

## GAMZE GÜRSOY

Yale University  
266 Whitney Ave.  
New Haven, CT 06520

[gamze.gursoy@yale.edu](mailto:gamze.gursoy@yale.edu)  
[gamzegursoy.org](http://gamzegursoy.org)  
[github.com/gursoygamze](https://github.com/gursoygamze)

### EDUCATION AND TRAINING

- **Postdoctoral Research Associate**, Nov 2016 – Present, Computational Biology & Bioinformatics  
Yale University, **Advisor:** Mark Gerstein  
NIH/NHGRI K99/R00 Pathway to Independence Award
- **Ph.D.**, Nov 2016, Bioinformatics / Bioengineering  
University of Illinois at Chicago (UIC), **Advisor:** Jie Liang  
**Thesis:** Three-dimensional Chromosome Organization in Eukaryotes: Novel Computational Approaches  
UIC Outstanding Dissertation Award (given to one Ph.D. among all STEM dissertations)  
UIC Chancellor's Graduate Research Fellowship
- **B.S.**, Jan 2008, Chemical Engineering  
Bogazici University, Istanbul – Turkey, **Advisors:** Mehmet Camurdan and Turkan Haliloglu  
Turkish Education Foundation Scholarship (tuition and stipend for 5 years)

### EMPLOYMENT

- **Postdoctoral Research Associate**, Nov 2016 – Present, Computational Biology & Bioinformatics  
Yale University, New Haven, CT
- **Research Assistant**, August 2009 – Nov 2016, Department of Bioengineering  
University of Illinois at Chicago, Chicago, IL
- **Teaching Assistant**, August 2008 – August 2009, Department of Bioengineering  
University of Illinois at Chicago, Chicago, IL
- **Visiting Researcher**, August 2007 – October 2007, Department of Chemical Engineering  
NASA Center for Advanced Microgravity Material Processing  
Northeastern University, Boston, MA

### HONORS AND AWARDS

- **K99/R00 NIH/NHGRI Pathway to Independence Award**
  - **Press:** <https://bioe.uic.edu/news-stories/searching-for-new-ways-to-keep-dna-data-secure/>
- **UIC Outstanding dissertation award**
- **2019**, Third place, iDASH Secure Genome Analysis Competition Track 1  
(<http://www.humangenomeprivacy.org/2019/>)
- **2018**, First place, iDASH Secure Genome Analysis Competition Track 1  
(<http://www.humangenomeprivacy.org/2018/>)
- **2018**, NIH/BD2K IBM Young Investigator Award (awarded to 5 young researchers); First prize for the best presentation among young investigators

- **2018**, ISCB / ISMB Travel Award
- **2018 – Present**, Sigma Xi full member
- **2016**, Travel Grant, Center for Nonlinear Studies, Los Alamos National Laboratory, 36<sup>th</sup> Annual Conference: Energy Landscapes: From Protein Folding to Molecular Assembly – Santa Fe, NM
- **2013 – 2015**, UIC Chancellor's Graduate Research Fellowship
- **2012/2013/2014/2015**, UIC Graduate Student Council Travel Awards
- **2012 and 2014**, UIC Presenter's Awards
- **2012**, NSF Fellow at 11<sup>th</sup> International Summer School on Biocomplexity from Gene to System – Istanbul, Turkey
- **2010**, Mathematical Sciences Research Institute travel support for the workshop “Algebraic, Geometric, and Combinatorial Methods for Optimization” – Berkeley, CA
- **2008**, Fulbright Travel Award to supplement travel to USA for graduate school
- **2008**, Turkish Petroleum Foundation Travel Award to supplement travel to USA for graduate school
- **2007**, Northeastern University Honorarium for visiting researcher position
- **2002 – 2007**, Turkish Education Foundation Scholarship (tuition and stipend for undergraduate studies)

## PUBLICATIONS

(Students who I directly mentored are underlined, \* denotes co-authorship)

### Book Chapters:

- **Gamze Gürsoy**. “Criticality of data sharing in genomic research and public views of genomic”, in Responsible Genomic Data Sharing: Challenges and Approaches, *Elsevier*, 2020

### Opinion & Commentary:

- **Gamze Gürsoy** and Mark Gerstein. “[As coronavirus testing expands, new personal privacy issues arise](#)” in Hartford Courant.
- **Gamze Gürsoy**, Megan Doerr, John Wilbanks, Jennifer K Wagner, Haixu Tang, Steven E Brenner. “Navigating ethical quandaries with the privacy dilemma of biomedical datatets”, *Proceedings of Pacific Symposium on Biocomputing*, 2020

- **Gamze Gürsoy**, Arif Harmanci, Haixu Tang, Erman Ayday, Steven E Brenner. “When Biology gets personal: Hidden Challenges of Privacy and Ethics in Biological Big Data”, *Proceedings of Pacific Symposium on Biocomputing*, 2019
- **Gamze Gürsoy** and Jie Liang. “3D Chromosome Structures from Energy Landscape“, *PNAS*, 2016, 113, (43), 11991-11993

#### First-author Pre-prints:

- **Gamze Gürsoy\***, Eduardo Chielle\*, Charlotte Brannon, Mihalis Maniatakos, and Mark Gerstein. “Privacy-preserving genotype imputation using homomorphic encryption”, doi: <https://doi.org/10.1101/2020.05.29.124412>  
Github: <https://github.com/gersteinlab/idash19he>
- **Gamze Gürsoy\***, Charlotte Brannon\*, Sarah Wagner, and Mark Gerstein. “Storing and analyzing a genome on a blockchain”, doi: <https://doi.org/10.1101/2020.03.03.975334> [revision submitted to **Genome Research**]  
Github: <https://github.com/gersteinlab/SAMChain>
- **Gamze Gürsoy**, Nancy Lu, Sarah Wagner, and Mark Gerstein. “Recovering genomes and phenotypes using allele-specific gene expression.”  
doi: <https://doi.org/10.1101/2020.11.11.377978>  
Github: <https://github.com/gersteinlab/privaseq4>

#### First-author Published Peer-reviewed Papers

- **Gamze Gürsoy**, Prashant Emani, Charlotte Brannon, Otto A. Jolanki, Arif Harmanci, J. Seth Strattan, J. Michael Cherry, Andrew Miranker, and Mark Gerstein. “Data sanitization to prevent private information leakage in functional genomics”, *Cell*, 183(4): 905-917, 2020  
Website: <https://privaseq3.gersteinlab.org>  
Github: <https://github.com/ENCODE-DCC/ptools>
  - [ASHG Press Release in 2018](#): New file type improves genomic data sharing while maintaining participant privacy.
  - [Yale Press Release](#): Yale team finds way to protect genetic privacy in research.
  - [Science Daily News](#): Researchers simulate privacy leaks in functional genomics studies.
  - [Q & A with The Scientist](#): A new tool for ensuring genetic privacy.
- **Gamze Gürsoy**, Charlotte Brannon, Fabio C.P. Navarro, and Mark Gerstein. “FANCY: Fast estimation of privacy risk in functional genomics data”, *Bioinformatics*, btaa661, 2020  
Website: <https://fancy.gersteinlab.org>  
Github: <https://github.com/gersteinlab/FANCY>
- **Gamze Gürsoy\***, Charlotte Brannon\*, Mark Gerstein. “Using Ethereum blockchain to store and query pharmacogenomics data via smart contracts”, *BMC Medical Genomics*, 13:74, 20  
Github: <https://github.com/gersteinlab/idash19bc>

- **Gamze Gürsoy**, Rob Bjornson, Molly E. Green, and Mark Gerstein. “Using blockchain to log genome dataset access: efficient storage and query”, *BMC Medical Genomics*, 13(Suppl 7):78, 2020  
**Github:** <https://github.com/gersteinlab/iDASH-blockchain>
- **Gamze Gürsoy**, Yun Xu, and Jie Liang. “Spatial organization of budding yeast genome in cell nucleus and identification of specific chromatin interactions from multi-chromosome constrained chromatin model”, *PLoS Comput Biol.*, 13(7):e1005658, 2017  
**Github:** <https://github.com/uic-lianglab/mCSAC>
- **Gamze Gürsoy\***, Yun Xu\*, Amy Kenter, and Jie Liang. “Computational construction of 3D chromatin ensembles and prediction of functional interactions of  $\alpha$ -globin locus from 5C data”, *Nucleic Acids Research*, 45(20):11547-11558, 2017  
**Github:** <https://github.com/uic-lianglab/nCSAC>
- **Gamze Gürsoy**, Anna Terebus, Youfang Cao, and Jie Liang. “Mechanisms of Stochastic Focusing and Defocusing in Biological Reaction Networks: Insight from Accurate Chemical Master Equation (ACME) Solutions”, *Conf Proc IEEE Eng Med Biol Soc.*, 1480-1483, 2016
- **Gamze Gürsoy**, Yun Xu, and Jie Liang. “Computational predictions of structures of budding yeast genome”, *Conf Proc IEEE Eng Med Biol Soc.*, 3945-8, 2014
- **Gamze Gürsoy\***, Yun Xu\*, Amy Kenter and Jie Liang. “Spatial confinement is a major determinant of folding landscape of human genome”, *Nucleic Acids Research*, 42(13):8223-8230, 2014  
**Github:** <https://github.org/uic-lianglab/CSAC>

#### Contributed Papers:

- Jing Zhang, Jason Liu, Donghoon Lee, Shaoke Lou, Zianlin Chen, **Gamze Gürsoy**, and Mark Gerstein. “DiNeR: a differential graphical model for analysis of co-regulation network rewiring”, *BMC Bioinformatics*, 21:281, 2020
- Jing Zhang, Donghoon Lee, ... , **Gamze Gürsoy**, ... , Mark Gerstein. “An integrative ENCODE resource for cancer genomics”, *Nature Communications*, 11:3696, 2020
- Jie Liang, Youfang Cao, **Gamze Gürsoy**, Hammad Naveed, Anna Terebus, and Jieliang Zhao. “Multiscale modeling of cellular epigenetic states and tissue patterning: stochasticity in molecular networks, chromatin folding in cell nucleus, and cell-cell interactions in tissue patterning”, *Crit Rev Biomed Eng.*, 43(4):323-46, 2015
- Sara M. Camp, Ermelinda Ceco, Carrie L. Evenoski, Sergei M. Danilov, Tong Zhou, Eddie T. Chiang, Liliana Moreno-Vinasco, Brandon Mapes, Jieliang Zhao, **Gamze Gürsoy**, Mary E. Brown, Djanybek M. Adyshev, Shahid S. Siddiqui, Hector Quijada, Saad Sammani, Eleftheria Letsiou, Laleh Saadat, Mohammed Yousef, Ting Wang, Jie Liang, and Joe G. N. Garcia. “Unique Toll-Like Receptor 4 Activation by NAMPT/PBEF Induces NF $\kappa$ B Signaling and Inflammatory Lung Injury”, *Scientific Reports*, 14(5):13135, 2015

- Reka Albert, Bhaskar DasGupta, Rashmi Hedge, Gowri Sangeetha Sivanathan, Anthony Gitter, **Gamze Gürsoy**, Pradyut Paul, Eduardo Sontag. “Computationally efficient measure of topological redundancy of biological and social networks”, *Physical Review E*, 84:036117, 2011
- Georgi Z. Genchev, Morten Kallberg, **Gamze Gürsoy**, Anuradha Mittal, Lalit Dubey, Ognjen Perisic, Gang Feng, and Hui Lu. “Mechanical signaling on the single protein level studies using steered molecular dynamics”, *Cell Biochemistry and Biophysics*, 55:141-152, 2009
- Mariam N. Ismail, Naftali D. Fraiman, Dennis M. Callahan Jr., **Gamze Gürsoy**, Edward Viveiros, Onnaz Ozkanat, Zhaoxia Ji, Ronald J. Willey, Juliusz Warzywoda and Albert Sacco Jr. “First unseeded hydrothermal synthesis of microporous vanadosilicate AM-6”, *Microporous and Mesoporous Materials*, 120:454-459, 2009

### Consortium Authorship

ENCODE Consortium: Co-lead of a working sub-group, integration of epigenomics data with personal genomes, co-lead of several analysis jamborees.

- ENCODE Consortium including **Gamze Gürsoy**. “An integrated encyclopedia of DNA elements in the human genome”, *Nature*, 489:57-74, 2020
- ENCODE Consortium including **Gamze Gürsoy**. “Perspectives on ENCODE”, *Nature*, 583: 693-698, 2020

PsychENCODE Consortium: Functional genomics data processing, quality control of the samples (e.g., sample swap detection).

- PsychENCODE Consortium including **Gamze Gürsoy**. “Comprehensive functional genomic resource and integrative model for the human brain”, *Science*, 362(6420):eaat8464, 2018
- PsychENCODE Consortium including **Gamze Gürsoy**. “Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder”, *Science*, 362(6420):eaat8127, 2018
- PsychENCODE Consortium including **Gamze Gürsoy**. “Transcriptome and epigenome landscape of human cortical development modeled in organoids”, *Science*, 362(6420):eaat6720, 2018
- PsychENCODE Consortium including **Gamze Gürsoy**. “Integrative functional genomic analysis of human brain development and neuropsychiatric risks”, *Science*, 362(6420):eaat7615, 2018

### TEACHING AND MENTORING

- **Fall 2019**: Guest Lecturer, Yale University
  - MB&B 594. Integrated workshop.
- **Spring 2013**: Guest Lecturer, UIC
  - BIOE 101. Introduction to Bioengineering.

- **Spring 2012:** Guest Lecturer, UIC
  - CS502. Algorithms in Computational Biology.
- **Fall 2008 – Summer 2009:** Teaching Assistant, UIC
  - BIOE 240. Modeling Physiological Data and Systems.
  - BIOE 594. Biodatamining and Machine Learning
  - BIOE 483. Molecular Modeling
- **Mentor for high school students:** Mr. Daniel Cui (currently at UC Berkeley), Ms. Rachel Hagani (currently at Carnegie Mellon University), Ms. Lindy Hong (currently at UC Berkeley), Ms. Michelle Zhu (currently at University of Illinois Urbana-Champaign), Isheng Hou (currently at University of Illinois Medical School).
- **Mentor for post-graduate trainees:** Mr. Gabriel Conte Cortez Martins (starting Oct 2020, Gerstein Lab), Ms. Charlotte Brannon (Gerstein Lab, currently grad student at Stanford), Ms. Molly Green, MS (Gerstein Lab), Heta Chokski, MS (Liang Lab).
- **Mentor for undergraduate students:**
  - Present: Amol Khanna (BME, Johns Hopkins), Vincent Schaffer (CS, Yale), Sanjna Bandaru (Biology, Brandeis), Megha Joshi (CS, Yale), Vaibhav Sharma (CS, Yale), Tucker Moses (CS, Yale), Kaitlyn Sandor (CS, Yale), Armaan Kalsi (MCDB, Yale), Leo Chen (Stat. senior thesis, Yale), Manuel Schneider (CS senior thesis, Yale), Megan Zhang (Stat., Yale), Susanna Liu (MCDB & Stat., Yale), Neehaar Gandhi (Stat., Yale), and Eva Syth (Stat., Yale).
  - Past: Mark Torres (Stat., Yale; currently analyst at DC Energy), Nancy Yu (MCDB & Stat. senior thesis, Yale; currently student at Harvard Medical School), Sarah Wagner (CS senior thesis, Yale; currently software engineer at Facebook), Samuel Berry (MB&B senior thesis, Yale; currently grad student at Harvard).

## FUNDING

- **Cancer Genomics Cloud Collaborative Project Grant:** \$30,000  
 “Pan-cancer characterization of tandem repeat expansions to understand gene dysregulation”  
**PIs:** Gamze Gursoy (Yale) & Graham S. Erwin (Stanford)
- **NIH/NHGRI K99/R00**  
 “Realistic quantification of potential privacy loss from genomic summary results”  
**PI:** Gamze Gursoy **Mentors:** Mark Gerstein (Yale) and Andrew Miranker (Yale)

## OUTREACH AND LEADERSHIP

- **Tutorial organizer** on genomics applications of homomorphic encryption, ACM-BCB 2020
- **Program committee**, GenoPri 2020
- **Mentor** at Athena by Women’s Inclusion in STEM (<https://www.athenabywistem.org>)
- **Program committee**, iDASH Privacy & Security Workshop 2018

- **Program committee**, ISMB 2019
- **500 Women Scientists** New Haven Pod Co-Coordinator
- Postdoctoral representative for **Yale MB&B Committee on Diversity and Climate** (2018-2019)
- **Co-organizer** of Biological Data Privacy session at **Pacific Symposium on Biocomputing** conference 2019 – Kona, HI
- **Co-chair** of Genome Security and Privacy session at **IEEE Biomedical and Health Informatics** conference 2019 – Chicago, IL
- **Co-organizer** of Ethics & Privacy workshop at **Pacific Symposium on Biocomputing** conference 2020 – Kona, HI
- **Spring 2018**: Panel Reviewer, Yale Institute for Biospheric Studies small grant program
- **April 2014**: Judge, Chicago Area Undergraduate Research Symposium
- **Memberships**: International Society for Computational Biology, The American Society of Human Genetics, The Biophysical Society

## INVITED TALKS AND SEMINARS

- “Quantification of private information leakage and privacy-preserving file formats for functional genomics data”, *November 2018, Biological Data Science, Cold Spring Harbor Laboratory Meeting*
- “Private information leakage from raw functional genomics data: Theoretical quantifications & practical privacy-aware file formats”, *October 2018, American Society of Human Genetics meeting, San Diego –CA*  
*Highlighted in an ASHG press release (<http://www.ashg.org/press/201810-privacy.shtml>)*
- “Privacy-preserving file formats for functional genomics data”, *October 2018, European Bioinformatics Institute (EMBL-EBI), in Hinxton near Cambridge, UK*
- “Quantification of private information leakage and privacy-preserving file formats for functional genomics data”, *Selected for presentation at NIH/BD2K ISMB 2018 Young Investigators special session (abstract competition & best presentation award winner)*
- “Quantification of private information leakage and privacy-preserving file formats for functional genomics data”, *July 2018, ISMB 2018 – HiTSeq session – Chicago, IL*
- “Conserved CTCF binding sites act as allosteric hotspots: A computational knock-out study using nC-SAC model”, *July 2018, ISMB 2018 – Chicago, IL*
- “Private information leakage in functional genomics data: Quantification, linking attacks & privacy-preserving file formats”, *February 2018, University of Bern – Bern, Switzerland*

- “Characterizing the chromatin folding landscape: Gene regulation via 3D chromatin organization in eukaryotes”, *July 2016, Yale University – New Haven, CT*
- “Computational predictions of structures of multi-chromosomes of budding yeast”, *IEEE Eng Med Biol Soc. – Chicago, IL*
- “Characterizing Chromatin Folding Landscape”, *December 2013, Koc University – Istanbul, Turkey*