

Hüseyin GÜNER

+90 352 224 88 00 (7307) | huseyin.guner@agu.edu.tr

LECTURER AND BIONFORMATICS SPECIALIST

Bioinformatics specialist with extensive experience in designing, implementing, testing and analyzing large-scale data-rich biological problems through computational and statistical approaches. Acquainted with numerous professional techniques, including scripting languages, object oriented languages, database structures and operating systems and (specialized) biological databases and specific tools/programs of special interest. Continuously learning basics of multivariate statistical analysis.

Computational Literacy , including

- Familiarity with Python, Perl, Tcl , Php etc.
- Experience in C# and C/C++
- Experience in SQL scripting
- Mysql, Postgresql, Access administration and programming
- Linux, FreeBSD installation/administration
- Web based/Windows (database) application development
- Data visualization and imaging tools
- R/Bioconductor statistical environment
- Familiarity with Matlab, SAS etc. commercial software

SELECTED WORK EXPERIENCE

UW-Madison, Human Proteomics Program

2008 – 2016

Bioinformatics Specialist as an Associate Research Specialist

High-throughput data analysis and elaboration of mass-spectrometry based techniques in search of biomarkers and/or post-translational modifications . Solving group members' everyday needs in terms of computational abstraction and implementations.

Accomplishments:

- Development of top-down/middle-down proteomics windows application suite, MASH SUITE, using .Net technologies. MASH suite has been used by more than 500 users in proteomics community. Built user interfaces , modules using C# utilizing (managed) C++ library of algorithms . This suite is heavily used by our group members and researchers all around the globe Visualization of spectral data and interpretation of found entities is automated and simplified through the program workflow. Core algorithms have been modified and enhanced after long use of application.
- Characterization, identification and quantitative analysis of proteins with a known/unknown sequence information. Localization of PTMs using in-house built suite and auxiliary tools
- Analyzed Metabolomics projects of different levels of organisms with diverse biological conditions. Identified key metabolites of certain regulation states. Differential analysis and clustering of biological replicates of tissues or (body) fluids and their technical replicates. Gene Ontology and Pathway association analysis of list of potential compounds/proteins through digging KEGG , Metlin and HMDB.
- Label-free quantitative proteomics data analysis
- Built auxiliary tools to fulfill researchers' data workflow initiatives using Excel's backend VBA or other scripting languages e.g. Python, Perl , R.
- Installation of stand-alone replica of genomic databases and running data-mining routines in order to correlate research data with their biological functions.
- Tracking of user charges and times of facility load and preparing billing statements on a web application. LAMP web server maintenance
- Large-scale data backup scheduling on daily basis and monitoring on the same web-server by the aid of Cron and Bash scripting
- Helped group members prepare their publications and presentations by applying routine statistical methods and preparing figures and charts

Export/Import Consultant and IT Specialist

Provided consultation on selective export procedures and international marketing opportunities. Took part in organization of events and lectures. Developed and designed export-document-processing web application using Php and Mysql.

EDUCATION & TRAINING

Middle East Technical University, Ankara, TURKEY

Bachelor of Science, Major in Physics

Advanced level Physics curriculum , and selected courses from Biology, Philosophy and Psychology

SELECTED PUBLICATIONS

Cai, W.; **Guner, H.**; Gregorich, Z. R.; Chen, A. J.; Ayaz-Guner, S.; Peng, Y.; Valeja, S. G.; Liu, X.; Ge, Y. MASH Suite Pro: A Comprehensive Software Tool for Top-down Proteomics, *Mol. Cell. Proteomics* mcp.O115.054387.

Gregorich Z. R.; Peng, Y.; Wolff, J. J.; Guo, W.; **Guner, H.**; Doop, J.; Hacker, T. A.; Ge, Y. Comprehensive assessment of regional and transmural heterogeneity in myofilament protein phosphorylation by topdown mass spectrometry, *J. Mol. Cell. Cardiol.* 2015, 87, 103-112

Chang, Y. H.; Ye, L.; Cai, W.; Lee, Y.; **Guner, H.**; Lee, Y.; Kamp, T. J.; Zhang, J.; Ge, Y. Quantitative Proteomics Reveals Differential Regulation of Protein Expression in Recipient Myocardium after Trilineage Cardiovascular Cell Transplantation. *Proteomics*. 2015, 15, 2560-2567 doi: 10.1002/pmic.201500131

Valeja, S. G.; Xiu, L.; Gregorich, Z. R.; **Guner, H.**; Jin, S.; Ge, Y. Three dimensional liquid chromatography coupling ion exchange chromatography/hydrophobic interaction chromatography/reverse phase chromatography for effective protein separation in top-down proteomics. **Anal Chem.** 2015, 87(10), 5363-71

Chang, Y.; Gregorich Z. R.; Chen, A. J.; Hwang L.; Guner, H.; Yu, D.; Zhang, J.; Ge, Y. New mass spectrometry-compatible degradable surfactant for tissue proteomics, *J. Proteome Res.*, 2015, 14, 1587- 1599

Zhang J, Guy MJ, Norman HS, Chen YC, Xu Q, Dong X, Guner H, Wang S, Kohmoto T, Young KH, Moss RL, Ge Y (2011) Top-down quantitative proteomics identified phosphorylation of cardiac troponin I as a candidate biomarker for chronic heart failure. *J Proteome Res.* 2;10 (9):4054-65.

Xu F, Xu Q, Dong X, Guy M, **Guner H**, Hacker TA, Ge Y (2011) Top-down high-resolution electron capture dissociation mass spectrometry for comprehensive characterization of post-translational modifications in Rhesus monkey cardiac troponin I. *Int. J Mass Spect.* 305: 2

Guner, H.; Close, P.L.; Cai, W.; Zhang, H.; Peng, Y.; Chen, Y.; Gregorich, Z. R. Ge, Y. MASH Suite: A user-friendly and versatile software interface for high-resolution mass spectrometry data interpretation and visualization, *J. Am. Soc. Mass Spectrom.* 2014, 25, 464-470.

Peng, Y.; Gregorich Z. R.; Valeja, S. G.; Zhang, H.; Cai, W.; Chen, Y.; **Guner, H.**; Chen, A. J.; Schwahn, D. J.; Hacker, T. A.; Liu, X.; Ge, Y. Top-down proteomics reveals concerted reductions in myofilament and Z-disc protein phosphorylation after acute myocardial infarction, *Mol. Cell. Proteomics* 06/2014