

Can Alkan

CONTACT INFORMATION

Department of Computer Engineering
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RESEARCH INTERESTS

Combinatorial algorithms for the analysis of high throughput sequencing data, genomic structural variation, human and primate segmental duplications, and hardware acceleration of bioinformatics algorithms.

EXPERIENCE

Department of Computer Engineering, Bilkent University, Bilkent, Ankara, Turkey

Associate Professor

April 2021 - present

Assistant Professor

January 2012 - April 2021

Seven Bridges Genomics, Cambridge, MA, United States

Visiting Scholar (on sabbatical)

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 - January 2012

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 Engineering and Information 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

RESEARCH
GRANTS

ACTIVE

- Horizon Europe EIC Pathfinder, 2022-2026
Title: Processing-in-memory architectures and programming libraries for bioinformatics algorithms (BioPIM)
Goal: Accelerate bioinformatics applications through leveraging the Processing-in-Memory (PIM) technologies.
Coordinator: Can Alkan
Team Leaders: Onur Mutlu (ETH Zürich), Rayan Chikhi (Institut Pasteur), Dominique Lavenier (CNRS), Abu Sebastian (IBM Zürich), Ran Ginosar (Technion), Yann Falevoz (UPMEM), Leonid Yavits (Bar-Ilan).
- NVIDIA Applied Research Accelerator Program, 2023-2025
Title: Fast pathogen screening using DNA sequencing in disaster-stricken areas
Goal: Sequencing-based identification of pathogens quickly using Jetson Nano kits.
PI: Can Alkan

PREVIOUS

- Afyon Health Sciences University, 2020-2021
Title: Developing rapid diagnostic kit for sepsis (Sepsi-Fast)
Goal: Determine antibiotic resistance and susceptibility in newborn sepsis cases.
PI: Nurullah Okumuş
- 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: Develop 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-2507-214Z130), 2015-2018
Elucidating the mechanisms of sequential trastuzumab/T-DM1 resistance *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-2505-215S364), 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: Develop 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: Develop 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: Develop assembly algorithms to 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)

POSTDOCTORAL FELLOWS

- **Nermin Çelik:** Postdoc, 2021 - present.

PH.D.

- **Zülal Bingöl:** Computer Engineering, Fall 2020 - present. Bilkent University.
- **Ricardo Román-Brenes:** Computer Engineering, Fall 2020 - present. Bilkent University.

M.Sc.

- **Rafi Çoktalaş:** Computer Engineering, Fall 2021 - present. Bilkent University.
- **Ömer Yavuz Öztürk:** Computer Engineering, Fall 2022 - present. Bilkent University.

- **Klea Zambaku:** Computer Engineering, Fall 2022 - present. Bilkent University.
- **Ecem İlğün:** Computer Engineering, Spring 2023 - present. Bilkent University.
- **Akmuhammet Ashyralyev:** Computer Engineering, Fall 2023 - present. Bilkent University.
- **Ebrar Bozkurt:** Computer Engineering, Fall 2023 - present. Bilkent University.

UNDERGRADUATE VOLUNTEERS

- **Sıla Özel:** B.Sc. student in Computer Engineering, Bilkent University. Since Fall 2023.
- **E Rana Emiroğlu:** B.Sc. student in Computer Engineering, Bilkent University. Since Fall 2023.
- **Şeyma Kılıç:** B.Sc. student in Computer Engineering, Bilkent University. Since Fall 2023.

STUDENTS AND INTERNS (ALUMNI)

POSTDOCTORAL FELLOWS

- **Malavi Sengupta:** Postdoc, co-advised with Ayça Ergül (Hacettepe University) and Mehmet Somel (Middle East Technical University), 2021 - 2022.
now: Instructor at Ashoka University, India

PH.D.

- **Arda Söylev:** Ph.D., Computer Engineering, Fall 2018. Bilkent University.
“Algorithms for structural variation discovery using multiple sequence signatures”
now: Postdoctoral Fellow at Heinrich Heine 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 and Instructor at ETH Zürich.

PH.D. (AS CO-SUPERVISOR)

- **Mona Shojaei:** Ph.D., Bioinformatics, Fall 2023. Co-supervised with Aybar Can Acar. Middle East Technical University Informatics Institute.
“An integrative framework for clinical diagnosis and knowledge discovery from exome sequencing data”
- **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.

- **Mahmud Sami Aydın:** M.Sc., Computer Engineering, Summer 2023. Bilkent University.
“Whole genome alignment via Alternating Lyndon Factorization Tree traversal”
now: Ph.D. student at Stockholm University.
- **Gözde Yazıcı:** M.Sc., Computer Engineering, Fall 2022. Bilkent University.
“Identification of protein-protein interaction bridges for multiple sclerosis”
now: Ph.D. student at Department of Industrial Engineering, Bilkent University.
- **Ezgi Ebren:** M.Sc., Computer Engineering, Fall 2020. Bilkent University.
“Large structural variation discovery using long reads with several degrees of error”
now: research engineer at UCLA.
- **Zülal Bingöl:** M.Sc., Computer Engineering, Summer 2020. Bilkent University. Co-supervisor: Özcan Öztürk.
“GateKeeper-GPU: accelerated pre-alignment filtering in short read mapping”
now: Ph.D. student at Bilkent University.
- **Alim Şükrücan Gökkaya:** M.Sc., Computer Engineering, Fall 2019. Bilkent University.
“Distributed stream-processing framework for graph-based sequence alignment”
now: software development engineer at Amazon London.

- **Emre Doğru:** M.Sc., 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”
after Bilkent: researcher at TÜBİTAK BİLGEM.
- **Halil İbrahim Özeran:** M.Sc., Computer Engineering, Summer 2019. Bilkent University.
“A cryptocurrency incentivized voluntary grid computing platform for DNA read alignment”
now: software engineer, Google London.
- **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”
after Bilkent: software engineer, K12Net.
- **Fatih Karaoğlanoglu:** 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 Firtina:** 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”
after Bilkent: Ph.D. at Boston University. now: bioinformatics scientist at Illumina.
- **Elif Dal:** M.Sc., Computer Engineering, Fall 2014. Bilkent University.
“Genome scaffolding using pooled clone sequencing”
now: software engineer at Siemens.
- **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”
- **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”
after Bilkent: Ph.D. at University of Waterloo.

UNDERGRADUATE VOLUNTEERS

- **Berk S Yilmaz:** B.Sc. student in Computer Engineering, Bilkent University. 2022 - 2023.
- **Oğuzhan Özçelik:** B.Sc. student in Computer Engineering, Bilkent University. Spring 2020 - Spring 2022.
- **Meryem Banu Cavlak:** B.Sc. student in Computer Engineering, Bilkent University. Summer 2019 - Spring 2021. *now: M.Sc. student at ETH Zürich.*
- **Naisila Puka:** B.Sc. student in Computer Engineering, Bilkent University. Spring 2019 - Spring 2020. *last seen: software engineer at Microsoft.*
- **Aldo Tali:** B.Sc. student in Computer Engineering, Bilkent University. Fall 2019.
- **Figali Taho:** B.Sc. student in Computer Engineering, Bilkent University. Fall 2017 - Spring 2018. *last seen: M.Sc. student at Simon Fraser University.*

- **Baraa Orabi:** B.Sc. student in Computer Engineering, Bilkent University. Spring 2016 - Summer 2017. *now: Ph.D. student at University of British Columbia.*
- **Ezgi Ebre:** 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 Özeran:** 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. *after Bilkent: Ph.D. at Carnegie Mellon University. now: software engineer, hardware acceleration at Bionano Genomics.*
- **Can Fırtına:** B.Sc. student in Computer Engineering, Bilkent University. Spring 2015.
- **Atalay Mert İleri:** B.Sc. student in Computer Engineering, Bilkent University. 2014. *after Bilkent: 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. *after Bilkent: Ph.D. student at Indiana University.*
- **Yiğit Küçük:** B.Sc. student in Computer Engineering, Bilkent University. 2012-2014. *after Bilkent: 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 SENIOR RESEARCH PROJECT COURSE

- **Arda İçöz:** Spring 2024.
- **Şebnem Türkoğlu:** Accelerating the String Decomposer algorithm. Fall 2023.
- **Ebrar Bozkurt:** Benchmarking of exome-based copy number variation calling learner (ECOLE) tool. Spring 2023.
- **Hacı Çakın:** Analyzing genomic sequences with Bloom Filters and Counter Bloom Filters using C++. Spring 2023.
- **Ege Demirkıran:** Structural variation discovery through genome homology maps. Fall 2022.
- **Gamze Güliter:** Benchmarking read-mapping tools for bacterial pangenomes. Spring 2022.
- **Akmuhammet Ashyralyev:** Breakpoint refinement of structural variations with exact locations given with confidence intervals. Spring 2022.
- **Ahmet Cemal Alıcioğlu:** Pairwise sequence alignment under block edit distance. Spring 2022.
- **Meryem Banu Cavlak:** Assembly-based genomic variation validation. Fall 2020.
- **Naisila Puka:** retroCNV discovery using high throughput sequencing. Spring 2020.
- **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

- **Elif Turan:** Intern in Summer 2022 at Bilkent.
- **Fatma Kahveci:** Ph.D. candidate, Computer Engineering, Fall 2014 - 2021. Bilkent University. Left the program in Fall 2021.
- **Mete Han Kahraman:** M.Sc. student, Computer Engineering, Fall 2019. Bilkent University. Left the program in Spring 2020.

- **Shatlyk Asyralyyev:** Ph.D. student, Computer Engineering, Fall 2013 - 2016. Bilkent University. Co-supervised with Cevdet Aykanat. Left the program in Fall 2016.
- **Fatemeh Hasiri:** Intern in Summer 2017 at Bilkent. *now: M.Sc. student at Simon Fraser University.*
- **Dilek Genç:** M.Sc. student, Computer Engineering, Fall 2015. Bilkent University. Left the program in Spring 2016.
- **Farnush Farhadi:** Intern between July and September 2014 at Bilkent.
- **Vineet Bhakhar:** Intern between May and July 2014 at Bilkent.
- **Farhad Hormozdiari:** Research Scientist at the Eichler Lab between February and September 2010. *last seen: Google Health.*
- **Sònia Casillas:** Visiting scientist at the Eichler Lab between February and July 2011.
- **Michael Duyzend:** Rotation student at the Eichler Lab between June and August 2010. *last seen: Resident Physician at Boston Children's Hospital.*
- **Pietro D'Addabbo:** Visiting scientist at the Eichler Lab between August and November 2009. *last seen: Staff scientist at University of Bari.*
- **Peter H. Sudmant:** Ph.D. student at the Eichler Lab between May 2009 and December 2011. *now: Assistant Professor at University of California, Berkeley.*
- **Jacob O. Kitzman:** Rotation student at the Eichler Lab between January and April 2009. *now: Associate Professor at University of Michigan.*
- **Iman Hajirasouliha:** Intern UW between February to July 2009 at UW. *now: Associate Professor at Weill Cornell Graduate School of Medical Sciences.*
- **Fereydoun Hormozdiari:** Intern between February to July 2008 at UW. *now: Associate Professor at the University of California, Davis.*
- **Kerry Hall:** Intern at UW in 2006.

THESIS
COMMITTEES
(CURRENT)

PH.D.

- **Halil İbrahim Kuru:** Ph.D., Computer Engineering, Summer 2022 - present. Advisors: Ercüment Çiçek, Öznur Taştan. Bilkent University.

THESIS
COMMITTEES
(PAST)

PH.D.

- **Dilek Koptekin:** Ph.D., Molecular Biology and Genetics, Summer 2022. Advisor: Mehmet Somel. Middle East Technical University.
- **Damla Şenol Çalı:** Ph.D., Computer Engineering, Summer 2021. Advisor: Onur Mutlu, Saugata Ghose. Carnegie Mellon University.
- **Nour M.N. Alserr:** Ph.D., Computer Engineering, Summer 2020. Advisors: Özgür Ulusoy, Erman Ayday. Bilkent University.
- **Gülden Olgun:** Ph.D., Computer Engineering, Summer 2019. Advisor: Öznur Taştan, 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 Otlı:** Ph.D., Computer Engineering, Spring 2017. Advisor: Tolga Can. Middle East Technical University.
- **Evrin 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.

- **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.
- **Gülşah Merve Dal:** Ph.D., Molecular Biology and Genetics, Fall 2014. Advisor: Tayfun Özçelik. Bilkent 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.

- **Haya Shamim Khan Khattak:** M.Sc., Computer Engineering, Fall 2022. Advisor: Çiğdem Gündüz Demir. Bilkent University.
- **Mubashira Zaman:** M.Sc., Computer Engineering, Fall 2021. Advisor: Uğur Doğrusöz. Bilkent University.
- **Kerem Ayöz:** M.Sc., Computer Engineering, Summer 2021. Advisor: Ercüment Çiçek. Bilkent University.
- **Doruk Çakmakçı:** M.Sc., Computer Engineering, Summer 2021. Advisor: Ercüment Çiçek. Bilkent University.
- **Furkan Özden:** M.Sc., Computer Engineering, Summer 2021. Advisor: Ercüment Çiçek. Bilkent University.
- **Mustafa Duymuş:** M.Sc., Computer Engineering, Spring 2021. Advisor: Cevdet Aykanat. Bilkent University.
- **Furkan Mustafa Akdemir:** M.Sc., Computer Engineering, Fall 2020. Advisors: Öznur Taştan, Ercüment Çiçek.
- **İlayda Beyreli:** M.Sc., Computer Engineering, Fall 2020. Advisor: Ercüment Çiçek.
- **Oğuzhan Karakahya:** M.Sc., Computer Engineering, Fall 2020. Advisor: Ercüment Çiçek.
- **Emin Onur Karakaşlar:** M.Sc., Computer Engineering, Summer 2020. Advisor: Ercüment Çiçek. Bilkent University.
- **Alper Eroğlu:** M.Sc., Computer Engineering, Summer 2020. Advisor: Ercüment Çiçek. Bilkent University.
- **Muhammed Çavuşoğlu:** M.Sc., Computer Engineering, Summer 2020. Advisor: Cevdet Aykanat. Bilkent University.
- **Simla Burcu Harma:** M.Sc., Computer Engineering, Fall 2019. Advisor: Oğuz Ergin. TOBB University of Economics and Technology.
- **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, 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.
- **Mehmet Başaran:** M.Sc. Computer Engineering, Fall 2014. Advisor: Cevdet Aykanat. Bilkent University.
- **Merve Çakır:** M.Sc. Computer Engineering, Spring 2013. Advisor: Uğur Doğrusöz. Bilkent University.
- **Fahrettin Can Koyuncu:** M.Sc. Computer Engineering, Fall 2012. Advisor: Çiğdem Gündüz Demir. Bilkent University.

ACADEMIC SERVICE

UNIVERSITY DUTIES

- Member of the Faculty Board and Faculty Executive Board, Faculty of Engineering, Bilkent University, since Fall 2021.
- Academic Coordinator for Erasmus+ and International Exchange Programs, Department of Computer Engineering, Bilkent University, since Summer 2014.
- CS491 Senior Design Project, Project Evaluator, Fall 2020.

EDITORIAL & PROGRAM COMMITTEES

- **Associate Editor**, Bioinformatics, 2021-*present*.
- **Member of the Editorial Board**, Genome Research, 2020-*present*.
- **Steering Committee Member**, RECOMB Conference on Biological Sequence Analysis (RECOMB-Seq), 2017-*present*.
- **General Co-Chair**, 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB), 2023.
- **Organization Committee Member**, ISCB COSI for High Throughput Sequencing and Applications (HiTSeq), 2016-*present*.
- **Associate Editor**, BMC Bioinformatics, 2010-2021.
- **Track and Area Co-Chair**, Annual International Conference on Intelligent Systems for Molecular Biology and the European Conference on Computational Biology (ISMB-ECCB).
 - ◊ ISMB: 2018 (Chicago, IL, USA), 2016 (Orlando, FL, USA)
 - ◊ ISMB-ECCB: 2021 (Lyon, France), 2019 (Basel, Switzerland), 2017 (Prague, Czech Republic).
- **Program Committee Chair**, 21st IEEE International Workshop on High-Performance Computational Biology (HiCOMB 2022), May 30, 2022, Lyon, France (held virtually).
- **Program Committee 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: 2024 (Cambridge, MA, USA), 2023 (İstanbul, Turkey), 2022 (San Diego, CA, USA), 2021 (Padova, Italy), 2020 (Padova, Italy), 2019 (Washington, DC, USA), 2016 (Santa Monica, CA, USA), 2011 (Vancouver, Canada).
- **PC Member**, Annual RECOMB Workshop on Massively Parallel Sequencing (RECOMB-Seq)
 - ◊ RECOMB-Seq: 2024 (Cambridge, MA, USA), 2018 (Paris, France), 2017 (Hong Kong), 2013 (Beijing, China), 2012 (Barcelona, Spain).
- **PC Member**, Annual International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB-ECCB)
 - ◊ ISMB: 2024 (Montreal, Canada), 2020 (online), ISMB 2014 (Boston, MA, USA), 2012 (Long Beach, CA, USA), 2010 (Boston, MA, USA).
 - ◊ ISMB-ECCB: 2015 (Dublin, Ireland), 2013 (Berlin, Germany), 2011 (Vienna, Austria).

- **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: 2022 (Chicago, IL, USA), 2021 (Virtual), 2020 (Virtual), 2019 (Niagara Falls, NY, USA), 2017 (Boston, MA, USA).
- **PC Member**, International Symposium on Health Informatics and Bioinformatics (HIBIT)
 - ◊ HIBIT: 2022 (Silifke, Turkey), 2021 (Ankara, Turkey), 2020 (Tuzla, Turkey), 2017 (Güzelyurt, Northern Cyprus), 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: 2021 (Virtual), 2019 (Berkeley, CA, USA), 2017 (Aveiro, Portugal), 2016 (Trujillo, Spain).
- **Session Chair**, 12th 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), 2010 (Big Island of Hawaii, USA).
- **PC Member**, The IEEE International Conference on Advanced Information Networking and Applications (AINA)
 - ◊ AINA: 2008 (Okinawa, Japan), 2007 (Niagara Falls, Canada)

SCIENTIFIC ADVISORY BOARDS

- Prototype Capital, Los Angeles, CA, United States. 2018 - 2020.
- Turkish Institutes of Health (TÜSEB) Genome Project, 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, 2019-2021.
- Genome in a Bottle Consortium, 2015-*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.

AD-HOC REVIEWER

- Nature Genetics, Nucleic Acids Research, Nature Reviews Genetics, Genome Research, PLoS Genetics, PLoS Computational Biology, Nature Microbiology, 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, 2022, 2023; Spring 2014, 2015, 2016, 2017, 2019, 2020, 2021, 2022.
- CS 481 Bioinformatics Algorithms: Fall 2012, 2013, 2016, 2017, 2019, 2020, 2021, 2022; Spring 2024.
- CS 681 Advanced Topics in Computational Biology: Spring 2012, 2013; Fall 2019, 2020.
- CS 202 Fundamental Structures of Computer Science II: Spring 2013, 2023, 2024; Fall 2021, 2023.
- CS 590/690 Research Topics (coordinator): Spring 2012, 2014, 2019, 2022.
- CS 319 Object Oriented Software Engineering: Summer 2012; Spring 2013; Fall 2013, 2014, 2015.

SENIOR PROJECT SUPERVISION

- RestoRun: Restaurant automation application. 2023-2024.
- Block Script: an educational visual programming language. 2023-2024.
- SoCoolBus: student school bus tracking system, 2022-2023.
- Vanny: virtual nanny, 2022-2023.
- Neutlan: NLP-based detection of gender discrimination in texts, 2022-2023.
- Tutorium: online tutoring system, 2022-2023.
- Cassett: bicyclist assistance tool, 2021-2022.
- ShopEye: personal assistant for visually impaired people, 2021-2022.
- Laber: real-time social media analysis, 2021-2022.
- onRoute: a road trip assistance tool, 2020-2021.
- LIBRA: Integrated web-based system to aid diagnosis using clinical sequencing, 2019-2020.
- Pengout: Mobile application to find events and organize group outings, 2019.
- 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

A total of 70 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 26, 2023.
- Invited Speaker, **Acceleration of read mapping through hardware/algorithm co-design.** Computational Genomics Summer Institute, University of California, Los Angeles, CA, United States, July 20, 2023.
- Invited Speaker, **Algorithms to characterize genomic structural variation using high throughput sequencing technologies.** Personalized Medicine and Functional Genomics Meeting, Sidra Medicine, Doha, Qatar, September 26, 2022.
- Invited Speaker, **Acceleration of read mapping through hardware/software co-design.** Computability in Europe 2020, Salerno, Italy, June 30, 2020.
- 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*) 12th National Medical Genetics Congress, Çeşme, Turkey, October 6, 2016.
- Invited Speaker, **High throughput sequencing and bioinformatics for characterization of diseases of genomic origin.** 24th 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 ‡.

GateKeeper-GPU: fast and accurate pre-alignment filtering in short read mapping. Z Bingöl, M Alser, O Mutlu, O Ozturk, C Alkan. *IEEE Transactions on Computers*, 73 (5): 1206-1218, 2024. *Preprint: arXiv 2103.14978*.

An integrative framework for clinical diagnosis and knowledge discovery from exome sequencing data. M Shojaei, N Mohammadvand, T Doğan, C Alkan, R Çetin Atalay, AC Acar. *Computers in Biology and Medicine*, 169: 107810, 2024.

ECOLE: Learning to call copy number variants on whole exome sequencing data. B Mandiracioglu*, F Ozden*, G Kaynar, MA Yilmaz, C Alkan, AE Cicek. *Nature Communications*, 15: 132, 2024. *Preprint: bioRxiv 2022.11.17.516880*.

Identification of protein-protein interaction bridges for multiple sclerosis. G Yazıcı, B Kurt Vatandaslar, I Aydin Canturk, FI Aydinli, O Arici Duz, E Karakoc, BE Kerman, C Alkan. *Bioinformatics*, 39 (4): btad175, 2023.

BLEND: a fast, memory-efficient, and accurate mechanism to find fuzzy seed matches. C Firtina, J Park, JS Kim, M Alser, D Senol Cali, T Shahroodi, N Mansouri-Ghiasi, G Singh, K Kanellopoulos, C Alkan, O Mutlu. *NAR Genomics and Bioinformatics*, 5 (1): lqad004, 2023. *Preprint: arXiv 2112.08687*.

CONGA: copy number variation genotyping in ancient genomes and low-coverage sequencing data. A Söylev, SS Çokoglu, D Koptekin, C Alkan, M Somel. *PLoS Comput Biol*. 18 (12): e1010788, 2022. *Preprint: bioRxiv 2021.12.17.473150*.

High coverage whole genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios. M Byrska-Bishop, US Evani, X Zhao, AO Basile, HJ Abel, AA Regier, A Corvelo, WE Clarke, R Musunuri, K Nagulapalli, S Fairley, A Runnels, L Winterkorn, E Lowy, **Human Genome Structural Variation Consortium**, P Flicek, S Germer, H Brand, IM Hall, ME Talkowski, G Narzisi, MC Zody. *Cell*, 185 (18): 3426-3440, 2022. *Preprint: bioRxiv 2021.02.06.430068*.

C Alkan is a member of The Human Genome Structural Variation Consortium.

FastRemap: a tool for quickly remapping reads between genome assemblies. JS Kim, C Firtina, MB Cavlak, D Senol Cali, C Alkan, O Mutlu. *Bioinformatics*, 38 (19): 4633-4635, 2022. *Preprint: arXiv 2201.06255*.

Polishing copy number variant calls on exome sequencing data via deep learning. F Özden, C Alkan†, AE Çiçek†. *Genome Research*, 32: 1170-1182, 2022. *Preprint: bioRxiv 2020.05.09.086082*.

Commentary: Implications of the first complete human genome assembly. C Alkan, L Carbone, M Dennis, J Ernst, G Evrony, S Girirajan, D Chi, Y Leung, CCY Cheng, D MacAlpine, T Ni, M Ramsay, H Rowe, P Gould, R Enriquez-Gasca, B Sullivan. *Genome Research*, 32 (4): 595-598, 2022.

Fast characterization of segmental duplication structure in multiple genome assemblies. H Işerić, C Alkan, F Hach, I Numanagić. *Algorithms Mol Biol.*, Mar 18; 17(1):4, 2022.

presented at the 21st International Workshop on Algorithms in Bioinformatics (WABI 2021), held virtually.

Technology dictates algorithms: recent developments in read alignment. M Alser, J Rotman, D Deshpande, K Taraszka, H Shi, P Icer Baykal, HT Yang, V Xue, S Knyazev, BD Singer, B Balliu, D Koslicki, P Skums, A Zelikovsky, C Alkan, O Mutlu, S Mangul. *Genome Biology*, Aug 26; 22: 249, 2021. *Preprint: arXiv 2003.00110*.

SneakySnake: a fast and accurate universal genome pre-alignment filter for CPUs, GPUs, and FPGAs. M Alser, T Shahroodi, J Gomez-Luna, C Alkan†, O Mutlu†. *Bioinformatics*, 36 (22-23), 5282-5290, 2020. *Preprint: arXiv 1910.09020*.

Accelerating Genome Analysis: a primer on an ongoing journey. M Alser, Z Bingöl, J Kim, D Senol Cali, S Ghose, C Alkan, O Mutlu. *IEEE Micro*, 40 (5): 65-75, 2020. *Preprint: arXiv 2008.00961*.

A robust benchmark for germline large deletion and insertion detection. JM Zook, NF Hansen, ND Olson, LM Chapman, JC Mullikin, C Xiao, S Sherry, S Koren, AM Phillippy, PC Boutros, SME Sahraeian, V Huang, A Rouette, N Alexander, CE Mason, I Hajirasouliha, C Ricketts, J Lee, R Tearle, IT Fiddes, A Martinez-Barrio, J Wala, A Carroll, N Ghaffari, OL Rodriguez, A Bashir, S Jackman, JJ Farrell, AM Wenger, C Alkan, A Soylev, MC Schatz, S Garg, G Church, T Marschall, K Chen, X Fan, AC English, JA Rosenfeld, W Zhou, RE Mills, JM Sage, JR Davis, MD Kaiser, JS Oliver, AP Catalano, MJP Chaisson, N Spies, FJ Sedlazeck, M Salit. *Nature Biotechnology*, Nov; 38 (11):1347-1355, 2020.

Apollo: A sequencing-technology-independent, scalable, and accurate assembly polishing algorithm. C Firtina, JS Kim, M Alser, D Senol Cali, AE Cicek, C Alkan[‡], O Mutlu[‡]. *Bioinformatics*, 36 (12): 3669-3679, 2020. *Preprint: arXiv 1902.04341*.

VALOR2: characterization of large-scale structural variants using linked-reads. F Karaoglanoglu*, C Ricketts*, E Ebren, M Eslami Rasekh, I Hajirasouliha[‡], C Alkan[‡]. *Genome Biology*, Mar 19; 21: 72, 2020. *Preprint: bioRxiv 394528*.

Automatic characterization of copy number polymorphism using high throughput sequencing. C Alkan. *Turkish J Elec Eng & Comp Sci*, 28: 253-261, 2020.

Shouji: fast and efficient computation of banded sequence alignment. M Alser, H Hassan, A Kumar, O Mutlu[‡], C Alkan[‡]. *Bioinformatics*, Nov 1; 35 (21): 4255-4263, 2019. *Preprint: arXiv 1809.07858*.

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. *Preprint: bioRxiv 393694*.

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. *Preprint: arXiv 1711.08774*.

Characterizing microsatellite polymorphisms using assembly-based and mapping-based tools. G Demir and C Alkan. *Turkish J Biol*, Aug; 43 (4): 264-273, 2019.

Evaluation of genome scaffolding tools using pooled clone sequencing. E Dal and C Alkan. *Turkish J Biol*, Dec; 42 (6): 471-476, 2018.

Fast characterization of segmental duplications in genome assemblies. I Numanagić, AS Gökkaya, L Zhang, B Berger, C Alkan[‡], F Hach[‡]. *Bioinformatics*, Sep 1; 34(17): i706-714, 2018. *Preprint: arXiv 1807.00205*.

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[‡], AE Cicek[‡]. *Nucleic Acids Research*, Nov 30; 46(21): e125, 2018. *Preprint: bioRxiv 233080*.

Realizing the potential of blockchain technologies in genomics. HI Ozercan, AM Ileri, E Ayday, C Alkan. *Genome Research*, Sep; 28(9): 1255-1263, 2018.

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*, May; 19 (Suppl 2): 89, 2018. *Preprint: arXiv 1711.01177*.

presented at the 16th Asia Pacific Bioinformatics Conference (APBC 2018), January 15-17, 2018, Yokohama, Japan.

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*, Apr; 37(17):2251-2269, 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. *Preprint: bioRxiv 043430*.

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. *Preprint: arXiv 1604.01789*.

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, YY Lin, I Numanagić, H Asghari, T Güngör, C Alkan[‡], F Hach[‡]. *Bioinformatics* (ISMB-ECCB 2017 issue), Jul 15; 33 (14): i161-i169, 2017.

presented at the 25th Annual International Conference on Intelligent Systems for Molecular Biology and 16th European Conference on Computational Biology (ISMB/ECCB 2017), July 21-25, 2017, Prague, Czech Republic.

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. Preprint: *arXiv 1707.01631*.

Building and improving reference genome assemblies. K Meltz-Steinberg, VA Schneider, C Alkan, MJ Montague, WC Warren, DM Church, RK 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, CT Amemiya, EE Eichler, F Antonacci[‡], C Alkan[‡]. *BMC Genomics*, Jan 10;18(1): 65, 2017.

Inter-varietal structural variation in grapevine genomes. MF Cardone, P D'Addabbo, C Alkan, C Bergamini, CR Catacchio, F Anacletio, 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. Preprint: *arXiv 1506.08235*.

Demographically-based evaluation of genomic regions under selection in domestic dogs. AH Freedman, RM Schweizer, D Ortega-Del Vecchyo, E Han, BW Davis, I Gronau, PM Silva, M Galaverni, Z Fan, P Marx, B Lorente-Galdos, O Ramirez, F Hormozdiari, C Alkan, C Vilà, K Squire, E Geffen, J Kusak, AR Boyko, HG Parker, C Lee, V Tadigotla, A Siepel, CD Bustamante, TT Harkins, SF Nelson, T Marques-Bonet, EA Ostrander, RK 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 Sarac, 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. PH Sudmant, T Rausch, EJ Gardner, RE Handsaker, A Abyzov, J Huddleston, Y Zhang, K Ye, G Jun, MH-Y Fritz, MK Konkel, A Malhotra, AM Stütz, X Shi, FP Casale, J Chen, F Hormozdiari, G Dayama, K Chen, M Malig, MJP Chaisson, K Walter, S Meiers, S Kashin, E Garrison, A Auton, HYK 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, JM Kidd, Y Kong, E-W Lameijer, S McCarthy, P Flicek, RAGibbs, G Marth, CE Mason, A Menelaou, DM Muzny, BJ Nelson, A Noor, NF Parrish, M Pendleton, A Quitadamo, B Raeder, EE Schadt, M Romanovitch, A Schlattl, R Sebra, AA Shabalina, A Untergasser, JA Walker, M Wang, F Yu, C Zhang, J Zhang, X Zheng-Bradley, W Zhou, T Zichner, J Sebat, MA Batzer, SA McCarroll, The 1000 Genomes Project Consortium, RE Mills, MB Gerstein, A Bashir, O Stegle, SE Devine, C Lee, EE Eichler, JO Korb. *Nature*, Oct 1; 526 (7571): 75-81, 2015.

Robustness of massively parallel sequencing platforms. P Kavak, B Yüksel, S Aksu, MO Kulekci, T Güngör, F Hach, SC Sahinalp, Turkish Human Genome Project, C Alkan[‡], MS Sağiroğlu[‡]. *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, SC 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. MJ Montague, G Li, B Gandolfi, R Khan, BL Aken, SMJ Searle, P Minx, L Hillier, DC Koboldt, BW Davis, CA Driscoll, CS Barr, K Blackstone, J Quilez, B Lorente-Galdos, T Marques-Bonet, C Alkan, GWC Thomas, M W Hahn, M Menotti-Raymond, SJ O'Brien, R Wilson, LA Lyons, WJ Murphy, WC 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, KP Koepfli, J Pontius, C A Driscoll, K Blackstone, C Barr, D Goldman, A Antunes, J Quilez, B Lorente-Galdos, C Alkan, T Marques-Bonet, M Menotti-Raymond, VA David, K Narfström, SJ O'Brien. *GigaScience*, Aug 5; 3(1): 13, 2014.

mrsFAST-Ultra: a compact, SNP-aware mapper for high performance sequencing applications. F Hach*, I Sarrafi*, F Hormozdiari, C Alkan, EE Eichler, SC 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. GM Dal, B Ergüner, MS Sağıroğlu, B Yüksel, OE Onat, C Alkan, T Özçelik. *J Med Genet*, 51(7): 455-459, 2014.

Genome sequencing highlights the dynamic early history of dogs. AH Freedman, I Gronau, RM Schweizer, D Ortega-Del Vecchyo, E Han, PM 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, AR Boyko, HG Parker, C Lee, V Tadigotla, A Siepel, CD Bustamante, TT Harkins, SF Nelson, EA Ostrander, T Marques-Bonet, RK 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, PH Sudmant, TA Graves, C Alkan, MY Dennis, RK Wilson, SW Turner, J Korlach, EE Eichler. *Genome Research*, 24(4): 688-96, 2014.

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

Great ape genetic diversity and population history. J Prado-Martinez, PH Sudmant, JM Kidd, H Li, JL Kelley, B Lorente-Galdos, KR Veeramah, AE Woerner, TD O'Connor, G Santpere, A Cagan, C Theunert, F Casals, H Laayouni, K Munch, A Hobolth, AE 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, ML Wilson, L Stevison, C Camprubi, T Carvalho, A Ruiz-Herrera, L Vives, M Mele, T Abello, I Kondova, RE Bontrop, A Pusey, F Lankester, JA Kiyang, RA Bergl, E Lonsdorf, S Myers, M Ventura, P Gagneux, D Comas, H Siegmund, J Blanc, L Agueda-Calpena, M Gut, L Fulton, SA Tishkoff, JC Mullikin, RK Wilson, IG Gut, M Katherine Gonder, OA Ryder, BH Hahn, A Navarro, JM Akey, J Bertranpetit, D Reich, T Mailund, MH Schierup, C Hvilsom, AM Andrés, JD Wall, CD Bustamante, MF Hammer, EE 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, JL Gomez-Skarmeta, M Gut, J Bertranpetit, IG Gut, T Abello, EE 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*, MY Dennis*, C Baker, M Malig, BP Coe, CD Campbell, K Mark, TH Vu, C Alkan, Z Cheng, LG Biesecker, R Bernier, EE 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.

presented at 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 Numanagiç, 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, JG Schraiber, F Jay, K Prüfer, C de Filippo, PH Sudmant, **C Alkan**, Q Fu, R Do, N Rohland, A Tandon, M Siebauer, RE Green, K Bryc, AW Briggs, U Stenzel, J Dabney, J Shendure, J Kitzman, MF Hammer, MV Shunkov, AP Derevianko, N Patterson, AM Andrés, EE 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. DM Bickhart, Y Hou, SG Schroeder, **C Alkan**, MF Cardone, LK Matukumalli, J Song, RD Schnabel, M Ventura, JF Taylor, JF Garcia, CP Van Tassell, TS Sonstegard, EE Eichler, GE Liu. *Genome Research*, Apr; 22(4): 778-90, 2012.

Detection of structural variants and indels within exome data. E Karakoc, **C Alkan**, BJ O’Roak, MY Dennis, L Vives, K Mark, MJ Rieder, DA Nickerson, EE 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, KG Paulson, EP Murchison, OK Afanasiev, **C Alkan**, JH Leonard, DR Byrd, GJ 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 AE Renton, E Majounie, A Waite, J Simón-Sánchez, S Rollinson, JR Gibbs, JC Schymick, H Laaksovirta, JC van Swieten, L Myllykangas, H Kalimo, A Paetau, Y Abramzon, AM Remes, A Kaganovich, SW Scholz, J Duckworth, J Ding, DW Harmer, DG Hernandez, JO Johnson, K Mok, M Ryten, D Trabzuni, RJ Guerreiro, RW Orrell, J Neal, A Murray, J Pearson, IE Jansen, D Sondervan, H Seelaar, D Blake, K Young, N Halliwell, JB Callister, G Toulson, A Richardson, A Gerhard, J Snowden, D Mann, D Neary, MA Nalls, T Peuralinna, L Jansson, VM Isoviiita, AL Kaivorinne, M Hölttä-Vuori, E Ikonen, R Sulkava, M Benatar, J Wu, A Chiò, G Restagno, G Borghero, M Sabatelli, The ITALSGEN Consortium, D Heckerman, E Rogaeva, L Zinman, JD Rothstein, M Sendtner, C Drepper, EE Eichler, **C Alkan**, Z Abdullaev, SD Pack, A Dutra, E Pak, J Hardy, A Singleton, NM Williams, P Heutink, S Pickering-Brown, HR Morris, PJ Tienari, BJ Traynor. *Neuron*, Oct 20; 72(2): 257-268, 2011.

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

Sensitive and fast mapping of di-base encoded reads. F Hormozdiari*, F Hach*, SC Sahinalp, EE Eichler, **C Alkan**. *Bioinformatics*, Jul 15; 27(14):1 915-21, 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, SC Sahinalp, EE Eichler. *Genome Research*, Jun; 21(6): 840-9, 2011.

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

***Cln4-2* genomic structure differs between the X locus in *Mus spretus* and the autosomal locus in *Mus musculus*: AT motif enrichment on the X.** DK Nguyen, F Yang, R Kaul, **C Alkan**, A Antonellis, KF Friery, B Zhu, PJ de Jong, CM Disteche. *Genome Research*, 21(3): 402-409, 2011.

Mapping copy number variation at fine scale by population scale genome sequencing. RE Mills*, K Walter*, C Stewart*, RE Handsaker*, K Chen*, **C Alkan***, A Abyzov*, SC Yoon*, K Ye*, RK Cheetham, A Chinwalla, DF Conrad, Y Fu, F Grubert, I Hajirasouliha, F Hormozdiari, LM Iakoucheva, Z Iqbal, S Kang, JM Kidd, MK Konkel, J Korn, E Khurana, D Kural, HYK Lam, J Leng, R Li, Y Li, C-Y Lin, R Luo, XJ Mu, J Nimesh, HE Peckham, T Rausch, A Scally, X Shi, MP Stromberg, AM Stütz, AE Urban, JA Walker, J Wu, Y Zhang, ZD Zhang, MA Batzer, L Ding, GT Marth, G McVean, J Sebat, M Snyder, J Wang, K Ye, EE Eichler, MB Gerstein, ME Hurles, C Lee, SA McCarroll, JO Korb. *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. JO Kitzman, AP MacKenzie, A Adey, JB Hiatt, RP Patwardhan, PH Sudmant, SB Ng, C Alkan, R Qiu, EE Eichler, J Shendure. *Nature Biotechnology*, 29(1): 59-63, 2011.

Limitations of next-generation genome assembly. C Alkan, S Sajjadian, EE 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*, MF Cardone*, CR Catacchio, F Antonacci, SJ O'Brien, OA Ryder, S Purgato, M Zoli, G Della Valle, EE Eichler, M Ventura. *Genome Research*, 21(1): 137-145, 2011.

Genetic history of an archaic hominin group from Denisova Cave in Siberia. D Reich, RE Green, M Kircher, J Krause, N Patterson, EY Durand, B Viola, AW Briggs, U Stenzel, PLF Johnson, T Maricic, JM Good, T Marques-Bonet, C Alkan, Q Fu, S Mallick, H Li, M Meyer, EE Eichler, M Stoneking, M Richards, S Talamo, MV Shunkov, AP 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. PH Sudmant, JO Kitzman, F Antonacci, C Alkan, M Malig, A Tsalenko, N Sampas, L Bruhn, J Shendure, The 1000 Genomes Project Consortium, EE 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, JM Kidd, T Marques-Bonet, B Teague, M Ventura, S Girirajan, C Alkan, CD Campbell, L Vives, M Malig, JA Rosenfeld, BC Ballif, LG Shaffer, TA Graves, RK Wilson, DC Schwartz, EE 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, EE Eichler, SC Sahinalp. *Nature Methods*, Aug; 7(8): 576-7, 2010.

A draft sequence of the Neandertal genome. RE Green, J Krause, AW Briggs, T Maricic, U Stenzel, M Kircher, N Patterson, H Li, W Zhai, MH-Y Fritz, NF Hansen, EY Durand, A-S Malaspina, JD Jensen, T Marques-Bonet, C Alkan, K Prüfer, M Meyer, HA Burbano, JM Good, R Schultz, A Aximu-Petri, A Butthof, B Höber, B Höffner, M Siegemund, A Weihmann, C Nusbaum, ES Lander, C Russ, N Novod, J Affourtit, M Egholm, C Verna, P Rudan, D Brajkovic, Z Kucan, I Gusic, VB Doronichev, LV Golovanova, C Lalueza-Fox, M de la Rasilla, J Fortea, A Rosas, RW Schmitz, PLF Johnson, EE Eichler, D Falush, E Birney, JC 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. JM Kidd, N Sampas, F Antonacci, T Graves, R Fulton, HS Hayden, C Alkan, M Malig, M Ventura, G Giannuzzi, J Kallicki, P Anderson, A Tsalenko, NA Yamada, P Tsang, R Kaul, RK Wilson, L Bruhn, EE 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, EE Eichler, SC Sahinalp. *Bioinformatics*, Jun 15; 26(12): i350-i357, 2010.

presented at the 18th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2010), July 11-13, 2010, Boston, MA, USA

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

presented at the Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2010), Special Interest Group of ISMB 2010: July 9-10 2010, Boston, MA, USA

Complete Khoisan and Bantu genomes from southern Africa. SC Schuster, W Miller, A Ratan, LP Tomsho, B Giardine, LR Kason, RS Harris, DC Petersen, F Zhao, J Qi, C Alkan, JM Kidd, Y Sun, DI Drautz, P Bouffard, DM Muzny, JG Reid, LV Nazareth, Q Wang, R Burhans, C Riemer, NE Wittekindt, P Moorjani, EA Tindall, CG Danko, WS Teo, AM Buboltz, Z Zhang, Q Ma, A Oosthuisen, AW Steenkamp, H Oosthuisen, P Venter, J Gajewski, Y Zhang, BF Pugh, KD Makova, A Nekrutenko, ER Mardis, N Patterson, TH Pringle, F Chiaromonte, JC Mullikin, EE Eichler, RC Hardison, RA Gibbs, TT Harkins, VM Hayes. *Nature*, Feb, 463(7283): 943-947, 2010.

Personalized copy-number and segmental duplication maps using next-generation sequencing. C Alkan, JM Kidd, T Marques-Bonet, G Aksay, F Antonacci, F Hormozdiari, J O Kitzman, C Baker, M Malig, O Mutlu, SC Sahinalp, R A Gibbs, EE 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. KJ McKernan, HE Peckham, GL Costa, SF McLaughlin, Y Fu, EF Tsung, CR Clouser, C Duncan, JK Ichikawa, CC Lee, Z Zhang, SS Ranade, ET Dimalanta, FC Hyland, TD Sokolsky, L Zhang, JA Sheridan, H Fu, CL Hendrickson, B Li, L Kotler, JR Stuart, JA Malek, JM Manning, AA Antipova, DS Perez, MP Moore, KC Hayashibara, MR Lyons, RE Beaudoin, BE Coleman, MW Laptewicz, AE Sannicandro, MD Rhodes, RK Gottimukkala, S Yang, V Bafna, A Bashir, A MacBride, C Alkan, JM Kidd, EE Eichler, MG Reese, FM De La Vega, AP 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, CR Catacchio, C Alkan, G Giannuzzi, F Antonacci, MF Cardone, G Della Valle, M Malig, M Rocchi, EE 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*, EE Eichler, SC Şahinalp. *Genome Research*, Jul, 19(7): 1270-8, 2009.

presented at the Thirteenth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2009), May 18-21, 2009 Tucson, AZ, USA

Comparative analysis of Alu repeats in primate genomes. GE Liu, C Alkan, L Jiang, S Zhao, EE 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, JM Kidd, P Siswara, J C Howard, EE Eichler. *PLoS Genetics*, Mar; 5(3): e1000403, 2009.

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

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

Optimal design of oligonucleotide microarrays for measurement of DNA copy number. AJ Sharp, A Itsara, Z Cheng, C Alkan, S Schwartz, EE 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, SC Şahinalp, EE Eichler. *PLoS Computational Biology*, Sep; 3(9): e181, 2007.

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

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

presented at 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.

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

The role of unequal crossover in alpha-satellite DNA evolution: a computational analysis. C Alkan, EE Eichler, JA Bailey, SC Şahinalp, E Tüzün. *Journal of Computational Biology*, 11(5): 933-944, 2004.

presented at the 13th International Conference on Genome Informatics, December 16-18, 2002, Tokyo, Japan, 18: 93-102, 2002.

The structure and evolution of centromeric transition regions within the human genome. X She, JE Horvath, Z Jiang, G Liu, T S Furey, L Christ, R Clark, T Graves, CL Gulden, C Alkan, JA Bailey, SC Şahinalp, M Rocchi, D Haussler, RK Wilson, W Miller, S Schwartz, EE 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, JA Bailey, SC Şahinalp, C Alkan, E Tüzün, ED Green, EE Eichler. *Genome Research*, 13(3): 358-368, 2003.

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

BOOK CHAPTERS

Whole-genome shotgun sequence CNV detection using read depth. F Kahveci, C Alkan. In: Bickhart D (eds) *Copy Number Variants. Methods in Molecular Biology*, vol 1833. Humana Press, New York, NY, pp 61-72, 2018.

PEER-REVIEWED CONFERENCE PROCEEDINGS

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 ‡.

AirLift: a fast and comprehensive technique for translating alignments between reference genomes. JS Kim, C Firtina, D Senol Cali, M Alser, N Hajinazar, C Alkan[‡], O Mutlu[‡]. *The 21st Asia Pacific Bioinformatics Conference (APBC 2023)*, Changsha, Hunan, China, April 14-16, 2023. *Preprint: arXiv:1912.08735*.

TargetCall: eliminating the wasted computation in basecalling via pre-basecalling filtering. MB Cavlak, G Singh, M Alser, C Firtina, J Lindegger, M Sadrosadati, N Mansouri Ghiasi, C Alkan, O Mutlu. *The 21st Asia Pacific Bioinformatics Conference (APBC 2023)*, Changsha, Hunan, China, April 14-16, 2023. *Preprint: arXiv 2212.04953*.

SeGraM: a universal hardware accelerator for genomic sequence-to-graph and sequence-to-sequence mapping. D Senol Cali, K Kanellopoulos, J Lindegger, Z Bingöl, GS Kalsi, Z Zuo, C Firtina, MB Cavlak, J Kim, N Mansouri Ghiasi, G Singh, J Gómez-Luna, N Almadhoun Alserr, M Alser, S Subramoney, C Alkan, S Ghose, O Mutlu. *49th Annual International Symposium on Computer Architecture (ISCA 2022)*, pp 638-655, New York, NY, United States, June 18-22, 2022. *Preprint: arXiv 2205.05883*.

BISER: fast characterization of segmental duplication structure in multiple genome assemblies. H Işerić, C Alkan, F Hach, I Numanagić. *21st International Workshop on Algorithms in Bioinformatics (WABI 2021)*, Aug 2-4, 2021, held virtually.

GenASM: a low-power, memory-efficient approximate string matching acceleration framework for genome sequence analysis. D Senol Cali, GS Kalsi, Z Bingöl, C Firtina, L Subramanian, JS Kim, R Ausavarungrun, M Alser, J Gómez-Luna, A Boroumand, A Nori, A Scibisz, S Subramoney, C Alkan, S Ghose, O Mutlu. *53rd IEEE/ACM International Symposium on Microarchitecture (MICRO 2020)*, October 17-21, 2020, Athens, Greece. *Preprint: arXiv:2009.07692*.

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[‡]. *10th 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, MŞ. Sağiroğlu, T Güngör and C Alkan. *12th Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB 2015)*, September 10-12, 2015, Naples, Italy.

RNA secondary structure prediction via energy density minimization. C Alkan*, E Karakoç*, SC 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.

UNPUBLISHED CONFERENCE TALKS AND POSTERS

SeGraM: a universal hardware accelerator for genomic sequence-to-graph and sequence-to-sequence mapping. D Senol Cali, K Kanellopoulos, J Lindegger, Z Bingöl, GS Kalsi, Z Zuo, C Firtina, MB Cavlak, JS Kim, N Mansouri Ghiasi, G Singh, J Gómez Luna, N Almadhoun Alserr, M Alser, S Subramoney, C Alkan, S Ghose, O Mutlu. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023), April 16-19, İstanbul, Türkiye. *Poster presentation by D Senol Cali.*

Copy number estimation using Counting Bloom Filters in *de novo* assembled genomes. K Zambaku, R Roman-Brenes, ÖY Öztürk, C Alkan, I Birol. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023), April 16-19, İstanbul, Türkiye. *Poster presentation by K Zambaku.*

Identification of protein-protein interaction bridges in multiple sclerosis. G Yazıcı, B Kurt Vatanaslar, E Karakoç, B Kerman, C Alkan. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023), April 16-19, İstanbul, Türkiye. *Poster presentation by G Yazıcı.*

Whole genome alignment via Alternating Lyndon Factorization Tree traversal. MS Aydın and C Alkan. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023), April 16-19, İstanbul, Türkiye. *Poster presentation by MS Aydın.*

Characterization of alignment and search algorithms for short read, long read, and graph mappers. E İlgin, ÖY Öztürk, K Zambaku, J Gómez Luna, M Alser, R Roman-Brenes, C Alkan and The BioPIM Project. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023), April 16-19, İstanbul, Türkiye. *Poster presentation by E İlgin.*

Pairwise sequence alignment with block and character edit operations. AC Ahcioğlu, MS Aydın, C Alkan. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023), April 16-19, İstanbul, Türkiye. *Poster presentation by MS Aydın.*

AirLift: a fast and comprehensive technique for remapping alignments between reference genomes. JS Kim, C Firtina, MB Cavlak, D Senol Cali, N Hajinazar, M Alser, C Alkan, O Mutlu. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023), April 16-19, İstanbul, Türkiye. *Poster presentation by C Firtina.*

Fast identification of sepsis antibiotic resistance. R Roman-Brenes, EG Güliter, C Alkan. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023), April 16-19, İstanbul, Türkiye. *Poster presentation by R Roman-Brenes.*

TargetCall: eliminating the wasted computation in basecalling via pre-basecalling filtering. MB Cavlak, G Singh, M Alser, C Firtina, J Lindegger, M Sadrosadati, N Mansouri Ghiasi, C Alkan, O Mutlu. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023), April 16-19, İstanbul, Türkiye. *Poster presentation by MB Cavlak.*

Pairwise sequence alignment with block and character edit operations. AC Ahcioğlu, MS Aydın, C Alkan. 13th RECOMB Satellite Conference on Biological Sequence Analysis (RECOMB-Seq 2023), April 14-15, İstanbul, Türkiye. *Oral presentation by MS Aydın.*

SeGraM: a universal hardware accelerator for genomic sequence-to-graph and sequence-to-sequence mapping. D Senol Cali, K Kanellopoulos, J Lindegger, Z Bingöl, GS Kalsi, Z Zuo, C Firtina, MB Cavlak, JS Kim, N Mansouri Ghiasi, G Singh, J Gómez Luna, N Almadhoun Alserr, M Alser, S Subramoney, C Alkan, S Ghose, O Mutlu. 13th RECOMB Satellite Conference on Biological Sequence Analysis (RECOMB-Seq 2023), April 14-15, İstanbul, Türkiye. *Poster presentation by D Senol Cali.*

Using minimizer interarrival distances for read-until human read detection from blood samples sequenced by Oxford Nanopore. S Barazandeh, MS Aydın, B Ucar, C Alkan, I Birol. 13th RECOMB Satellite Conference on Biological Sequence Analysis (RECOMB-Seq 2023), April 14-15, İstanbul, Türkiye. *Poster presentation by MS Aydın.*

Characterization of alignment and search algorithms for short read, long read, and graph mappers. E İlğün, ÖY Öztürk, K Zambaku, J Gómez Luna, M Alser, R Roman-Brenes, C Alkan and The BioPIM Project. 13th RECOMB Satellite Conference on Biological Sequence Analysis (RECOMB-Seq 2023), April 14-15, İstanbul, Türkiye. *Poster presentation by E İlğün.*

Copy number estimation using Counting Bloom Filters in *de novo* assembled genomes. K Zambaku, R Roman-Brenes, ÖY Öztürk, C Alkan, I Birol. 13th RECOMB Satellite Conference on Biological Sequence Analysis (RECOMB-Seq 2023), April 14-15, İstanbul, Türkiye. *Poster presentation by K Zambaku.*

Identification of protein-protein interaction bridges in multiple sclerosis. G Yazıcı, B Kurt Vatanaslar, E Karakoç, B Kerman, C Alkan. 21st European Conference on Computational Biology (ECCB 2022), September 12-21, Sitges, Spain. *Poster presentation by G Yazıcı.*

Polishing copy number variant calls on exome sequencing data via deep learning. F Özden, C Alkan[‡], AE Çiçek[‡]. 29th Annual International Conference Intelligent Systems for Molecular Biology (ISMB/ECCB 2021), *HiTSeq Track*, July 27, 2021, held virtually. *Oral presentation by F Özden.*

GateKeeper-GPU: accelerated pre-alignment filtering in short read mapping. Z Bingol, M Alser, O Ozturk, C Alkan. 20th IEEE International Workshop on High Performance Computational Biology (HiCOMB), May 17, 2021, Portland, OR, United States. *Oral presentation by Z Bingol.*

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 Ebre, M Eslami Rasekh, I Hajirasouliha, C Alkan. 27th 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. 27th 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, JS Kim, Z Bingol, M Alser, C Alkan, S Ghose, O Mutlu. 27th 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, JS Kim, M Alser, D Senol Cali, AE Cicek, C Alkan, O Mutlu. 27th 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, TF Jesus, JA 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, AE Cicek. 26th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2018), July 7-10, 2018, Chicago, IL, United States. *Oral presentation by AE Cicek.*

Nanopore sequencing technology and tools for genome assembly: computational analysis of the current state, bottlenecks, and future directions. D Senol Cali, JS Kim, S Ghose, C Alkan, O Mutlu. 22nd 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, JS 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 Ebre, AB Dinçer, C Alkan. 25th Annual International Conference on Intelligent Systems for Molecular Biology and 16th European Conference on Computational Biology (ISMB/ECCB 2017), July 21-25, 2017, Prague, Czech Republic. *Poster presentation by E Ebre.*

Discovery of long genomic inversions using long range information. F Karaoğlu, 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 Karaoğlu*.

A profile HMM-based hybrid error correction algorithm for long sequencing reads. C Firtina, Z Bar-Joseph, AE 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 Firtina*.

LEAP: a generalization of the Landau-Vishkin algorithm with custom gap penalties. H Xin, JS Kim, S Nahar, C Kingsford, [C Alkan](#), O Mutlu. The Seventh RECOMB Satellite Workshop on Massively Parallel Sequencing, May 7-8, 2017, Hong Kong. *Oral presentation by H Xin*.

Yapısal varyasyonların karakterizasyonu. A Söylev, [C Alkan](#). 12th 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 F Balci*.

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 M Alser*.

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

Coinami: a cryptocurrency with DNA sequence alignment as proof-of-work. AM Ileri, HI Ozeran, A Gundogdu, AK Senol, MY Ozkaya, [C Alkan](#). *The 6th Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2015)*, July 10-11, 2015, Dublin, Ireland. *Oral and poster presentation by C Alkan*.

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 6th Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2015)*, July 10-11, 2015, Dublin, Ireland. *Poster presentation by H Xin*.

Discovery of large genomic inversions using pooled clone sequencing. ME Rasekh, G Chiatante, M Miroballo, J Tang, M Ventura, CT Amemiya, EE Eichler, F Antonacci[†], [C Alkan](#)[†]. *The 6th Conference on High Throughput Sequencing Analysis and Algorithms (HiTSeq 2015)*, July 10-11, 2015, Dublin, Ireland. *Poster presentation by M Eslami Rasekh. Preprint: bioRxiv 015156*.

A hypergraph-based model for hybrid de novo assembly. S Ashyralyev, C Firtina, C Aykanat, [C Alkan](#). Bertinoro Computational Biology Meeting, June 17, 2015, Bertinoro, Italy. *Oral presentation by S Ashyralyev*.

Massively parallel mapping of next generation sequence reads using GPUs. A Nouri, RO 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 A Nouri*.

PREPRINTS

Older preprints that are later published in a journal or a peer-reviewed conference are moved from this section to their relative sections.

Pairwise sequence alignment with block and character edit operations. AC Alıcıoğlu, MS Aydın, [C Alkan](#). *arXiv:2311.11082*, posted Nov 18, 2023.

Pre-processing of paleogenomes: Mitigating reference bias and postmortem damage in ancient genome data. D Koptekin, E Yapar, KB Vural, E Sağlıcan, NE Altınışık, AS Malaspinas, [C Alkan](#), M Somel. *bioRxiv*, doi: 10.1101/2023.11.11.566695, posted Nov 13, 2023.

GateSeeder: Near-memory CPU-FPGA acceleration of short and long read mapping. J Eudine, M Alser, G Singh, [C Alkan](#), O Mutlu. *arXiv:2309.17063*, posted Sep 29, 2023.

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. AM Ileri, HI Ozeran, A Gundogdu, AK Senol, MY Ozkaya, [C Alkan](#). *arXiv:1602.03031*, posted Feb 9, 2016.

SOFTWARE

- Multiple alignment Manipulator (MaM). <https://github.com/BilkentCompGen/mam>
- 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>
- 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>
- GateKeeper: FPGA design for accelerating pre-alignment in DNA short read mapping.
<https://github.com/BilkentCompGen/GateKeeper>
- GateKeeper-GPU: GPGPU design and implementation for the GateKeeper algorithm.
<https://github.com/BilkentCompGen/GateKeeper-GPU>
- 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>
- Apollo: Profile HMM-based genome assembly polishing tool. <https://github.com/CMU-SAFARI/Apollo>
- BISER: Characterization of segmental duplication evolutionary structure across genome assemblies.
<https://github.com/0xTCG/biser>
- RinsLR: Discovery of mid-range novel sequence insertions using long-read sequencing.
<https://github.com/vpc-ccg/rinslr>
- DeCoNT: CNV prediction polisher on whole exome sequencing data.
<https://github.com/ciceklab/DECoNT>
- GenASM: approximate string matching (ASM) acceleration framework for genome sequence analysis.
<https://github.com/CMU-SAFARI/GenASM>
- SeGraM: universal genomic mapping accelerator that supports both sequence-to-graph mapping and sequence-to-sequence mapping for both short and long reads.
<https://github.com/CMU-SAFARI/SeGraM>
- FastRemap: Tool for quickly remapping reads between genome assemblies.
<https://github.com/CMU-SAFARI/FastRemap>
- BLEND: Fast, memory-efficient, and accurate mechanism to find fuzzy seed matches in genome analysis.
<https://github.com/CMU-SAFARI/BLEND>
- AirLift: Fast and comprehensive technique for translating alignments between reference genomes.
<https://github.com/CMU-SAFARI/AirLift>
- BriFin: Identification of bridges in intercellular PPI networks. <https://github.com/BilkentCompGen/briFin>
- TargetCall: Pre-basecalling filter for the Oxford Nanopore platform.
<https://github.com/CMU-SAFARI/TargetCall>
- SABER: Sequence alignment using block edits and rearrangements.
<https://github.com/BilkentCompGen/saber>
- Linden: Alternating Lyndon Factorization Tree for whole-genome alignments.
<https://github.com/BilkentCompGen/linden>

SOFTWARE (DEPRECATED)

- taveRNA: RNA suite for RNA folding, RNA-RNA interaction prediction and search.
<http://compbio.cs.sfu.ca/taverna>
- VariationHunter/CommonLAW: Structural variation calling algorithm for paired-end, next-generation sequencing data (replaced by TARDIS). <http://variationhunter.sourceforge.net>
- NovelSeq: a computational pipeline to detect novel sequence insertions using second-generation sequencing (replaced by Pamir). <http://novelseq.sourceforge.net>
- RepeatNet: an algorithm to characterize centromeric satellite sequences from paired-end sequence data.
<https://github.com/BilkentCompGen/repeatnet>
- SEDEF: Characterization of segmental duplications within genome assemblies (replaced by BISER).
<https://github.com/vpc-ccg/sedef/>