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**

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

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.
- 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

Active

- 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
- 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
- European Molecular Biology Organization Installlation 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-1001-214Z130), 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 am serving 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 am serving as a consultant for this project for the *de novo* assembly work package.
  PI: Ali Ergül

Previous

- 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, Ankara, Turkey.
- **Mohammed Alser:** Ph.D. student, Computer Engineering, Fall 2014 - present. Bilkent University, Ankara, Turkey. Co-supervisor: Onur Mutlu.
- **Arda Söylev:** Ph.D. student, Computer Engineering, Fall 2014 - present. Bilkent University, Ankara, Turkey.
- **Volkan Yazar:** Ph.D. student, Molecular Biology and Genetics, Fall 2013 - present. Bilkent University, Ankara, Turkey. Co-supervised. Main supervisor: İhsan Gürsel.

M.Sc.

- **F. Tuğba Doğan:** M.Sc. student, Computer Engineering, Fall 2015 - present. Bilkent University, Ankara, Turkey.
- **Halil İbrahim Özercan:** M.Sc. student, Computer Engineering, Fall 2016 - present. Bilkent University, Ankara, Turkey.
- **Fatih Karaoğlanoğlu:** M.Sc. student, Computer Engineering, Spring 2017 - present. Bilkent University, Ankara, Turkey.
- **Alim Şükrü Gökkaya:** M.Sc. student, Computer Engineering, Spring 2017 - present. Bilkent University, Ankara, Turkey.
- **Balanur İçen:** M.Sc. student, Computer Engineering, Spring 2017 - present. Bilkent University, Ankara, Turkey. *started the program in Fall 2016 under the supervision of Assoc. Prof. Selim Aksoy.*
- **Ezgi Ebren:** M.Sc. student, Computer Engineering, Summer 2017 - present. Bilkent University, Ankara, Turkey.
- **Emre Doğru:** M.Sc. student, Computer Engineering, Summer 2017 - present. Bilkent University, Ankara, Turkey. *started the program in Spring 2016 under the supervision of Prof. Cevdet Aykanat.*
- **Zülal Bingöl:** M.Sc. student, Computer Engineering, Fall 2017 - present. Co-supervisor: Özcan Öztürk. Bilkent University, Ankara, Turkey.

Undergraduate Volunteers (Current)

- **Figali Taho:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. Since Fall 2017.

Students and Interns (Alumni)

Ph.D.

- **Pınar Kavak:** Ph.D., Computer Engineering, Spring 2017. Boğaziçi University, İstanbul, Turkey. Co-supervised with Tunga Güngör.
  Thesis title: "Developing new approaches for multi-platform and multi-individual genomic sequence assembly"

M.Sc.

- **Can Fırtına:** M.Sc., Computer Engineering, Fall 2017. Bilkent University, Ankara, Turkey.
  Thesis title: "Assessment and correction of errors in DNA sequencing technologies"
  now: Research associate at ETH Zürich.
- **Gülfem Demir:** M.Sc., Computer Engineering, Spring 2017. Bilkent University, Ankara, Turkey.
  Thesis title: "Characterization of short tandem repeats using local assembly"
  now: R&D engineer at Seven Bridges Genomics.
- **Azita Nouri:** M.Sc., Computer Engineering, Spring 2016. Bilkent University, Ankara, Turkey.
  Thesis title: "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, Ankara, Turkey.
  Thesis title: "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, Ankara, Turkey.
  Thesis title: "Genome scaffolding using pooled clone sequencing"
  now: software engineer at TÜBİTAK Software Technologies Research Institute.
- **Fatma Kahveci (née Balcı):** M.Sc., Computer Engineering, Spring 2014. Bilkent University, Ankara, Turkey.
  Thesis title: "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, Ankara, Turkey. Co-supervised with Cevdet Aykanat.
  Thesis title: "Massively parallel mapping of next generation sequence reads using GPU"
  last seen: Ph.D. student at University of Waterloo.

Undergraduate volunteers

- **Baraa Orabi:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. Spring 2016 - Summer 2017. *now: M.Sc. student at Simon Fraser University.*
- **Ezgi Ebren:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. Summer 2016 - 2017. *now: M.Sc. student at Bilkent University.*
- **Abdullah Alperen:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. Since Spring 2015 - 2017. *now: Ph.D. student at Michigan State University.*
- **Halil İbrahim Özercan:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. Fall 2015 - Spring 2016. *now: M.Sc. student at Bilkent University.*
- **Ayhun Tekat:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. Summer 2015. *now: M.Sc. student at Technische Universität München.*
- **Damla Şenol:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. Spring 2015. *now: Ph.D. student at Carnegie Mellon University.*
- **Can Fırtına:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. Spring 2015. *now: M.Sc. student at Bilkent University.*
- **Atalay Mert İleri:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. 2014. *now: Ph.D. student at MIT.*
- **Gülfem Demir:** B.Sc. student in Computer Engineering, Middle East Technical University, Ankara, Turkey. 2013-2014. *now: R&D engineer at Seven Bridges Genomics.*
- **Can Koçkan:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. 2012-2014. *last seen: Ph.D. student at Indiana University.*

- **Yiğit Küçük:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. 2012-2014. *last seen: Ph.D. student at Case Western Reserve University.*
- **Serhat Kıyak:** B.Sc. student in Computer Engineering, Bilkent University, Ankara, Turkey. 2013-2014. *last seen: Ph.D. student at Carnegie Mellon University.*

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, Ankara, Turkey. Co-supervised with Cevdet Aykanat. Left the program in Fall 2016.
- **Dilek Genç:** M.Sc. student, Computer Engineering, Fall 2015. Bilkent University, Ankara, Turkey. 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: M.D./Ph.D. student at University of Washington.*
- **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

- **Fahrettin Can Koyuncu:** Ph.D. candidate, Computer Engineering, since Spring 2014. Advisor: Çiğdem Gündüz Demir. Bilkent University, Ankara, Turkey.
- **Abdullah Atmaca:** Ph.D. candidate, Computer Engineering, since Spring 2015. Advisors: Yavuz Oruç and Cevdet Aykanat. Bilkent University, Ankara, Turkey.

Past

- **Onur Baloğlu:** Ph.D. candidate, Biology, since Fall 2015. I left the committee in Spring 2018. Advisor: Mehmet Somel. Middle East Technical University, Ankara, Turkey.
- **Arif Yılmaz:** Ph.D., Bioinformatics, Spring 2018. Advisor: Yeşim Aydın Son. Middle East Technical University, Ankara, Turkey.
- **Burçak Otlu:** Ph.D., Computer Engineering, Spring 2017. Advisor: Tolga Can. Middle East Technical University, Ankara, Turkey.
- **Evrim Tekeli:** Ph.D., Anthropology, Spring 2017. Advisor: Timur Gültekin. Ankara University, Ankara, Turkey.
- **M. Yağmur Şahin:** M.Sc. Computer Engineering, Fall 2016. Advisor: Buğra Gedik. Bilkent University, Ankara, Turkey.

- **Mona Shojaei:** M.Sc. Bioinformatics, Summer 2016. Advisor: Rengül Çetin Atalay. Middle East Technical University Informatics Institute, Ankara, Turkey.
- **Melike Dönertaş:** M.Sc. Biology, Spring 2016. Advisor: Mehmet Somel. Middle East Technical University, Ankara, Turkey.
- **Doğukan Çağatay:** M.Sc. Computer Engineering, Fall 2015. Advisor: Buğra Gedik. Bilkent University, Ankara, Turkey.
- **Gülsüm Ece Ekşi:** M.Sc. Computer Engineering, Fall 2015. Advisor: Bedir Tekinerdoğan. Bilkent University, Ankara, Turkey.
- **Onur Özdemir:** M.Sc. Computer Engineering, Fall 2015. Advisor: Bedir Tekinerdoğan. Bilkent University, Ankara, Turkey.
- **Daria Iakovishina:** Ph.D., Bioinformatics, November 2015. Advisor: Valentina Boeva. École Polytechnique, Palaiseau, France. *last seen: Bioinformatician at iBinom, 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.*
- **Havva Gülay Gürbüz:** M.Sc. Computer Engineering, Summer 2014. Advisor: Bedir Tekinerdoğan. Bilkent University, Ankara, Turkey. *last seen: Software Development Engineer at Microsoft, Redmond, WA, USA..*
- **Mehmet Başaran:** M.Sc. Computer Engineering, Fall 2014. Advisor: Cevdet Aykanat. Bilkent University, Ankara, Turkey. *last seen: Ph.D. student at Bilkent University, Ankara, Turkey.*
- **Gülşah Merve Dal:** Ph.D., Molecular Biology and Genetics, Fall 2014. Advisor: Tayfun Özçelik. Bilkent University, Ankara, Turkey. *last seen: Postdoctoral fellow at Department of Biology, Middle East Technical University, Ankara, Turkey.*
- **Merve Çakır:** M.Sc. Computer Engineering, Spring 2013. Advisor: Uğur Doğrusöz. Bilkent University, Ankara, Turkey. *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, Ankara, Turkey. *last seen: Ph.D. student at Bilkent University, Ankara, Turkey.*
- **Özlem Tufanlı:** Ph.D. candidate, Molecular Biology and Genetics, since Fall 2013. I left the committee in Spring 2015. Advisor: Ebru Erbay. Bilkent University, Ankara, Turkey.

Academic Service

University Duties

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

Editorial

- Steering Committee Member, RECOMB Workshop on Massively Parallel Sequencing (RECOMB-Seq), 2017-*present*.
- Associate Editor, BMC Bioinformatics, 2010-*present*.
- Track co-chair, 26^{th} Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2018), High Throughput Sequencing Analysis and Algorithms (HiTSeq) track, July 6-10, 2018, Chicago, IL, United States.
- PC Member, Eighth Annual RECOMB Workshop on Massively Parallel Sequencing (RECOMB-Seq 2018), April 19-20, 2018, Paris, France.
- PC Member, HPCA 2018 Workshop on Accelerator Architecture in Computational Biology and Bioinformatics, February 24, 2018, Vienna, Austria
- PC Member, 8^{th} ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2017), August 21-24, 2017, Boston, MA, USA.
- PC Member, 10^{th} International Symposium on Health Informatics and Bioinformatics (HIBIT), June 28-30, 2017, Güzelyurt / Northern Cyprus.
- PC Member, Seventh Annual RECOMB Workshop on Massively Parallel Sequencing (RECOMB-Seq 2017), May 7-8, 2017, Hong Kong.
- PC Member, Next Generation Sequencing Conference (NGS 2017), April 3-5, 2017, Barcelona, Spain.

- Track co-chair, 25^{rd} Annual International Conference on Intelligent Systems for Molecular Biology and 16^{th} European Conference on Computational Biology (ISMB/ECCB 2017), High Throughput Sequencing Analysis and Algorithms (HiTSeq) track, July 21-25, 2017, Prague, Czech Republic.
- PC Member, the 4^{th} International Conference on Algorithms for Computational Biology (AlCoB 2017), June 5-7, 2016, Aveiro, Portugal.
- Session Chair, 12^{th} National Medical Genetics Congress, Çeşme, Turkey, October 7, 2016.
- PC Member, 24^{th} Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2016), July 8-12, 2016, Orlando, FL, USA.
- Co-chair, 7^{th} Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2016), July 8-9, 2016, Orlando, FL, USA.
- PC Member, the 3^{rd} International Conference on Algorithms for Computational Biology (AlCoB 2016), June 21-23, 2016, Trujillo, Spain.
- PC Member, the 20^{th} Annual International Conference on Research in Computational Molecular Biology (RECOMB 2016), April 17-21, 2016, Santa Monica, CA, USA.
- PC Member, 6^{th} Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2015), July 10-11, 2015, Dublin, Ireland.
- Co-Chair, Bertinoro Computational Biology Meeting, June 14-17, 2015, Bertinoro, Italy.
- PC Member, 23^{rd} Annual International Conference on Intelligent Systems for Molecular Biology and 14^{th} European Conference on Computational Biology (ISMB/ECCB 2015), July 10-14, 2015, Dublin, Ireland.
- PC Member, 22^{nd} Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2014), July 13-15, 2014, Boston, MA, USA.
- PC Member, 8^{th} International Symposium on Health Informatics and Bioinformatics, (HIBIT), September 25-27, 2013, Ankara, Turkey.
- PC Member, 21^{st} Annual International Conference on Intelligent Systems for Molecular Biology and 12^{th} European Conference on Computational Biology (ISMB/ECCB 2013), July 19-23, 2013, Berlin, Germany.
- PC Member, Third Annual RECOMB Workshop on Massively Parallel Sequencing (RECOMB-seq), April 11-12, 2013, Beijing, China.
- PC Member, 20^{th} Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2012), July 15-17, 2012, Long Beach, CA, USA.
- PC Member, Second Annual RECOMB Workshop on Massively Parallel Sequencing (RECOMB-seq), April 19-20, 2012, Barcelona, Spain.
- PC Member, 19^{th} Annual International Conference on Intelligent Systems for Molecular Biology and 10^{th} European Conference on Computational Biology (ISMB/ECCB 2011), July 15-19, 2011, Vienna, Austria.
- Chair, First Annual RECOMB Workshop on Massively Parallel Sequencing (RECOMB-seq), March 26-27, 2011, Vancouver, BC, Canada.
- PC Member, the 15^{th} Annual International Conference on Research in Computational Molecular Biology (RECOMB 2011), March 28-31, 2011, Vancouver, BC, Canada.
- Session Co-Chair, Session on Personal Genomics at the Pacific Symposium for Biocomputing (PSB 2011), January 3-7, 2011, The Big Island of Hawaii, USA.
- PC Member, 18^{th} Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2010), July 9-14, 2010, Boston, MA, USA.
- Session Co-Chair, Session on Personal Genomics at the Pacific Symposium for Biocomputing (PSB 2010), January 4-8, 2010, The Big Island of Hawaii, USA.
- PC Member, The IEEE 22nd International Conference on Advanced Information Networking and Applications 2008 (AINA-08).
- PC Member, The IEEE 21st International Conference on Advanced Information Networking and Applications 2007 (AINA-07).

Scientific Advisory Boards

- Turkish Institutes of Health (TÜSEB), Ankara, Turkey. 2016 - *present*.
- 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.
- 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.
- CS 481 Bioinformatics Algorithms, Fall 2012, 2013, 2016, 2017.
- CS 319 Object Oriented Software Engineering, Summer 2012; Spring 2013; Fall 2013, 2014, 2015.
- CS 681 Advanced Topics in Computational Biology, Spring 2012, 2013.
- CS 202 Fundamental Structures of Computer Science II, Spring 2013.
- CS 590/690 Research Topics (coordinator), Spring 2012, 2014.

Senior Project Supervision

- 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

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

Conference and Invited Talks

- Faculty Member, **Next-generation sequence characterization of complex genome structural variation.** Computational Genomics Summer Institute, University of California, Los Angeles, CA, United States, July 11, 2017.
- Invited Speaker, **Kodlamayan genomu anlamlandırmak.** *(in Turkish)* 3^{rd} Course on Neurogenetics, İstanbul, Turkey, June 1, 2017.
- Invited Speaker, **Discovery of large genomic inversions using long range information.** Institute for Molecular Medicine, University of Lisboa, Lisbon, Portugal, April 7, 2017.
- Invited Speaker, **Discovery of large genomic inversions using long range information.** Institute for Computational Biomedicine, Weill Cornell Medicine, New York, NY, USA, January 27, 2017.
- Invited Speaker, **Kodlamayan genomu anlamlandırmak.** *(in Turkish)* 12^{th} National Medical Genetics Congress, Çeşme, Turkey, October 6, 2016.
- Invited Speaker, **Characterization of structural genomic variation.** International Genomics and Bioinformatics Conference, İzmir Biomedicine and Genome Center, Dokuz Eylül University, İzmir, Turkey, May 7, 2016.
- Invited Speaker, **Dünyada ve Türkiye'de Genom Çalışmaları ve Biyoenformatik.** *(in Turkish)* TÜSEB 1. Türk Genom Çalıştayı, İstanbul Technical University, İstanbul, Turkey, February 12, 2016.
- Invited Speaker, **Dijital Yaşam Bilimleri.** *(in Turkish)* Gelecekhane Life 2.0 Workshop, Acıbadem University, İstanbul, Turkey, December 3, 2015.
- Invited Speaker, **A cryptocurrency with DNA Sequence Alignment as Proof-of-work.** School of Medicine, Koç University, İstanbul, Turkey, December 2, 2015.
- Invited Speaker (two talks), **Discovery of large genomic inversions using pooled clone sequencing.** SeqBio2015 Workshop, Université Paris-Sud, Orsay, France, November 27, 2015.
- Invited Speaker (two talks), **A cryptocurrency with DNA Sequence Alignment as Proof-of-work.** SeqBio2015 Workshop, Université Paris-Sud, Orsay, France, November 27, 2015.
- Invited Speaker, **A cryptocurrency with DNA Sequence Alignment as Proof-of-work.** Middle East Technical University, Ankara, Turkey, October 21, 2015.
- Invited Speaker, **A cryptocurrency with DNA Sequence Alignment as Proof-of-work.** 9^{th} International Symposium on Health Informatics and Bioinformatics (HIBIT 2015), Muğla, Turkey, October 16, 2015.
- Workshop Talk, **Can you really anonymize the donors of genomic data in today's digital world?** 10^{th} International Workshop on Data Privacy Management (DPM 2015), September 21, 2015, Vienna, Austria.
- Workshop Short Talk, **Characterization of structural variation and segmental duplications for the GiaB Project.** Genome in a Bottle Workshop, National Institute of Standards and Technology, Gaithersburg, MD, USA, August 27, 2015.
- Invited Speaker, **Discovery of large genomic inversions using pooled clone sequencing.** Georgia Institute of Technology, Atlanta, GA, USA, August 26, 2015.
- Conference Talk, **Coinami: A cryptocurrency with DNA Sequence Alignment as Proof-of-work.** High Throughput Sequencing Algorithms and Applications (HiTSeq 2015), Dublin, Ireland, July 10, 2015.
- Invited Speaker, **Discovery of large genomic inversions using pooled clone sequencing.** İzmir Biomedicine and Genome Center, Dokuz Eylül University, İzmir, Turkey, April 20, 2015.
- 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.
- Invited Speaker, **Genetik Hastalıkların Karakterizasyonunda Yüksek Ölçekli Dizileme ve Biyoenformatik.** *(in Turkish)*, İzmir Biomedicine and Genome Center, Dokuz Eylül University, İzmir, Turkey, October 8, 2014
- Invited Speaker, **Characterization of genome structural variation and large inversions using NGS.** IU Bioinformatics Clinic, July 17, 2014.
- Conference Talk, **Characterization of large inversions using pooled clone sequencing.** European Molecular Biology Organization, Young Investigator Meeting, Heidelberg, Germany, May 14-16, 2014.

- Invited Lecturer, **Characterization of mobile element insertions using NGS.** ALLBIO Course on Next Generation Sequencing (NGS) methods for identification of mutations and large structural variants, Lausanne, Switzerland, March 11-12, 2014.
- Invited Speaker, **Next-generation sequence characterization of complex genome structural variation.** İzmir Biomedicine and Genome Center, Dokuz Eylül University, İzmir, Turkey, October 8, 2014.
- Instructor, **EMBO Practical Course: Computational biology: From genomes to cells and systems.** Cappadocia, Nevşehir, Turkey. September 29 - October 4, 2013.
- Invited Speaker, **Next-generation sequence characterization of complex genome structural variation.** Sabancı University, Tuzla, İstanbul, Turkey. April 17, 2013.
- Invited Speaker, **Yeni nesil dizileme ile karmaşık genom yapısal farklılıkların karakterizasyonu.** *(in Turkish)*, MBG Weekend Seminars VIII, Boğaziçi University, March 23, 2013.
- Invited Speaker, **Genetik Hastalıkların Keşfinde Yüksek Ölçekli Dizileme ve Biyoinformatik.** *(in Turkish)*, 10^{th} National Medical Genetics Congress, Bursa, Turkey, December 20, 2012.
- Invited Speaker, **Next-generation sequence characterization of complex genome structural variation.** Swiss Institute of Allergy and Asthma Research (SIAF), Davos, Switzerland, September 3, 2012.
- 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.** School of Medicine, Koç University, İstanbul, Turkey, May 21, 2012.
- Invited Speaker, **Next-generation sequence characterization of complex genome structural variation.** Department of Molecular Biology and Genetics, Bilkent University, Ankara, Turkey, March 14, 2012.
- Invited Speaker, **Initial analysis results of the Turkish Genome Project.** Boğaziçi University, İstanbul, Turkey, January 20-21, 2012.
- Invited Speaker, *Alu* **repeat discovery and characterization within human genomes.** FASEB Meeting on Mobile DNA in Mammalian Genomes, Snowmass Village, CO, USA, August 12, 2011.
- 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.
- Invited Speaker, **Next-generation sequence characterization of complex genome structural variation.** Brigham and Women's Hospital, Harvard Medical School, Boston, MA, USA, February 22, 2011.
- Invited Speaker, **Next-generation sequence characterization of complex genome structural variation.** Keystone Symposium on Functional Consequences of Structural Variation in the Genome, Steamboat Springs, CO, USA, January 10, 2011.
- Tutorial Presenter, **Session tutorial: Personal Genomics**. Pacific Symposium for Biocomputing (PSB 2011), The Big Island of Hawaii, USA, January 3, 2011.
- Invited Speaker, **Discovery and characterization of copy-number variants with next-gen sequencing technologies**. TÜBİTAK Informatics and Information Security Research Center, Gebze, Turkey, August 6, 2010.
- Invited Speaker, **Characterization of novel sequence insertions through both clone-based and clone-free sequencing**. Illumina Sequencing Expert Panel Meeting, Toronto, ON, Canada, July 22, 2010.
- Tutorial Presenter, **Session tutorial: Personal Genomics**. Pacific Symposium for Biocomputing (PSB 2010), January 4, 2010, The Big Island of Hawaii, USA.
- Invited Speaker, **Structural variation discovery and characterization of segmental duplications with next-gen sequencing technologies**. Simon Fraser University, Vancouver, BC, Canada, November 19, 2009.
- Invited Speaker, **Structural variation discovery and characterization of segmental duplications with next-gen sequencing technologies**. Universitat Pompeu Fabra, Barcelona, Spain, November 16, 2009.

- Invited Speaker, **Structural variation discovery and characterization of segmental duplications with next-gen sequencing technologies**. Università di Bologna, Bologna, Italy, November 11, 2009.
- Invited Speaker, **Structural variation discovery and characterization of segmental duplications with next-gen sequencing technologies**. Università degli Studi di Bari, Bari, Italy, November 9, 2009.
- 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.
- Invited Speaker, **Characterization of structural variation and segmental duplications using next-gen sequencing technology**. The Mediterranean Medical Genetics Meeting 2009, Ankara, Turkey, June 30, 2009.
- Conference Talk, **Organization and evolution of primate centromeric DNA from whole genome shotgun sequence data**. 16^{th} Annual International Conference Intelligent Systems for Molecular Biology (ISMB 2008), *Highlights Track*, Toronto, ON, Canada, July 22, 2008.
- Workshop Talk, **Personalized copy-number and segmental duplication maps using next-gen sequencing technology**. Special Interest Group on Algorithms for Short Read Assembly, Alignment & Variation Analysis at the 16^{th} Annual International Conference Intelligent Systems for Molecular Biology (ISMB 2008), Toronto, ON, Canada, July 19, 2008.
- Invited Speaker, **Organization and evolution of primate centromeric DNA from whole genome shotgun sequence data**. Bilkent University Center for Bioinformatics, Ankara, Turkey, July 20, 2007.
- Invited Speaker, **Towards a model for the evolution of alpha-satellite DNA**. BC Genome Sciences Centre, Vancouver, BC, Canada April 12, 2006.
- 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.
- Workshop Talk, **RNA-RNA interactions and miRNA target prediction**. MITACS-PIMS Pacific Northwest Bioinformatics Day, Simon Fraser University, Burnaby, BC, Canada, May 20, 2004.

Publications

Journal Publications

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

Genome Read In-Memory (GRIM) Filter: fast seed location filtering in DNA read mapping using processing-in-memory technologies. J. Kim, D. Senol Cali, H. Xin, D. Lee, S. Ghose, M. Alser, H. Hassan, O. Ergin, **C. Alkan**‡, O. Mutlu‡. *BMC Genomics*, *to appear*.

Targeting PLK1 overcomes T-DM1 resistance via CDK1-dependent phosphorylation and inactivation of Bcl-2/xL in HER2-positive breast cancer. Ö. Saatci, S. Borgoni, Ö. Akbulut, S. Durmuş, U. Raza, E. Eyüpoğlu, **C. Alkan**, A. Akyol, Ö. Kütük, S. Wiemann, Ö. Şahin. *Oncogene*, [epub Feb 2; doi: 10.1038/s41388-017-0108-9], 2018.

Computational pan-genomics: status, promises and challenges. Computational Pan-Genomics Consortium. *Briefings in Bioinformatics*, [epub Oct 21, 2016], Jan 1;19(1):118-135, 2018.

GateKeeper: a new hardware architecture for accelerating pre-alignment in DNA short read mapping. M. Alser, H. Hassan, H. Xin, O. Ergin, O. Mutlu‡, **C. Alkan**‡. *Bioinformatics*, Nov 1; 33(21):3335-63, 2017.

Toolkit for automated and rapid discovery of structural variants. A. Soylev, C. Kockan, F. Hormozdiari‡, **C. Alkan**‡. *Methods*, Oct 1, 129:3-7, 2017.

Discovery and genotyping of novel sequence insertions in many sequenced individuals. P. Kavak, Y-Y. Lin, I. Numanagić, H. Asghari, T. Güngör, **C. Alkan**‡, F. Hach‡. *Bioinformatics* (ISMB-ECCB 2017 issue), Jul 15; 33 (14): i161-i169, 2017.

MAGNET: understanding and improving the accuracy of genome pre-alignment filtering. M. Alser, O. Mutlu‡, **C. Alkan**‡. *IPSI Transactions on Internet Research*, 13(2), 2017.

Building and improving reference genome assemblies. K. Meltz-Steinberg, V.A. Schneider, **C. Alkan**, M.J. Montague, W.C. Warren, D.M. Church, R.K. Wilson. *Proceedings of the IEEE*, Mar 3, 105(3): 422-435, 2017.

Discovery of large genomic inversions using long range information. M. Eslami Rasekh, G. Chiatante, M. Miroballo, J. Tang, M. Ventura, C.T. Amemiya, E.E. Eichler, F. Antonacci‡, **C. Alkan**‡. *BMC Genomics*, Jan 10;18(1):65, 2017.

Inter-varietal structural variation in grapevine genomes. M.F. Cardone, P. D'Addabbo, **C. Alkan**, C. Bergamini, C.R. Catacchio, F. Anaclerio, G. Chiatante, A. Marra, G. Giannuzzi, R. Perniola, M. Ventura, D. Antonacci. *Plant Journal*, 88(4): 648-661, 2016.

On genomic repeats and reproducibility. C. Firtina and **C. Alkan**. *Bioinformatics*, Aug 1;32(15): 2243-7, 2016.

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‡. *Bioinformatics*, Jun 1;32(11):1632-42, 2016.

Demographically-based evaluation of genomic regions under selection in domestic dogs. A.H. Freedman, R.M. Schweizer, D. Ortega-Del Vecchyo, E. Han, B.W. Davis, I. Gronau, P.M. Silva, M. Galaverni, Z. Fan, P. Marx, B. Lorente-Galdos, O. Ramirez, F. Hormozdiari, **C. Alkan**, C. Vilà, K. Squire, E. Geffen, J. Kusak, A.R. Boyko, H.G. Parker, C. Lee, V. Tadigotla, A. Siepel, C.D. Bustamante, T.T. Harkins, S.F. Nelson, T. Marques-Bonet, E.A. Ostrander, R.K. Wayne, J. Novembre. *PLoS Genetics*, 12(3):e1005851, 2016.

Determining the origin of synchronous multifocal bladder cancer by exome sequencing. Ö. Acar*, E. Özkurt*, G. Demir, H. Saraç, **C. Alkan**, T. Esen, M. Somel‡, Nathan A Lack‡. *BMC Genomics*, Nov 9; 15:871, 2015.

A global reference for human genetic variation. The 1000 Genomes Project Consortium. *Nature*, Oct 1; 526 (7571):98-74, 2015.

An integrated map of structural variation in 2,504 human genomes. P.H. Sudmant, T. Rausch, E.J. Gardner, R.E. Handsaker, A. Abyzov, J. Huddleston, Y. Zhang, K. Ye, G. Jun, M.H-Y. Fritz, M.K. Konkel, A. Malhotra, A.M. Stütz, X. Shi, F.P. Casale, J. Chen, F. Hormozdiari, G. Dayama, K. Chen, M. Malig, M.J.P. Chaisson, K. Walter, S. Meiers, S. Kashin, E. Garrison, A. Auton, H.Y.K. Lam, X. J. Mu, **C. Alkan**, D. Antaki, T. Bae, E. Cerveira, P. Chines, Z. Chong, L. Clarke, E. Dal, L. Ding, S. Emery, X. Fan, M. Gujral, F. Kahveci, J.M. Kidd, Y. Kong, E-W. Lameijer, S. McCarthy, P. Flicek, R.A.Gibbs, G. Marth, C.E. Mason, A. Menelaou, D.M. Muzny, B.J. Nelson, A. Noor, N.F. Parrish, M. Pendleton, A. Quitadamo, B. Raeder, E.E. Schadt, M. Romanovitch, A. Schlattl, R. Sebra, A.A. Shabalin, A. Untergasser, J.A. Walker, M. Wang, F. Yu, C. Zhang, J. Zhang, X. Zheng-Bradley, W. Zhou, T. Zichner, J. Sebat, M.A. Batzer, S.A. McCarroll, The 1000 Genomes Project Consortium, R.E. Mills, M.B. Gerstein, A. Bashir, O. Stegle, S.E. Devine, C. Lee, E.E. Eichler, J.O. Korbel. *Nature*, Oct 1; 526 (7571):75–81, 2015.

Robustness of massively parallel sequencing platforms. P. Kavak, B. Yüksel, S. Aksu, M.O. Kulekci, T. Güngör, F. Hach, S.C. Sahinalp, Turkish Human Genome Project, **C. Alkan**‡, M.S. Sağıroğlu‡. *PLoS ONE*, Sep 18;10(9):e0138259, 2015.

Fast and accurate mapping of Complete Genomics reads. D. Lee, F. Hormozdiari, H. Xin, F. Hach, O. Mutlu‡, **C. Alkan**‡. *Methods*, Jun;79-80:3-10, 2015.

Shifted Hamming Distance: a fast and accurate SIMD-friendly filter to accelerate alignment verification in read mapping. H. Xin, J. Greth, J. Emmons, G. Pekhimenko, C. Kingsford, **C. Alkan**‡, O. Mutlu‡. *Bioinformatics*, May 15;31(10):1553-60, 2015.

Activating mutations of STAT5B and STAT3 in lymphomas derived from $\gamma\delta$-T or NK cells. C. Kucuk, B. Jiang, X. Hu, W. Zhang, J. Chan, W. Xiao, N. Lack, **C. Alkan**, J. Williams, K. Avery, P. Kavak, A. Scuto, E. Sen, P. Gaulard, L. Staudt, J. Iqbal, W. Zhang, A. Cornish, Q. Gong, Q. Yang, H. Sun, F. d'Amore, S. Leppä, W. Liu, K. Fu, L. de Leval, T. McKeithan. *Nature Communications*, Jan 14;6:6025, 2015.

Whole genome sequencing of Turkish genomes reveals functional private alleles and impact of genetic interactions with Europe, Asia and Africa. C. Alkan, P. Kavak, M. Somel, O. Gokcumen, S. Uğurlu, E. Dal, K. Buğra-Bilge, T. Güngör, S.C. Sahinalp, N. Özören, C. Bekpen. *BMC Genomics*, 15 (1):963, 2014.

Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. M.J. Montague, G. Li, B. Gandolfi, R. Khan, B.L. Aken, S.M.J. Searle, P. Minx, L. Hillier, D.C. Koboldt, B.W. Davis, C.A. Driscoll, C.S. Barr, K. Blackistone, J. Quilez, B. Lorente-Galdos, T. Marques-Bonet, **C. Alkan**, G.W.C. Thomas, M. W. Hahn, M. Menotti-Raymond, S.J. O'Brien, R. Wilson, L.A. Lyons, W.J. Murphy, W.C. Warren. *Proc Natl Acad Sci*, Dec 2;111(48):17230-17235, 2014.

Annotated features of domestic cat – *Felis catus* genome. G. Tamazian, S. Simonov, P. Dobrynin, A. Makunin, A. Logachev, A. Komissarov, A. Shevchenko, V. Brukhin, N. Cherkasov, A. Svitin, K-P. Koepfli, J. Pontius, C. A Driscoll, K. Blackistone, C. Barr, D. Goldman, A. Antunes, J. Quilez, B. Lorente-Galdos, **C. Alkan**, T. Marques-Bonet, M. Menotti-Raymond, V.A. David, K. Narfström, S.J. O'Brien. *GigaScience*, Aug 5; 3:(13), 2014.

mrsFAST-Ultra: a compact, SNP-aware mapper for high performance sequencing applications. F. Hach*, I. Sarrafi*, F. Hormozdiari, **C. Alkan**, E.E. Eichler, S.C. Sahinalp. *Nucl Acids Research*, Jul;42(Web Server issue):W494-500, 2014.

Early postzygotic mutations contribute to de novo variation in a healthy monozygotic twin pair. G.M. Dal, B. Ergüner, M.S. Sağıroğlu, B. Yüksel, O.E. Onat, **C. Alkan**, T. Özçelik. *J Med Genet*, 51(7):455-459, 2014.

Genome sequencing highlights the dynamic early history of dogs. A.H. Freedman, I. Gronau, R.M. Schweizer, D. Ortega-Del Vecchyo, E. Han, P.M. Silva, M. Galaverni, Z. Fan, P. Marx, B. Lorente-Galdos, H. Beale, O. Ramirez, F. Hormozdiari, **C. Alkan**, C. Vilà, K. Squire, E. Geffen, J. Kusak, A.R. Boyko, H.G. Parker, C. Lee, V. Tadigotla, A. Siepel, C.D. Bustamante, T.T. Harkins, S.F. Nelson, E.A. Ostrander, T. Marques-Bonet, R.K. Wayne, J. Novembre. *PLoS Genetics*, 10(1): e1004016, 2014.

Reconstructing complex regions of genomes using long-read sequencing technology. J. Huddleston, S. Ranade, M. Malig, F. Antonacci, M. Chaisson, L. Hon, P.H. Sudmant, T.A. Graves, **C. Alkan**, M.Y. Dennis, R.K. Wilson, S.W. Turner, J. Korlach, E.E. Eichler. *Genome Research*, 24(4):688-96, 2014.

Rates and patterns of great ape retrotransposition. F. Hormozdiari, M.K. Konkel, J. Prado-Martinez, G. Chiatante, I. Hernando-Herraez, J.A. Walker, B. Nelson, **C. Alkan**, P.H. Sudmant, J. Huddleston, C.R. Catacchio, A. Ko, M. Malig, C. Baker, T. Marques-Bonet, M. Ventura, M.A. Batzer, and E.E. Eichler. *Proc Natl Acad Sci*, Aug 13;110(33):13457-62, 2013.

Great ape genetic diversity and population history. J. Prado-Martinez, P.H. Sudmant, J.M. Kidd, H. Li, J.L. Kelley, B. Lorente-Galdos, K.R. Veeramah, A.E. Woerner, T.D. O'Connor, G. Santpere, A. Cagan, C. Theunert, F. Casals, H. Laayouni, K. Munch, A. Hobolth, A.E. Halager, M. Malig, J. Hernandez-Rodriguez, I. Hernando-Herraez, K. Prüfer, M. Pybus, L. Johnstone, M. Lachmann, **C. Alkan**, D. Twigg, N. Petit, C. Baker, F. Hormozdiari, M. Fernandez-Callejo, M. Dabad, M.L. Wilson, L. Stevison, C. Camprubí, T. Carvalho, A. Ruiz-Herrera, L. Vives, M. Mele, T. Abello, I. Kondova, R.E. Bontrop, A. Pusey, F. Lankester, J.A. Kiyang, R.A. Bergl, E. Lonsdorf, S. Myers, M. Ventura, P. Gagneux, D. Comas, H. Siegismund, J. Blanc, L. Agueda-Calpena, M. Gut, L. Fulton, S.A. Tishkoff, J.C. Mullikin, R.K. Wilson, I.G. Gut, M. Katherine Gonder, O.A. Ryder, B.H. Hahn, A. Navarro, J.M. Akey, J. Bertranpetit, D. Reich, T. Mailund, M.H. Schierup, C. Hvilsom, A.M. Andrés, J.D. Wall, C.D. Bustamante, M.F. Hammer, E.E. Eichler, T. Marques-Bonet. *Nature*, 499(7459):471-475, 2013.

The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. J. Prado-Martinez, I. Hernando-Herraez, B. Lorente-Galdos, M. Dabad, O. Ramirez, C. Baeza-Delgado, C. Morcillo-Suarez, **C. Alkan**, F. Hormozdiari, E. Raineri, J. Estellé, M. Fernandez-Callejo, M. Valles, L. Ritscher, T. Schöneberg, E. de la Calle-Mustienes, S. Casillas, R. Rubio-Acero, M. Melé, J. Engelken, M. Caceres, J.L. Gomez-Skarmeta, M. Gut, J. Bertranpetit, I.G. Gut, T. Abello, E.E. Eichler, I. Mingarro, C. Lalueza-Fox, A. Navarro, T. Marques-Bonet. *BMC Genomics*, May 31;14(1):363, 2013.

Refinement and discovery of new hotspots of copy-number variation associated with autism spectrum disorder. S. Girirajan*, M.Y. Dennis*, C. Baker, M. Malig, B.P. Coe, C.D. Campbell, K. Mark, T.H. Vu, **C. Alkan**, Z. Cheng, L.G. Biesecker, R. Bernier, E.E. Eichler. *Am J Hum Genet.*, Feb 7;92(2):221-37, 2013.

Accelerating read mapping with FastHASH. H. Xin, D. Lee, F. Hormozdiari, S. Yedkar, O. Mutlu[‡], **C. Alkan**[‡]. *BMC Genomics*, 14(Suppl 1):S13, 2013.

Special issue for the 11th Asia Pacific Bioinformatics Conference, Jan. 21-23, 2013, Vancouver, BC, Canada

An integrated map of genetic variation from 1,092 human genomes. The 1000 Genomes Project Consortium. *Nature*, Nov 1;491(7422):56-65, 2012.

SCALCE: boosting sequence compression algorithms using locally consistent encoding. F. Hach, I. Numanagiċ, **C. Alkan**, S. Cenk Sahinalp. *Bioinformatics*, Dec 1;28(23):3051-57, 2012.

A high-coverage genome sequence from an archaic Denisovan individual. M. Meyer, M. Kircher, M-T. Gansauge, H. Li, F. Racimo, S. Mallick, J.G. Schraiber, F. Jay, K. Prüfer, C. de Filippo, P.H. Sudmant, **C. Alkan**, Q. Fu, R. Do, N. Rohland, A. Tandon, M. Siebauer, R.E. Green, K. Bryc, A.W. Briggs, U. Stenzel, J. Dabney, J. Shendure, J. Kitzman, M.F. Hammer, M.V. Shunkov, A.P. Derevianko, N. Patterson, A.M. Andrés, E.E. Eichler, M. Slatkin, D. Reich, J. Kelso, S. Pääbo. *Science*, 338(6014):222-226, 2012.

The bonobo genome compared with the chimpanzee and human genomes. The International Gorilla Genome Sequencing and Analysis Consortium. *Nature*, 486(7404):527-531, 2012.

Insights into hominid evolution from the gorilla genome sequence. The International Gorilla Genome Sequencing and Analysis Consortium. *Nature*, 483(7388): 169-175, 2012.

Copy number variation of individual cattle genomes using next-generation sequencing. D.M. Bickhart. Y. Hou, S.G. Schroeder, **C. Alkan**, M.F. Cardone, L.K. Matukumalli, J. Song, R.D. Schnabel, M. Ventura, J.F. Taylor, J.F. Garcia, C.P. Van Tassell, T.S. Sonstegard, E.E. Eichler, G.E. Liu. *Genome Research*, Apr;22(4):778-90, 2012.

Detection of structural variants and indels within exome data. E. Karakoc, **C. Alkan**, B.J. O'Roak, M.Y. Dennis, L. Vives, K. Mark, M.J. Rieder, D.A. Nickerson, E.E. Eichler. *Nature Methods*, 9(2): 176-178, 2012.

Identification and validation of a novel mature microRNA encoded by the Merkel cell polyomavirus in human Merkel cell carcinomas. S. Lee, K.G. Paulson, E.P. Murchison, O.K. Afanasiev, **C. Alkan**, J.H. Leonard, D.R. Byrd, G.J. Hannon, P. Nghiem. *J Clin Virol.* Nov; 52(3):272-275, 2011.

A hexanucleotide repeat expansion in C9ORF72 is the cause of chromosome 9p21-linked ALS-FTD. A.E. Renton, E. Majounie, A. Waite, J. Simón-Sánchez, S. Rollinson, J.R. Gibbs, J.C. Schymick, H. Laaksovirta, J.C. van Swieten, L. Myllykangas, H. Kalimo, A. Paetau, Y. Abramzon, A.M. Remes, A. Kaganovich, S.W. Scholz, J. Duckworth, J. Ding, D.W. Harmer, D.G. Hernandez, J.O. Johnson, K. Mok, M. Ryten, D. Trabzuni, R.J. Guerreiro, R.W. Orrell, J. Neal, A. Murray, J. Pearson, I.E. Jansen, D. Sondervan, H. Seelaar, D. Blake, K. Young, N. Halliwell, J.B. Callister, G. Toulson, A. Richardson, A. Gerhard, J. Snowden, D. Mann, D. Neary, M.A. Nalls, T. Peuralinna, L. Jansson, V.M. Isoviita, A.L. Kaivorinne, M. Hölttä-Vuori, E. Ikonen, R. Sulkava, M. Benatar, J. Wuu, A. Chiò, G. Restagno, G. Borghero, M. Sabatelli, The ITALSGEN Consortium, D. Heckerman, E. Rogaeva, L. Zinman, J.D. Rothstein, M. Sendtner, C. Drepper, E.E. Eichler, **C. Alkan**, Z. Abdullaev, S.D. Pack, A. Dutra, E. Pak, J. Hardy, A. Singleton, N.M. Williams, P. Heutink, S. Pickering-Brown, H.R. Morris, P.J. Tienari, B.J. Traynor. *Neuron*, Oct 20; 72(2):257-268, 2011.

Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. M. Ventura, C.R. Catacchio, **C. Alkan**, T. Marques-Bonet, S. Sajjadian, T.A. Graves, F. Hormozdiari, A. Navarro, M. Malig, C. Baker, C. Lee, E.H. Turner, L. Chen, J.M. Kidd, N. Archidiacono, J. Shendure, R.K. Wilson, E.E. Eichler. *Genome Research*, Oct;21(10):1640-9, 2011.

Sensitive and fast mapping of di-base encoded reads. F. Hormozdiari*, F. Hach*, S.C. Sahinalp, E.E. Eichler, **C. Alkan**. *Bioinformatics*, Jul 15;27(14):1915-21, 2011.

Alu* repeat discovery and characterization within human genomes**. F. Hormozdiari*, **C. Alkan, M. Ventura*, I. Hajirasouliha, M. Malig, F. Hach, D. Yorukoglu, P. Dao, M. Bakshi, S.C. Sahinalp, E.E. Eichler. *Genome Research*, Jun;21(6):840-9, 2011.

Genome structural variation discovery and genotyping. **C. Alkan**, B.P. Coe, E.E. Eichler. *Nature Reviews Genetics*, 12:363-376, 2011.

***Clcn4-2* genomic structure differs between the X locus in Mus spretus and the autosomal locus in Mus musculus: AT motif enrichment on the X**. D.K. Nguyen, F. Yang, R. Kaul, **C. Alkan**, A. Antonellis, K.F. Friery, B. Zhu, P.J. de Jong, C.M. Disteche. *Genome Research*, 21(3):402-409, 2011.

Mapping copy number variation at fine scale by population scale genome sequencing. R.E. Mills*, K. Walter*, C. Stewart*, R.E. Handsaker*, K. Chen*, **C. Alkan***, A. Abyzov*, S.C. Yoon*, K. Ye*, R.K. Cheetham, A. Chinwalla, D.F. Conrad, Y. Fu, F. Grubert, I. Hajirasouliha, F. Hormozdiari, L.M. Iakoucheva, Z. Iqbal, S. Kang, J.M. Kidd, M.K. Konkel, J. Korn, E. Khurana, D. Kural, H.Y.K. Lam, J. Leng, R. Li, Y. Li, C-Y. Lin, R. Luo, X.J. Mu, J. Nemesh, H.E. Peckham, T. Rausch, A. Scally, X. Shi, M.P. Stromberg, A.M. Stütz, A. E. Urban, J.A. Walker, J. Wu, Y. Zhang, Z.D. Zhang, M.A. Batzer, L. Ding, G.T. Marth, G. McVean, J. Sebat, M. Snyder, J. Wang, K. Ye, E.E. Eichler, M.B. Gerstein, M.E. Hurles, C. Lee, S.A. McCarroll, J.O. Korbel. *Nature*, 470(7332):56-65, 2011.

Comparative and demographic analysis of orangutan genomes. International Orangutan Genome Sequencing and Analysis Consortium. *Nature*, 469(7331):529-533, 2011.

Haplotype resolved genome sequencing of a Gujarati Indian individual. J.O. Kitzman, A.P. MacKenzie, A. Adey, J.B. Hiatt, R.P. Patwardhan, P.H. Sudmant, S.B. Ng, **C. Alkan**, R. Qiu, E.E. Eichler, J. Shendure. *Nature Biotechnology*, 29(1):59-63, 2011.

Limitations of next-generation genome assembly. **C. Alkan**, S. Sajjadian, E.E. Eichler. *Nature Methods*, 8(1):61-65, 2011.

Highlighted in "Assemblies: the good, the bad, the ugly", E. Birney, Nature Methods, 8(1):59-60, 2011.

Genome-wide characterization of centromeric satellites from multiple mammalian genomes. **C. Alkan***, M.F. Cardone*, C.R. Catacchio, F. Antonacci, S.J. O'Brien, O.A. Ryder, S. Purgato, M. Zoli, G. Della Valle, E.E. Eichler, M. Ventura. *Genome Research*, 21(1): 137-145, 2011.

Genetic history of an archaic hominin group from Denisova Cave in Siberia. D. Reich, R.E. Green, M. Kircher, J. Krause, N. Patterson, E.Y. Durand, B. Viola, A.W. Briggs, U. Stenzel, P.L.F. Johnson, T. Maricic, J.M. Good, T. Marques-Bonet, **C. Alkan**, Q. Fu, S. Mallick, H. Li, M. Meyer, E.E. Eichler, M. Stoneking, M. Richards, S. Talamo, M.V. Shunkov, A.P. Derevianko, J-J. Hublin, J. Kelso, M. Slatkin, S. Pääbo. *Nature*, Dec; 468(7327):1053-1060, 2010.

Diversity of human copy number variation and multicopy genes. P.H. Sudmant, J.O. Kitzman, F. Antonacci, **C. Alkan**, M. Malig, A. Tsalenko, N. Sampas, L. Bruhn, J. Shendure, The 1000 Genomes Project Consortium, E.E. Eichler. *Science*, Oct; 330(6004):641-646, 2010.

A map of human genome variation from population scale sequencing. The 1000 Genomes Project Consortium. *Nature*, Oct; 467(7319):1061-1073, 2010.

A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. F. Antonacci, J.M. Kidd, T. Marques-Bonet, B. Teague, M. Ventura, S. Girirajan, **C. Alkan**, C.D. Campbell, L. Vives, M. Malig, J.A. Rosenfeld, B.C. Ballif, L.G. Shaffer, T.A. Graves, R.K. Wilson, D.C. Schwartz, E.E. Eichler. *Nature Genetics*, Sep; 42(9):745-750, 2010.

mrsFAST: a cache-oblivious algorithm for short-read mapping. F. Hach, F. Hormozdiari, **C. Alkan**, F. Hormozdiari, I. Birol, E.E. Eichler, S.C. Sahinalp. *Nature Methods*, Aug;7(8):576-7, 2010.

A draft sequence of the Neandertal genome. R.E. Green, J. Krause, A.W. Briggs, T. Maricic, U. Stenzel, M. Kircher, N. Patterson, H. Li, W. Zhai, M.H-Y. Fritz, N.F. Hansen, E.Y. Durand, A-S. Malaspinas, J.D. Jensen, T. Marques-Bonet, **C. Alkan**, K. Prüfer, M. Meyer, H.A. Burbano, J.M. Good, R. Schultz, A. Aximu-Petri, A. Butthof, B. Höber, B. Höffner, M. Siegemund, A. Weihmann, C. Nusbaum, E.S. Lander, C. Russ, N. Novod, J. Affourtit, M. Egholm, C. Verna, P. Rudan, D. Brajkovic, Z. Kucan, I. Gusic, V.B. Doronichev, L.V. Golovanova, C. Lalueza-Fox, M. de la Rasilla, J. Fortea, A. Rosas, R.W. Schmitz, P.L.F. Johnson, E.E. Eichler, D. Falush, E. Birney, J.C. Mullikin, M. Slatkin, R. Nielsen, J. Kelso, M. Lachmann, D. Reich, S. Pääbo. *Science*, 7 May, 328 (5979):710-722, 2010.

Recipient of the 2010 AAAS Newcomb Cleveland Prize.

Characterization of missing human genome sequences and copy-number polymorphic insertions. J.M. Kidd, N. Sampas, F. Antonacci, T. Graves, R. Fulton, H.S. Hayden, **C. Alkan**, M. Malig, M. Ventura, G. Giannuzzi, J. Kallicki, P. Anderson, A. Tsalenko, N.A. Yamada, P. Tsang, R. Kaul, R.K. Wilson, L. Bruhn, E.E. Eichler. *Nature Methods*, May, 7 (5):365-371, 2010.

Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. F. Hormozdiari, I. Hajirasouliha, P. Dao, F. Hach, D. Yorukoglu, **C. Alkan**, E.E. Eichler, S.C. Sahinalp. *Bioinformatics*, Jun 15; 26(12):i350-i357, 2010.

Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. I. Hajirasouliha*, F. Hormozdiari*, **C. Alkan***, J.M. Kidd, I. Birol, E.E. Eichler, S.C. Sahinalp. *Bioinformatics*, May 15;26(10):1277-83, 2010.

Complete Khoisan and Bantu genomes from southern Africa. S.C. Schuster, W. Miller, A. Ratan, L.P. Tomsho, B. Giardine, L.R. Kasson, R.S. Harris, D.C. Petersen, F. Zhao, J. Qi, **C. Alkan**, J.M. Kidd, Y. Sun, D.I. Drautz, P. Bouffard, D.M. Muzny, J.G. Reid, L.V. Nazareth, Q. Wang, R. Burhans, C. Riemer, N.E. Wittekindt, P. Moorjani, E.A. Tindall, C.G. Danko, W.S. Teo, A.M. Buboltz, Z. Zhang, Q. Ma, A. Oosthuysen, A.W. Steenkamp, H. Oostuisen, P. Venter, J. Gajewski, Y. Zhang, B.F. Pugh, K.D. Makova, A. Nekrutenko, E.R. Mardis, N. Patterson, T.H. Pringle, F. Chiaromonte, J.C. Mullikin, E.E. Eichler, R.C. Hardison, R.A. Gibbs, T.T. Harkins, V.M. Hayes. *Nature*, Feb, 463(7283):943-947, 2010.

Personalized copy-number and segmental duplication maps using next-generation sequencing. **C. Alkan**, J.M. Kidd, T. Marques-Bonet, G. Aksay, F. Antonacci, F. Hormozdiari, J. O. Kitzman, C. Baker, M. Malig, O. Mutlu, S.C. Sahinalp, R. A. Gibbs, E.E. Eichler. *Nature Genetics*, Oct, 41(10):1061-1067, 2009.

Highlighted in "Mapping duplicated sequences", DY Chiang and SA McCarroll, Nature Biotechnology, Nov; 27(11):1001-2, 2009.

Sequence and structural variation in a human genome uncovered by short-read, massively parallel ligation sequencing using two base encoding. K.J. McKernan, H.E. Peckham, G.L. Costa, S.F. McLaughlin, Y. Fu, E.F. Tsung, C.R. Clouser, C. Duncan, J.K. Ichikawa, C.C. Lee, Z. Zhang, S.S. Ranade, E.T. Dimalanta, F.C. Hyland, T.D. Sokolsky, L. Zhang, J.A. Sheridan, H. Fu, C.L. Hendrickson, B. Li, L. Kotler, J.R. Stuart, J.A. Malek, J.M. Manning, A.A. Antipova, D.S. Perez, M.P. Moore, K.C. Hayashibara, M.R. Lyons, R.E. Beaudoin, B.E. Coleman, M.W. Laptewicz, A.E. Sannicandro, M.D. Rhodes, R.K. Gottimukkala, S. Yang, V. Bafna, A. Bashir, A. MacBride, **C. Alkan**, J.M. Kidd, E.E. Eichler, M.G. Reese, F.M. De La Vega, A.P. Blanchard. *Genome Research*, Sep, 19(9): 1527-1541, 2009.

New insights into centromere organization and evolution from the white-cheeked gibbon and marmoset. A. Cellamare, C.R. Catacchio, **C. Alkan**, G. Giannuzzi, F. Antonacci, M.F. Cardone, G. Della Valle, M. Malig, M. Rocchi, E.E. Eichler, M. Ventura. *Mol Biol Evol*, Aug; 26(8):1889-1900, 2009.

MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions. S. Lee, F. Hormozdiari, **C. Alkan**, M. Brudno. *Nature Methods*, Jul, 6(7):473-4, 2009.

Combinatorial algorithms for structural variation detection in high throughput sequenced genomes. F. Hormozdiari*, **C. Alkan***, E.E. Eichler, S.C. Şahinalp. *Genome Research*, Jul, 19(7):1270-8, 2009.

Comparative analysis of Alu repeats in primate genomes. G.E. Liu, **C. Alkan**, L. Jiang, S. Zhao, E.E. Eichler. *Genome Research*, 19(5):876-885, 2009.

Death and resurrection of the human *IRGM* gene. C. Bekpen, T. Marques-Bonet, **C. Alkan**, F. Antonacci, M. B. Leogrande, M. Ventura, J.M. Kidd, P. Siswara, J. C. Howard, E.E. Eichler. *PLoS Genetics*, March 2009; 5(3):e1000403, 2009.

A burst of segmental duplications in the genome of the African great ape ancestor. T. Marques-Bonet, J.M. Kidd, M. Ventura, T.A. Graves, Z. Cheng, L.W. Hillier, Z. Jiang, C. Baker, R. Malfavon-Borja, L.A. Fulton, **C. Alkan**, G. Aksay, S. Girirajan, P. Siswara, L. Chen, M.F. Cardone, A. Navarro, E.R. Mardis, R.K. Wilson, E.E. Eichler. *Nature*, Feb 12 2009; 457(7231):877-881, 2009.

Mapping and sequencing of structural variation from eight human genomes. J.M. Kidd, G.M. Cooper, W.F. Donahue, H.S. Hayden, N. Sampas, T. Graves, N. Hansen, B. Teague, **C. Alkan**, F. Antonacci, E. Haugen, T. Zerr, N.A. Yamada, P. Tsang, T.L. Newman, E. Tüzün, Z. Cheng, H.M. Ebling, N. Tusneem, R. David, W. Gillett, K.A. Phelps, D. Saranga, A. Brand, W. Tao, E. Gustafson, K. McKernan, L. Chen, M. Malig, J.D. Smith, S.A. McCarroll, D.A. Altshuler, D.A. Peiffer, M. Dorschner, J. Stamatoyannopoulos, D. Schwartz, D.A. Nickerson, J.C. Mullikin, R.K. Wilson, L. Bruhn, M.V. Olson, R. Kaul, D.R. Smith, E.E. Eichler. *Nature*, May 1, 2008; 453(7191):56-64, 2008.

Optimal design of oligonucleotide microarrays for measurement of DNA copy number. A.J. Sharp, A. Itsara, Z. Cheng, **C. Alkan**, S. Schwartz, E.E. Eichler. *Human Molecular Genetics*, Nov 15; 16(22):2770-2779, 2007.

Organization and evolution of primate centromeric DNA from whole genome shotgun sequence data. **C. Alkan**, M. Ventura, N. Archidiacono, M. Rocchi, S.C. Şahinalp, E.E. Eichler. *PLoS Computational Biology*, 3(9): e181, September 2007.

taveRNA: a web suite for RNA algorithms and applications. C. Aksay, R. Salari, E. Karakoç, **C. Alkan**, S.C. Şahinalp. *Nucleic Acids Research*, July 1, 2007; Vol. 35 (Web Server Issue): W325-329, 2007.

RNA-RNA interaction prediction and antisense RNA target search. **C. Alkan**, E. Karakoç, J. Nadeau, S.C. Şahinalp, K. Zhang. *Journal of Computational Biology*, March 2006; Vol 13, No 2: 267-282, 2006.

Manipulating multiple sequence alignments via MaM and WebMaM. **C. Alkan**, E. Tüzün, J. Buard, F. Lethiec, E.E. Eichler, J.A. Bailey, S.C. Şahinalp. *Nucleic Acids Research*, July 1, 2005; Vol. 33 (Web Server issue): W295-W298, 2005.

The role of unequal crossover in alpha-satellite DNA evolution: a computational analysis. **C. Alkan**, E.E. Eichler, J.A. Bailey, S.C. Şahinalp, E. Tüzün. *Journal of Computational Biology*, Vol. 11, No.5: 933-944, 2004.

The structure and evolution of centromeric transition regions within the human genome. X. She, J.E. Horvath, Z. Jiang, G. Liu, T. S. Furey, L. Christ, R. Clark, T. Graves, C.L. Gulden, **C. Alkan**, J.A. Bailey, S.C. Şahinalp, M. Rocchi, D. Haussler, R.K. Wilson, W. Miller, S. Schwartz, E.E. Eichler. *Nature*, Aug 19, 2004; 430(7002):857-64, 2004.

Analysis of primate genomic variation reveals a repeat-driven expansion of the human genome. G. Liu, NISC Comparative Sequencing Program, S. Zhao, J.A. Bailey, S.C. Şahinalp, **C. Alkan**, E. Tüzün, E.D. Green, E.E. Eichler. *Genome Research*, 13(3):358-368, 2003.

Divergent origins and concerted expansion of two segmental duplications on chromosome 16. E.E. Eichler, M.E. Johnson, **C. Alkan**, E. Tüzün, C. Şahinalp, D. Misceo, N. Archidiacono, and M. Rocchi. *Journal of Heredity*, 92: 462-468, 2001.

Peer-Reviewed Conference Publications

Note: In CS disciplines papers in highly ranked conferences are fully refereed and are regarded as highly as the top journal papers. In computational molecular biology RECOMB and ISMB are generally accepted as the top conferences, with 10-15% acceptance rates. Joint first authors are marked with * in case of equal contribution. Joint last authors are marked with ‡.

Genome Read In-Memory (GRIM) Filter: fast seed location filtering in DNA read mapping using processing-in-memory technologies. J. Kim, D. S. Cali, H. Xin, D. Lee, S. Ghose, M. Alser, H. Hassan, O. Ergin, **C. Alkan**‡, O. Mutlu‡. The 16^{th} Asia Pacific Bioinformatics Conference (APBC 2018), January 15-17, 2018, Yokohama, Japan.

Discovery and genotyping of novel sequence insertions in many sequenced individuals. Pınar Kavak, Yen-Yi Lin, Ibrahim Numanagić, Hossein Asghari, Tunga Güngör, **C. Alkan**‡, Faraz Hach‡. 25^{th} 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.

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.

Accelerating read mapping with FastHASH. H. Xin, D. Lee, F. Hormozdiari, S. Yedkar, O. Mutlu‡, **C. Alkan**‡. *Proc. of the 11^{th} Asia Pacific Bioinformatics Conference, Jan. 21-23, 2013, Vancouver, BC, Canada*

Detection of characterization of novel sequence insertions using paired-end next-generation sequencing, I. Hajirasouliha*, F. Hormozdiari*, **C. Alkan***, J.M. Kidd, I. Birol, E.E. Eichler, S.C. Sahinalp. *Proc. of the 11^{th} Conference on High Throughput Sequencing Analysis and Algorithms, Special Interest Group of ISMB 2010 (HiTSeq 2010): July 9-10 2010, Boston, MA, USA*

Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. F. Hormozdiari, I. Hajirasouliha, P. Dao, F. Hach, D. Yorukoglu, **C. Alkan**, E.E. Eichler, S.C. Sahinalp. *Proc. of the 18^{th} Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2010)*, July 11-13, 2010, Boston, MA, USA

Combinatorial algorithms for structural variation detection in high throughput sequenced genomes. F. Hormozdiari*, **C. Alkan***, E.E. Eichler, S.C. Şahinalp. *Proc. of the Thirteenth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2009)*, May 18-21, 2009 Tucson, AZ, USA

RNA secondary structure prediction via energy density minimization. **C. Alkan***, E. Karakoç*, S.C. Şahinalp, P. Unrau, H. A. Ebhardt, K. Zhang, J. Buhler. *Proc. of the Tenth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2006 - LNBI 3909)*, pp. 130-142, April 2-5, 2006 Venice, Italy, 2006.

RNA-RNA interaction prediction and antisense RNA target search. **C. Alkan**, E. Karakoç, J. Nadeau, S.C. Şahinalp, K. Zhang. *Proc. of the Ninth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2005 - LNBI 3500)*, pp 152-171, May 14-18, 2005 Cambridge, MA, USA, 2005.

An algorithmic analysis of the role of unequal crossover in alpha-satellite DNA evolution. **C. Alkan**, J.A. Bailey, E.E. Eichler, S.C. Şahinalp, E. Tüzün. *The 13th International Conference on Genome Informatics*, December 16-18, 2002, Tokyo, Japan, vol.18 pp 93-102, 2002.

Unpublished Conference Talks and Posters

Algorithms for structural variation discovery using hybrid sequencing technologies. Ezgi Ebren, Ayşe Berceste Dinçer, Can 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. Fatih Karaoğlanoğlu, Marzieh Eslami Rasekh, Can 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. Can Fırtına, Ziv Bar-Joseph, Ercüment Çiçek, Can 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.*

LEAP: a generalization of the Landau-Vishkin algorithm with custom gap penalties. Hongyi Xin, Jeremie Kim, Sunny Nahar, Carl Kingsford, Can Alkan, Onur Mutlu. The Seventh RECOMB Satellite Workshop on Massively Parallel Sequencing, May 7-8, 2017, Hong Kong. *Oral presentation by H. Xin.*

Yapısal varyasyonların karakterizasyonu. Arda Söylev, **C. Alkan**. 12^{th} National Medical Genetics Congress, October 7, 2016, Çeşme, Turkey. *Oral presentation by A. Söylev (in Turkish).*

A new inference attack against kin genomic privacy. F. Balci, H. Kulan, **C. Alkan**‡, and E. Ayday‡. *Privacy-aware computational genomics (PRIVAGEN 2015)*, September 8, 2015, Tokyo, Japan. *Oral and poster presentation by Fatma Balcı.*

Identifying anonymous donors of genetic information. M. Alser, N. Almadhoun, A. Nouri, **C. Alkan**‡, and E. Ayday‡. *Privacy-aware computational genomics (PRIVAGEN 2015)*, September 8, 2015, Tokyo, Japan. *Poster presentation by Mohammed Alser.*

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.*

Discovery of large genomic inversions using pooled clone sequencing. M.E. Rasekh, G. Chiatante, M. Miroballo, J. Tang, M. Ventura, C.T. Amemiya, E.E. Eichler, F. Antonacci‡, **C. Alkan**‡. *The 6^{th} Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2015)*, July 10-11, 2015, Dublin, Ireland. *Poster presentation by Marzieh Eslami Rasekh.*

A hypergraph-based model for hybrid de novo assembly. S. Ashyralyyev, C. Firtina, C. Aykanat, **C. Alkan**. Bertinoro Computational Biology Meeting, June 17, 2015, Bertinoro, Italy. *Oral presentation by Shatlyk Ashyralyyev*

Massively parallel mapping of next generation sequence reads using GPUs.. A. Nouri, R.O. Selvitopi, O. Ozturk, O. Mutlu‡, **C. Alkan**‡. *The 20^{th} 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

Hercules: a profile HMM-based hybrid error correction algorithm for long reads. C. Firtina, Z. Bar-Joseph, **C. Alkan**‡, E. Cicek‡. *bioRxiv*, doi: 10.1101/233080, posted Dec 13, 2017.

Nanopore sequencing technology and tools: computational analysis of the current state, bottlenecks, and future directions. Damla Senol Cali, Jeremie Kim, Saugata Ghose, **C. Alkan**‡, O. Mutlu‡. *arXiv:1711.08774*, posted Nov 23, 2017.

LEAP: a generalization of the Landau-Vishkin algorithm with custom gap penalties. H. Xin, J. Kim, S. Nahar, **C. Alkan**‡, O. Mutlu‡. *bioRxiv*, doi: 10.1101/133157, posted May 7, 2017.

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