, **Characterization of mobile element insertions using high throughput sequencing.** 63rd Fujihara Seminar: A new horizon of retroposon research, Kyoto, Japan, August 2, 2012.
- Invited Speaker, **Next-generation sequence characterization of complex genome structural variation.** Department of Genetics, Yale University, New Haven, CT, USA, May 11, 2011.
- Invited Speaker, **Dark side of genomes: what is missing in current sequence assemblies?** Genome 10K Project Genome Assembly Workshop, Santa Cruz, CA, USA, March 16, 2011.
- Keynote Speaker, **Structural variation discovery and characterization of segmental Duplications with next-gen sequencing technologies**. Spanish and Portuguese Bioinformatics Conference (Jornadas de Bioinformática), Lisbon, Portugal, November 6, 2009.
- Conference Talk, **RNA-RNA interaction prediction and antisense RNA target search**. Ninth Annual Conference on Research in Computational Molecular Biology (RECOMB 2005), Cambridge, MA, USA, May 14, 2005.

Publications

Journal Publications

Joint first authors are marked with * in case of equal contribution. Joint last authors are marked with ‡.

Discovery of tandem and interspersed segmental duplications using high throughput sequencing. A. Soylev*, T. Le*, H. Amini, **C. Alkan**‡, F. Hormozdiari‡. *Bioinformatics*, Oct 15; 35(20):3923-3930, 2019.

Automatic characterization of copy number polymorphism using high throughput sequencing. **C. Alkan**. *Turkish J. Elec Eng & Comp Sci, in press*, doi: 10.3906/elk-1903-135.

Nanopore sequencing technology and tools for genome assembly: computational analysis of the current state, bottlenecks and future directions. D. Senol Cali, J. Kim, S. Ghose, **C. Alkan**‡, O. Mutlu‡. *Briefings in Bioinformatics*, [epub Apr 2, 2018], Jul; 20(4):1542–1559, 2019.

Characterizing microsatellite polymorphisms using assembly-based and mapping-based tools. G. Demir and **C. Alkan**. *Turkish J. Biol*, 432, 264-273, 2019.

Shouji: Fast and Efficient Computation of Banded Sequence Alignment. M. Alser, H. Hassan, A. Kumar, O. Mutlu‡, **C. Alkan**‡. *Bioinformatics*, [epub Mar 28; doi: 10.1093/bioinformatics/btz234], 2019.

Evaluation of genome scaffolding tools using pooled clone sequencing. E. Dal and **C. Alkan**. *Turkish J. Biol*, 42, 471-476, 2018.

Fast characterization of segmental duplications in genome assemblies. I. Numanagić, A.S. Gökkaya, L. Zhang, B. Berger, **C. Alkan**‡, F. Hach‡. *Bioinformatics*, Sep 1; 34(17): i706-714, 2018.

presented at the 17th European Conference for Computational Biology (ECCB 2018), September 8-12, 2018, Athens, Greece.

Hercules: a profile HMM-based hybrid error correction algorithm for long reads. C. Firtina, Z. Bar-Joseph, **C. Alkan**‡, A.E. Cicek‡. *Nucleic Acids Research*, [epub Aug 16; doi: 10.1093/nar/gky724], 2018.

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Book Chapters

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Note that selected papers accepted to some conferences such as ISMB and RECOMB are published in special issues of journals. Such publications are listed under Journal Publications with a note to the conference above. Joint first authors are marked with * in case of equal contribution. Joint last authors are marked with ‡.

Can you really anonymize the donors of genomic data in today's digital world? M. Alser, N. Almadhoun, A. Nouri, **C. Alkan**‡, and E. Ayday‡. *10^{th} International Workshop on Data Privacy Management (DPM 2015)*, September 21-22, 2015, Vienna, Austria.

Improving genome assemblies using multi-platform sequence data. P. Kavak, B. Ergüner, D. Üstek, B. Yüksel, M.Ş. Sağıroğlu, T. Güngör and **C. Alkan**. *12^{th} Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB 2015)*, September 10-12, 2015, Naples, Italy.

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Discovery of structural variations in ancient genomes. A. Soylev, **C. Alkan**, M. Somel. Twelfth International Symposium on Health Informatics and Bioinformatics (HIBIT), October 17-18, 2019, İzmir, Turkey. *Oral presentation by A. Soylev.*

Characterization of large-scale structural variants using Linked-Reads. F. Karaoglanoglu, C. Ricketts, E. Ebren, M. Eslami Rasekh, I. Hajirasouliha, **C. Alkan**. 27^{th} Annual International Conference Intelligent Systems for Molecular Biology (ISMB/ECCB 2019), *HiTSeq Track*, July 23, 2019, Basel, Switzerland. *Oral presentation by C. Alkan.*

SneakySnake: a fast and efficient pre-alignment filter for accelerating approximate string matching. M. Alser, **C. Alkan**, O. Mutlu. 27^{th} Annual International Conference Intelligent Systems for Molecular Biology (ISMB/ECCB 2019), *HiTSeq Track*, July 22-23, 2019, Basel, Switzerland. *Poster presentation by M. Alser.*

BitMAC: an in-memory accelerator for bitvector-based sequence alignment of both short and long genomic reads. D. Senol Cali, C. Firtina, J.S. Kim, Z. Bingol, M. Alser, **C. Alkan**, S. Ghose, O. Mutlu. 27^{th} Annual International Conference Intelligent Systems for Molecular Biology (ISMB/ECCB 2019), *HiTSeq Track*, July 22-23, 2019, Basel, Switzerland. *Poster presentation by C. Firtina.*

Apollo: a sequencing-technology-independent, scalable, and accurate assembly polishing algorithm. C. Firtina, J.S. Kim, M. Alser, D. Senol Cali, A.E. Cicek, **C. Alkan**, O. Mutlu. 27^{th} Annual International Conference Intelligent Systems for Molecular Biology (ISMB/ECCB 2019), *HiTSeq Track*, July 22-23, 2019, Basel, Switzerland. *Poster presentation by C. Firtina.*

Graph based plasmid identification in bacteria. F. Kahveci, Ö. Kalay, A. Jain, T.F. Jesus, J.A. Carriço, **C. Alkan**. Eleventh International Symposium on Health Informatics and Bioinformatics (HIBIT), October 25-27, 2018, Antalya, Turkey. *Oral presentation by F. Kahveci.*

Hercules: a profile HMM-based hybrid error correction algorithm for long reads. C. Firtina, Z. Bar-Joseph, **C. Alkan**, A.E. Cicek. 26^{th} Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2018), Chicago, IL, United States, July 7-10, 2018. *Oral presentation by A.E. Cicek.*

Nanopore Sequencing Technology and Tools for Genome Assembly: Computational Analysis of the Current State, Bottlenecks, and Future Directions. D. Senol Cali, J.S. Kim, S. Ghose, **C. Alkan**, O. Mutlu. 22^{nd} Annual International Conference on Research in Computational Molecular Biology (RECOMB 2018), April 21-24, 2018, Paris, France. *Poster presentation by D. Senol Cali.*

Accelerating Approximate Pattern Matching with Processing-In-Memory (PIM) and Single-Instruction Multiple-Data (SIMD) Programming. D. Senol Cali, Z. Bingol, J.S. Kim, R. Ausavarungnirun, S. Ghose, **C. Alkan**, O. Mutlu. The Eighth RECOMB Satellite Workshop on Massively Parallel Sequencing, April 19-20, 2018, Paris, France. *Poster presentation by D. Senol Cali. Best Poster Award Winner.*

Algorithms for structural variation discovery using hybrid sequencing technologies. E. Ebren, A.B. Dinçer, **C. Alkan**. 25^{rd} Annual International Conference on Intelligent Systems for Molecular Biology and 16^{th} European Conference on Computational Biology (ISMB/ECCB 2017), July 21-25, 2017, Prague, Czech Republic. *Poster presentation by E. Ebren.*

Discovery of long genomic inversions using long range information. F. Karaoğlanoğlu, M. Eslami Rasekh, **C. Alkan**. Tenth International Symposium on Health Informatics and Bioinformatics (HIBIT), June 28-30, 2017, Güzelyurt, Turkish Republic of North Cyprus. *Oral presentation by F. Karaoğlanoğlu.*

A Profile HMM-based hybrid error correction algorithm for long sequencing reads. C. Fırtına, Z. Bar-Joseph, A.E. Çiçek, **C. Alkan**. Tenth International Symposium on Health Informatics and Bioinformatics (HIBIT), June 28-30, 2017, Güzelyurt, Turkish Republic of North Cyprus. *Poster presentation by C. Fırtına.*

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BioPeer: A fast and secure peer-to-peer data sharing tool. C. Oge, F.T. Dogan, G. Goktepe, F. Koc, C. Sevim, **C. Alkan**. *The 6^{th} Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2015)*, July 10-11, 2015, Dublin, Ireland. *Poster presentation by Cihad Öge.*

Coinami: A cryptocurrency with DNA sequence alignment as proof-of-work. A.M. Ileri, H.I. Ozercan, A. Gundogdu, A.K. Senol, M.Y. Ozkaya, **C. Alkan**. *The 6^{th} Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2015)*, July 10-11, 2015, Dublin, Ireland. *Oral and poster presentation by H. İbrahim Özercan.*

Optimal Seed Solver: optimizing seed selection in read mapping. H. Xin, S. Nahar, R. Zhu, J. Emmons, G. Pekhimenko, C. Kingsford, **C. Alkan**[‡], O. Mutlu[‡]. *The 6^{th} Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2015)*, July 10-11, 2015, Dublin, Ireland. *Poster presentation by Hongyi Xin.*

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Massively parallel mapping of next generation sequence reads using GPUs. A. Nouri, R.O. Selvitopi, O. Ozturk, O. Mutlu[‡], **C. Alkan**[‡]. *The 20th International Conference on Architectural Support for Programming Languages and Operating Systems (ASPLOS 2015)*, March 14-18, 2015, İstanbul, Turkey. *Short talk and poster presented by Azita Nouri.*

Preprints

Apollo: A sequencing-technology-independent, scalable, and accurate assembly polishing algorithm. C. Firtina, J.S. Kim, M. Alser, D. Senol Cali, A.E. Cicek, **C. Alkan**[‡], O. Mutlu[‡]. *arXiv:1902.04341*, posted Feb 12, 2019.

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Coinami: a cryptocurrency with DNA sequence alignment as proof-of-work. A.M. Ileri, H.I. Ozercan, A. Gundogdu, A.K. Senol, M.Y.Ozkaya, **C. Alkan**. *arXiv:1602.03031* , posted Feb 9, 2016.

Software

- Multiple alignment Manipulator (MaM).
  `https://github.com/BilkentCompGen/mam`
- taveRNA: RNA suite for RNA folding, RNA-RNA interaction prediction and search.
  `http://compbio.cs.sfu.ca/taverna`
- micro-read Fast Alignment Search Tools (mrFAST, mrsFAST, drFAST, and sirFAST).
  `https://github.com/BilkentCompGen/mrfast`, `https://github.com/sfu-compbio/mrsfast`,
  `https://github.com/BilkentCompGen/drfast`, `https://github.com/BilkentCompGen/sirfast`
- mrCaNaVaR: characterization of segmental duplications and absolute copy number prediction from read depth.
  `https://github.com/BilkentCompGen/mrcanavar`
- VariationHunter/CommonLAW: Structural variation calling algorithm for paired-end, next generation sequencing data.
  `http://variationhunter.sourceforge.net`
- NovelSeq: computational pipeline fo detect novel sequence insertions using second generation sequencing.
  `http://novelseq.sourceforge.net`
- RepeatNet: algorithm to characterize centromeric satellite sequences from paired end sequence data.
  `https://github.com/BilkentCompGen/repeatnet`
- SCALCE: Tool to compress FASTQ files.
  `https://github.com/sfu-compbio/scalce`
- VALOR: Structural variation discovery using long range information.
  `https://github.com/BilkentCompGen/valor`
- Pamir: Novel sequence insertion discovery in multiple samples.
  `https://github.com/vpc-ccg/pamir`
- TARDIS: Toolkit for the automated and rapid discovery of structural variants.
  `https://github.com/BilkentCompGen/tardis`
- Hercules: Profile HMM-based hybrid error correction algorithm for long reads.
  `https://github.com/BilkentCompGen/hercules`
- LaVa: Large structural variation discovery using hybrid sequence data.
  `https://github.com/BilkentCompGen/lava`
- SEDEF: Characterization of segmental duplications within genome assemblies.
  `https://github.com/vpc-ccg/sedef/`
- GateKeeper: FPGA design for accelerating pre-alignment in DNA short read mapping.
  `https://github.com/BilkentCompGen/GateKeeper`
- MAGNET: FPGA-based filtering strategy with high accuracy across different edit distance thresholds.
  `https://github.com/BilkentCompGen/MAGNET`
- Shouji: fast and efficient computation of banded sequence alignment.
  `https://github.com/CMU-SAFARI/Shouji`
- SneakySnake: approximate alignment computation on CPU, GPU, and FPGA by reducing alignment problem to single net routing problem.
  `https://github.com/CMU-SAFARI/SneakySnake`
- BROSV: structural variation breakpoint resolution refiner using split reads.
  `https://github.com/BilkentCompGen/brosv`