

ERAY TÜZÜN

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EDUCATION:

Middle Eastern Technical University, Ankara, Turkey
Ph.D. in Information Systems 2009-2012(Expected)

Case Western Reserve University, Cleveland, OH
Master of Science in Computer Science (Concentration in Bioinformatics) December 2002
Major GPA: 3.63 /4.00
Case Prime Fellowship Award for tuition and other expenses in CWRU (2000-2002)

Bilkent University, Ankara, Turkey
Bachelor of Science in Computer Science May 2000
Full scholarship awarded by the Bilkent University for tuition and other expenses (1996-2000)

Ankara Atatürk Anadolu High School, Ankara, Turkey June 1996

WORK EXPERIENCE:

Havelsan
Research and Development Group Ankara, Turkey
Senior Software Engineer Nov 2008-Present

- Leads Software Test and Software Process Improvement teams
- Member of Command and Control Systems Framework Project, responsible for implementing a Data Distribution Service (DDS) vendor independent data layer. .

Microsoft
Communications/Collaborations Services Seattle, WA
Software Design Engineer March 2007-Nov 2008

- Worked on a Configuration Management Solution for large Data Centers. Main aim of the project is monitoring/updating the configuration state of a Data Center from a central location. (Using remote PowerShell, WinRm, CMDB, XML, C#)
- Designed/Implemented a Patching Solution for Microsoft Online (New Software as a service platform from Microsoft). (Using WSUS, PowerShell, F5 Load Balancer API, C#)
- Designed/Implemented a Virtual Server Automation Environment to enable other developers in the team to simulate Data Center environment on their own development computers. (Provided PowerShell cmdlets by utilizing Microsoft Virtual Server API)

University of Washington/Howard Hughes Medical Institute
Department of Genetics Seattle, WA
Senior Bioinformatics Specialist May 2004-March 2007

- Designed/Implemented an innovative set of algorithms to detect Structural Variation in genomes using pair-end mapping (First in this area)
- Primarily responsible for the design, implementation, testing and maintenance of software (programs and/or scripts) that facilitate large-scale data-mining of genomic, genetic and expression databases
(Programming languages used: C, Perl, Java. Environment: 50-node using Sun Grid Engine (SGE), 12Tb Linux GPFS Cluster)

- Construct specialized MySQL databases for the collection and comparison of sequence properties
- Lead a team of Junior-Level programmer analysts as well as computational students

Case Western Reserve University

Center for Computational Genomics

Software Engineer/Bioinformatics Programmer

Cleveland, OH

February 2003-May 2004

- Primarily responsible for the design, implementation, testing and maintenance of software (programs and/or scripts) that facilitate large-scale data-mining of genomic, genetic and expression databases (Programming languages used: C, Perl, XML)
- Optimization of computational pipeline for the detection and characterization of recent segmental duplications within eukaryotic genomes.
- Responsible for technical support and maintenance of the software delivered
- Implemented a Multiple Alignment Software Application
Available at: <http://compbio.cs.sfu.ca/MAM.htm>
- Collaborated with Genetics Department on several research projects

Case Western Reserve University

Department of Computer Science and Electrical Engineering

Graduate Assistant

Cleveland, OH

August 2000- December 2002

- Teaching Assistant of Computer Security, Software Engineering, Introduction to Algorithms
- Research Assistant in Bioinformatics

IBM

Research and Development Lab

Software Engineer

Stuttgart, Germany

Summer 1999

- Main Project: "PWS Code Processing via FTP" implemented in REXX
Reengineered PWS Code Mirroring process that solves the accessing problem for non-local users
- Programmed several REXX applications (installation programs, test programs)

IBM

Information Systems Administrator

Ankara, Turkey

Summer 1998

- Responsible for Network Administration and Information support of approximately 150 employees
- Participated in OV/VM-Lotus Notes Migration Project

COMPUTER SKILLS:

Programming Languages: C/C++/C#, Java, Perl, SQL, Visual Basic, Turbo Pascal, REXX, XML, Shell Scripts, PowerShell, ASP .NET

Operating Systems: Windows (All Flavors), Linux (Ubuntu), Mac OS X, IBM OS/2, MS-DOS

Computer Applications/Tools: Eclipse, Microsoft Visual Studio 2008, Microsoft Virtual Server 2005, SPSS, Microsoft SQL Server 2005, Microsoft Windows Update Services 3.0, Microsoft Product Studio, mySQL, Microsoft Exchange Server 2007, Microsoft System Center for Operations Manager. 2007, Microsoft Office Applications

Bioinformatic Applications/Tools: Blast, Repeat Masker, ClustalW, Genome Browser

HONORS & ACTIVITIES:

- Organized Bilkent Alumni Activities in Seattle
- Founder & President(2001-2004) of Cleveland Turkish Community
- Ranked 63rd in Turkish Graduate Record Examination among 30.000 graduate students in 2000
- Ranked 225th in Turkish University Entrance Exam(OYS) among 1.5 million students in 1996
- Ranked 13th in Turkey Chess Championship
- Member of National Physics Olympiad Team in 1995
- Refereed papers in Bioinformatics

SELECTED PUBLICATIONS:

- **Fine-Scale Structural Variation of the Human Genome.**
Tuzun E, Sharp AJ, Bailey JA, Kaul R, Morrison VA, Pertz LM, Haugen E, Hayden H, Albertson D, Pinkel D, Olson MV, Eichler EE.
Nat Genet. 2005 Jul;37(7):727-32. Epub 2005 May 15. (Cited By 455 papers)
- **Manipulating multiple sequence alignments via MaM and WebMaM.**
Alkan C, **Tuzun E**, Buard J, Lethiec F, Eichler EE, Bailey JA, Sahinalp SC.
Nucleic Acids Res 2005 Jul 1;33(Web Server issue):W295-8.
- **A genome-wide survey of structural variation between human and chimpanzee.**
Newman TL, **Tuzun E**, Morrison A, Hayden KE, Ventura M, McGrath SD, Rocchi M, Eichler EE.
Genome Res. 2005 Oct;15(10):1344-56. Epub 2005 Sep 16
- **Recent segmental duplications in the working draft assembly of the brown norway rat.**
Tuzun, E, Bailey, J. A, Eichler, EE.
Genome Research 2004 Apr;14(4):493-506.
- **Shotgun sequence assembly and recent segmental duplications within the human genome.**
She X, Jiang Z, Clark RA, Liu G, Cheng Z, **Tuzun E**, Church DM, Sutton G, Halpern AL, Eichler EE.
Nature 2004 Oct 21;431(7011):927-30
- **Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution.**
International Chicken Genome Sequencing Consortium
Nature. 2004 Dec 9;432(7018):695-716. Erratum in: *Nature.* 2005 Feb 17;433(7027):777.
- **Sequence and Evolution of the Genome of the Brown Norway Rat.**
Rat Genome Sequencing Project Consortium (2004)
Nature. 2004 Apr 1;428(6982):493-521.
- **Analysis of Primate Genomic Variation Reveals a Repeat-Driven Expansion of the Human Genome.**
Liu G, Program NI, Zhao S, Bailey JA, Sahinalp SC, Alkan C, **Tuzun E**, Green ED, Eichler EE.
Genome Research, 2003 Mar 1; 13(3): 358-368.
- **An algorithmic analysis of the role of unequal crossover in alpha-satellite DNA evolution**
Can Alkan, Jeff Bailey, Evan Eichler, S. Cenk Sahinalp, **Eray Tuzun**
Genome Informatics Workshop 2002, Tokyo, Japan, 2002