

# GÜNGÖR BUDAK, MSc

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## EDUCATION

2016 (ongoing) – PhD, Computer Engineering, Middle East Technical University (METU)

Ankara, TURKEY

CGPA: TBD / 4.00 – GPA: TBD / 4.00

- ❑ Network modeling and analysis of the temporal signaling networks for ovarian cancer patients when there is a delay in freezing tumor tissue after the removal (ongoing study)

2016 – MSc, Bioinformatics, Middle East Technical University (METU)

Ankara, TURKEY

CGPA: 3.86 / 4.00 (95.80 / 100) – GPA: 3.83 / 4.00 (94.90 / 100)

- ❑ Network modeling and analysis of the temporal signaling network in *Salmonella*-infected human cells (MSc thesis work)

2014 – BSc, Biology, Middle East Technical University (METU)

Ankara, TURKEY

CGPA: 3.32 / 4.00 (83.20 / 100) – GPA: 3.75 / 4.00 (92.50 / 100)

- ❑ Design of a biosensor that can detect MRSA (Methicillin-resistant *S. aureus*)
- ❑ Developing a web-based software that constructs functional genetic devices with the input and output parameters which are defined as the activator of promoters and the production of coding sequences, respectively

2009 – Mathematics and Science, Kirami Refia Alemdaroğlu High School

Ankara, TURKEY

Diploma grade: 83 / 100

## WORK EXPERIENCE

2016 (ongoing) – Bioinformatics Analyst (full-time)

Seven Bridges Genomics, Inc.

Ankara, TURKEY

2016 (8 months) – Research Scholar (full-time)

School of Informatics and Computing, Indiana University Purdue University Institute

Indianapolis, IN, USA

- ❑ Developing a Python package and a React.js application for systematic identification and comparison of processes, phenotypes and diseases associated with RNA-binding proteins from condition-specific CLIP-seq profiles
- ❑ Transcriptome analysis of developing mouse lens tissue including novel transcript discovery and alternative splicing alterations
- ❑ Developing a database of transcriptome profiles encompassing known and novel transcripts across multiple developmental stages in eye tissues in mouse; the data have been curated from Sequence Read Archive (SRA) and European Nucleotide Archive (ENA) and quality check, alignment, transcript discovery and transcript quantification have been performed
- ❑ Developing a web resource for prognostic analyses of exons across human cancers using clinical transcriptomes obtained from The Cancer Genome Atlas (TCGA)

2015 (6 months) – Software Specialist (part-time)

Evias Pharmaceuticals R&D, Co., Ltd.

Ankara, TURKEY

- ❑ Developing a cloud-based (AWS EC2) high performance virtual screening for drug discovery web service by integrating different tools such as JSmol, JSME, Google Charts, Autodock 4, Autodock Vina, MolPort Web Services using Django (Python) web framework

2014 (10 months) – Intern (part-time)

Atlas Biotechnologies, Co., Ltd.

Ankara, TURKEY

- ❑ Communicating with foreign biotechnology product suppliers, giving orders and tracking the process including customs regulations
- ❑ Detecting possible mutations in sequences obtained from ABI format files by blasting against reference genomes database or aligning to the corresponding reference genome

2013 (3 months) – Intern (full-time)

Bioinformatics Department (BiGCaT), Maastricht University

Maastricht, THE NETHERLANDS

- ❑ Analysis of the dataset on four breast cancer cell lines to build network models that represent the active cell signaling pathways in breast cancer

2012 (3 months) – Intern (Erasmus Internship Program - full-time)

Bioinformatics Unit (HUSAR), German Cancer Research Center (DKFZ)

Heidelberg, GERMANY

- ❑ Contaminant detection and identification in Next-Generation Sequencing data by developing a pipeline which extracts the unmapped reads and compares the possible contaminant genomes in different databases using Perl programming language

## PUBLICATIONS

- ❑ **Budak, G.**, Srivastava, R., & Janga, S. C. (2017). Seten: A tool for systematic identification and comparison of processes, phenotypes and diseases associated with RNA-binding proteins from condition-specific CLIP-seq profiles. *RNA*, rna-059089.  
<https://www.ncbi.nlm.nih.gov/pubmed/28336542>
- ❑ Hashemikhabir, S., **Budak, G.**, & Janga, S. C. (2016). ExSurv: A Web Resource for Prognostic Analyses of Exons Across Human Cancers Using Clinical Transcriptomes. *Cancer Informatics*, 15(Suppl 2), 17.  
<https://www.ncbi.nlm.nih.gov/pubmed/27528797>
- ❑ Hill, S. M., Heiser, L. M., Cokelaer, T., Unger, M., Nesser, N. K., Carlin, D. E., **The HPN-DREAM Consortium**, ... & Graim, K. (2016). Inferring causal molecular networks: empirical assessment through a community-based effort. *Nature methods*, 13(4), 310-318.  
<https://www.ncbi.nlm.nih.gov/pubmed/26901648>
- ❑ **G. Budak**, O. Eren-Ozsoy, Y. Aydin-Son, T. Can, and N. Tuncbag, Reconstruction of the temporal signaling network in Salmonella-infected human cells, *Front. Microbiol.*, 6:00730, 2015. doi:10.3389/fmicb.2015.00730  
<https://www.ncbi.nlm.nih.gov/pubmed/26257716>

## PRESENTATIONS

- ❑ 2016 – Poster presentation titled ‘Seten: A tool for systematic identification and comparison of processes, phenotypes and diseases associated with RNA-binding proteins from condition-specific CLIP-seq profiles’ at GLBIO/CCBC Great Lakes Bioinformatics and the Canadian Computational Biology Conference 2016 / University of Toronto, Toronto, CANADA  
Published on F1000Research: <https://f1000research.com/posters/5-2586>
- ❑ 2015 – Poster presentation titled ‘Reconstruction of the temporal signaling network in *Salmonella*-infected human cells’ at ISMB/ECCB 2015, Intelligent Systems for Molecular Biology / European Conference on Computational Biology 2015 / The Convention Centre Dublin, Dublin, IRELAND  
Published on F1000Research: <http://f1000research.com/posters/4-292>
- ❑ 2013 – Poster presentation titled ‘CONTAMINATION: detect contaminating sequences in high-throughput sequencing data’ at ISMB/ECCB 2013, Intelligent Systems for Molecular Biology / European Conference on Computational Biology 2013 / Messe Berlin, Berlin, GERMANY (Contributed study was presented by co-authors)  
Published on F1000Research: <http://f1000research.com/posters/1094020>
- ❑ 2012 – Oral presentation titled ‘METU Biology and Genetics Student Club Introduction’ at FBI - DIYbio Outreach Workshop / Marriott Hotel, Walnut Creek, CA, USA
- ❑ 2012 – Paper presentation titled ‘M4B: A Novel Method for Designing and Ordering Genetic Constructs’ at HIBIT 2012, 7th International Symposium on Health Informatics and Bioinformatics / Cappadocia, Nevsehir, TURKEY (Contributed study was presented by co-authors)  
Published on IEEE Xplore: <http://ieeexplore.ieee.org/xpl/articleDetails.jsp?arnumber=6209054>

## COMPUTER / BIOINFORMATICS SKILLS

- ❑ Python, R, JavaScript, Perl, PHP, Java, C/C++
- ❑ HTML, CSS coding; MySQL, SQLite, NoSQL (MongoDB)
- ❑ RNA-Seq, ChIP-Seq and CLIP-Seq analyses, network modeling, virtual screening for drug discovery (docking)
- ❑ FASTX Toolkit, FastQC, HISAT, SAMtools, MACS2, StringTie, Cytoscape, NetworkX, UCSC Chimera, AutoDock4
- ❑ BLAST, Clustal family, MUSCLE, ExpASy tools, BioPython, BioPerl, Ensembl API
- ❑ Android Studio, Adobe Photoshop/Illustrator, MS Office tools, MS Windows, Unix/GNU/Linux, macOS

## LANGUAGES

- ❑ Turkish (native)
- ❑ English (fluent) / METU EPE score: 91.0 / 100 (2014)
- ❑ French (beginner)

## AWARDS AND CERTIFICATES

- ❑ 2015 – Travel funding to ISMB/ECCB 2015, Intelligent Systems for Molecular Biology / European Conference on Computational Biology 2015 by BMC Bioinformatics
- ❑ Certificate of high honor / certificate of honor: 2012 – 2013 spring, 2013 – 2014 fall / 2010 – 2011 fall, 2011 – 2012 fall, 2011 – 2012 spring, 2012 – 2013 fall
- ❑ 2011 – iGEM (International Genetically Engineered Machines) Competition World Championship ‘Software Division: Best Use of Registry’ Award / Massachusetts Institute of Technology, Cambridge, MA, USA
- ❑ 2011 – iGEM (International Genetically Engineered Machines) Competition European Jamboree Silver Medal / Vrije University, Amsterdam, THE NETHERLANDS
- ❑ 2011 – Hacettepe University Technopolis Technovation Competition Mention Award / Hacettepe University, Ankara, TURKEY

## **VOLUNTEERING**

- ❑ 2015 – Lilly AMECA 2015, Lilly Africa, Middle East and Central Asia (AMECA) 2015 / Indianapolis, IN, USA
- ❑ 2015 – ISMB/ECCB 2015, Intelligent Systems for Molecular Biology / European Conference on Computational Biology 2015 / Dublin, IRELAND
- ❑ 2013 – TEDxMaastricht / Maastricht, THE NETHERLANDS
- ❑ 2010 - 2014 – Organizing various scientific conferences on biodiversity, evolutionary biology and many other fields in biology as a member of METU Biology and Genetics Student Club / Ankara, TURKEY

## **MEMBERSHIPS**

- ❑ International Society for Computational Biology, ISCB (as a member since 2015)
- ❑ Tree of Evolution Movement (as the co-founder and developer since November, 2010) <http://www.evrimagaci.org>
- ❑ METU Biology and Genetics Student Club (as a member since September, 2009, as a member of administrative board between September, 2010 – February, 2011, as the head of the administrative board between February, 2011 – June, 2012, as a member of supervising council between June, 2012 – January, 2014)

## **INTERESTS AND HOBBIES**

- ❑ Biology, molecular biology, genetics, computer science, statistics, bioinformatics, coding, programming, website development
- ❑ Blogging on bioinformatics and English language; playing guitar; doing sports; playing basketball and football, volunteering

## **REFERENCES**

Assist. Prof. Dr. Nurcan TUNCBAG

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