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## Intelligent workflows for automated analysis of mass spectrometry-based proteomics data

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## Appendices

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## Curriculum Vitae

Arzu Tuğçe Güler was born on 24<sup>th</sup> of August, 1988 in Ankara, Turkey. She did her primary and secondary education in TED Ankara College and graduated from high school in 2005 as an honor student with a major in mathematics and natural sciences. She started studying Computer Engineering at TOBB Economy and Technology University (TOBB ETU) in Ankara in 2006. During the second year of her studies in 2008, she was selected by her department for the Erasmus Placement program and did a 4-month internship in Brussels, Belgium at the Turkish Research and Business Organizations Office, mainly working on tasks in relation to the EU 7<sup>th</sup> Framework Program and liaised with the national researchers. Between 2008 and 2009, she worked part-time at TOBB ETU's external affairs office as their website manager. During the third year of her studies, she did her second 4-month internship at a private information technology company where she worked on database management of the national healthcare system. She did her third and final internship during the last year of her bachelor studies at the same company and worked on a web application development project. Being always interested in bioinformatics, she did her graduation project on "algorithm development for p53 binding site prediction" and graduated with a Bachelor's degree in Computer Engineering from the Faculty of Engineering at TOBB ETU in 2010. In the fall of 2010, she started her master's studies in Bioinformatics at the Faculty of Bioscience Engineering at Katholieke Universiteit Leuven in Leuven, Belgium. She did her master's thesis at the Department of Electrical Engineering on "computational description and assessment of synonymous variations in the human genome". In 2013, she graduated with a Master's degree in Bioinformatics with a major in Bioscience Engineering. In January 2014 she moved to Leiden, The Netherlands to begin her PhD studies under the supervision of dr. Magnus Palmblad at the Center for Proteomics and Metabolomics at Leiden University Medical Center (LUMC), initially having emeritus prof. dr. Andre M. Deelder as the promotor till September 2017 and prof. dr. Manfred Wuhrer as the current promotor. During her research she attended various scientific conferences, gave talks and poster presentations, published in scientific journals, took several courses and also assisted with teaching short courses and (co-)supervised students at LUMC-Lomonosov Moscow State University Bioinformatics summer schools organized in 2014, 2015, and 2016. The papers that resulted from her PhD research are combined in this thesis entitled "Intelligent Workflows for Automated Analysis of Mass Spectrometry Based Proteomics Data". Since April 2018, she continues her research career as a Post-Doc in Reit's Group at Amsterdam UMC – AMC, focusing on proteomics of Huntington's Disease.



## PhD Portfolio

### Courses and certifications

|  |                                |
|--|--------------------------------|
| Basic course for clinical investigators (BROK)<br><i>Course &amp; National Exam</i> NFU, The Netherlands   | 6 October 2016 - 31 March 2017 |
| Introduction to 'omics data integration<br><i>Course</i><br>EMBL-EBI, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, UK  | 7 - 10 March 2017              |
| Computational methods for the analysis and interpretation of mass-spectrometric high-throughput data<br><i>Summer School</i><br>Leibniz-Zentrum für Informatik, Castle Dagstuhl, Wadern, Germany | 26 - 30 September 2016         |
| Data Stewardship for Scientific Discovery and Innovation<br><i>Summer School</i><br>LERU Doctoral Summer School, Leiden, The Netherlands   | 10-15 July 2016                |
| Advanced Proteomics Bioinformatics Workshop<br><i>Workshop</i><br>X <sup>th</sup> Annual Congress of the EuPA, Istanbul, Turkey  | 21 June 2016                   |
| Basic Methods and Reasoning in Biostatistics<br><i>Course</i><br>LUMC, Leiden, The Netherlands   | 12-16 September 2016           |
| Bioinformatics for Protein Identification<br><i>Course</i><br>64 <sup>th</sup> ASMS Conference, San Antonio, Texas, USA  | 4-5 June 2016                  |
| Proteomics Informatics Course<br><i>Course</i><br>14 <sup>th</sup> HUPO World Congress, Vancouver, B.C., Canada  | 22-25 September, 2015          |
| Communication in Science<br><i>Hands-on Training</i><br>Leiden University, Leiden, The Netherlands   | 15 January – 12 February 2015  |
| Fundamentals of Mass Spectrometry<br><i>Short Course</i><br>20 <sup>th</sup> IMSC, Geneva, Switzerland   | 23-24 August 2014              |

## **Teaching and supervision experience**

### **Teaching assistant**

6 April 2017

Short course: *"Introduction to Cytoscape"*  
LUMC, Leiden, The Netherlands

### **Lecturer**

24 August 2016

Topic: *"Taverna workflows"*  
Workshop on Computational Biology, Department for Biochemistry and Molecular Biology, University of South Denmark

### **Co-supervisor to two undergrad students**

July-August 2016

Project: *"Splitting tandem MS datasets into molecular classes using machine learning"*  
LUMC-Lomonosov Moscow State University Bioinformatics Summer School, LUMC, Leiden, The Netherlands

### **Supervisor to two undergrad students**

July-August 2015

Project: *"Visualization of gene and protein expression data in spatial context"*  
LUMC-Lomonosov Moscow State University Bioinformatics Summer School, LUMC, Leiden, The Netherlands

### **Teaching assistant**

26-27 January 2015

Short course: *"Linux and basic scripting short course"*  
LUMC, Leiden, The Netherlands

### **Co-supervisor to two undergrad students**

July-August 2014

Project: *"Barcoding of life using shotgun tandem mass spectrometry"*  
LUMC-Lomonosov Moscow State University Bioinformatics Summer School. LUMC, Leiden, The Netherlands

## **Poster Presentations**

**Guler, A. T.**, Palmblad, M. Experimental setup independent automated internal calibration of LC-MS data for non-targeted proteomics analysis. *65<sup>th</sup> American Society for Mass Spectrometry Conference on Mass Spectrometry and Allied Topics*. Indianapolis, Indiana, USA, Jun 4 - 8, 2017.

**Guler, A. T.**, Travin, D., Mohammed, Y., Palmblad, M. Scientific workflows for data analysis and visualization in quantitative proteomics. *64<sup>th</sup> American Society for Mass Spectrometry Conference on Mass Spectrometry and Allied Topics*. San Antonio, Texas, USA, Jun 5 - 9, 2016.

**Guler, A. T.**, Palmblad, M. Intelligent workflows for proteomics data analysis. *Human Proteome Organization World Congress*. Vancouver, Canada, Sep 27 - 30, 2015.

**Guler, A. T.,** Waaijer, C. J. F., Palmblad, M. Mapping scientific pedigrees and collaborative patterns using bibliometrics: six former presidents of the ASMS. *63<sup>rd</sup> American Society of Mass Spectrometry Conference on Mass Spectrometry and Allied Topics*. St. Louis, USA, May 31 - Jun 4, 2015.

**Guler, A. T.,** Palmblad, M. Protein quantitation combining MS and MS/MS data with intelligent workflows. *63<sup>rd</sup> American Society of Mass Spectrometry Conference on Mass Spectrometry and Allied Topics*. St. Louis, USA, May 31 - Jun 4, 2015.

**Guler, A. T.,** Mohammed, Y., Palmblad, M. Intelligent workflows for label-free, quantitative proteomics. *Dutch Techcentre for Life Sciences on track*. Amersfoort, The Netherlands, Dec 1, 2014.

### **Oral Presentations**

**Guler, A. T.** Scientific workflows for combining MS and MS/MS data and improving mass measurement accuracy in proteomics. *2<sup>nd</sup> Annual Danish Bioinformatics Conference*. Odense, Denmark, Aug 25 - 26, 2016.

**Guler, A. T.** Integration and visualization of multi-omics data in animal models. *X Annual Congress of the European Proteomics Association*. Istanbul, Turkey, Jun 22 - 25, 2016.

**Guler, A. T.** Use of ontologies for automated data processing and their challenges: a bioinformatics view. *The Information Universe Conference*. Groningen, The Netherlands, Oct 7 - 9, 2015.

**Guler, A. T.,** Waaijer, C. J. F., Palmblad, M. Scientific workflows for bibliometrics. *15<sup>th</sup> International Conference on Scientometrics and Informetric*. Istanbul, Turkey, Jun 29 - Jul 4, 2015.

**Guler, A. T.** Scientific workflows for proteomics. *11<sup>th</sup> Ardgour Symposium*. Ardgour, Scotland, Sep 8 - 12, 2014.



## List of Publications

Sap, K. A.\*, **Guler, A. T.\***, Bury, A., Dekkers, D., Demmers, J. A. A., Reits, E. A. [Identification of Full-Length Wild-Type and Mutant Huntingtin Interacting Proteins by Crosslinking Immunoprecipitation in Mice Brain Cortex](#). *J. Huntington's Dis.* **10**, 335-347 (2021). (\*shared first authors)

Sap, K. A., **Guler, A. T.**, Bezstarosti, K., Bury, A. E., Juenemann, K., Demmers, J. A. A., Reits, E. A. [Global Proteome and Ubiquitinome Changes in the Soluble and Insoluble Fractions of Q175 Huntington Mice Brains](#). *Mol. Cell. Proteomics* **18**, 1705-1720 (2019).

Travin, D., Popov, I., **Guler, A. T.**, Medvedev, D., van der Plas-Duivesteyn, S., Alvarez, M. V., Kolder, I. C. R. M., Meijer, A. H., Spaink, H., Palmblad, M. [COMICS: Cartoon visualization of omics data with spatial context using anatomical ontologies](#). *Journal of Proteome Research*, **17**, 739-744 (2018). [This thesis]

Farnham, A., Kurz, C., Ozturk, M. A., Solbiati, M., Myllyntaus O., Meekes, J., Pham, T. M., Paz, C., Langiewicz, M., Andrews, S., Kanninen, L., Agbembabiese, C., **Guler, A. T.**, Durieux, J., Jasim, S., Viessmann, O., Frattini, S., Yembergenova, D., Benito, C. M., Porte, M., Grangeray-Vilmint, A., Curiel, R. P., Rehncrona, C., Malas, T., Esposito, F., Hettne, K. [Early Career Researchers Want Open Science](#). *Genome Biology*, **18**, 221 (2017).

Hussaarts, L., Kaisar, M. M. M., **Guler, A. T.**, Dalebout, H., Everts, B., Deelder, A. M., Palmblad, M., Yazdanbakhsh, M. [Human dendritic cells with Th2-polarizing capacity: analysis using label-free quantitative proteomics](#). *International Archives of Allergy and Immunology*, **174**, 170-182 (2017).

Kolder, I. C. R. M., van der Plas-Duivesteyn, S. J., Tan, G., Wiegertjes, G. F., Forlenza, M., **Guler, A. T.**, Travin, D. Y., Nakao, M., Moritomo, T., Irnazarow, I., den Dunnen, J. T., Anvar, S. Y., Jansen, H. J., Dirks, R. P., Palmblad, M., Lenhard, B., Henkel, C. V., Spaink, H. P. [A full-body transcriptome and proteome resource for the European common carp](#). *BMC Genomics*, **17**, 701 (2016).

**Guler, A. T.**, Waaijer, C. J. F., Mohammed, Y., Palmblad, M. [Automating bibliometric analysis using Taverna scientific workflows: A tutorial on integrating Web Services](#). *Journal of Informetrics*, **10**, 830-841 (2016). [This thesis]

**Guler, A. T.**, Waaijer, C. J. F., Palmblad, M. [Scientific workflows for bibliometrics](#). *Scientometrics*, **107**, 385-398 (2016766). [This thesis]



