

# Ting Huang

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## PERSONAL INFORMATION

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Address: West Village H 310C (Khoury), Northeastern University, Boston, Massachusetts, USA  
Google Scholar: <http://scholar.google.com/citations?user=rUFbIE4AAAAJ&hl=en>  
Website: <https://huang704.github.io/PersonalSite/dist/>

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## EDUCATION

<i>PhD candidate</i> , Computer Science. Advisor: Olga Vitek Khoury College of Computer Sciences Northeastern University, USA	05/2015-now
<i>PhD program</i> , Statistics. Advisor: Olga Vitek Department of Statistics Purdue University, USA	08/2014-05/2015
<i>MS</i> , Computer Applied Technology. Advisor: Zengyou He School of Software Dalian University of Technology, P.R. China	09/2011-06/2014
<i>Bachelor</i> in Software Engineering School of Software Dalian University of Technology, P.R. China	09/2007-06/2011

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## RESEARCH INTERESTS

My research area is computational biology and biostatistics. My current focus is on developing methods of statistical inference and computational tools for mass spectrometry-based relative protein quantification. I'm the main developer and maintainer of R/Bioconductor package MSstatsTMT.

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## EXPERIENCE

### Summer intern:

Research and development team, Biognosys AG, Switzerland	05/2017-08/2017
<ul style="list-style-type: none"><li>• Design benchmarking experiments for relative protein quantification in data-independent acquisition (DIA).</li><li>• Combine precursor and fragment information for improved detection of differential abundance in data independent acquisition (DIA).</li></ul>	

### Graduate Research Assistant:

Olga Vitek's Lab, Northeastern University	05/2015-present
<ul style="list-style-type: none"><li>• Develop statistical methods and open-source softwares for relative protein quantification and group comparison in mass spectrometry-based experiments with isobaric labeling (iTRAQ and TMT).</li><li>• Develop simulation-based methods and open-source software for sample size estimation and optimal design of mass spectrometry-based proteomic experiments.</li></ul>	
Olga Vitek's Lab, Purdue University	05/2017-08/2017
<ul style="list-style-type: none"><li>• Develop, evaluate and implement a statistical approach for identifying multivariate but robust, interpretable and accurate panels of gene biomarkers of drug therapy response.</li></ul>	
Zengyou He's Lab, Dalian University of Technology	09/2011-06/2014
<ul style="list-style-type: none"><li>• Develop a linear programming model for protein inference problem in shotgun proteomics (DDA).</li></ul>	

- Develop a constrained Lasso regression approach to utilize peptide detectability for protein inference problem in shotgun proteomics(DDA).

#### Teaching Assistant:

College of Computer and Information Science 01/2016-05/2016

- *Topics in Statistics and Data Analysis*. Grading, office hours support for 14 graduate students.

School of Software, Dalian University of Technology 09/2012-12/2012

- *Data Structures & Algorithms*. Exercises, grading, lab tutorials for 30 undergraduate students.

## HONORS AND AWARDS

#### Travel stipend:

- Annual Conference of American Society for Mass Spectrometry (ASMS), 2019
- Annual Conference of the US Human Proteome Organization (USHUPO), 2017, 2018, 2019
- Annual World Congress of the Human Proteome Organization (HUPO), 2018

Northeastern University Dissertation Completion Fellowship award, 2021

Wolfgang Goetzinger-Amgen Memorial Scholar Award in Life Science Analysis, 2016

- The award was established by Amgen in memory of Wolfgang Goetzinger. It provides \$5,000 to support student travel, education or research expenses.

Lucille Zanghi '72 and Jim Dow '72 Graduate Fellowship in Bioinformatics, 2015

- The fellowship supports promising graduate students conducting bioinformatics research related to chemotherapy. It offers \$2,500 for conference travel and other research expenses.

Scholar Star of Graduate, 2013

- Each year, Dalian University of Technology selects 10 out of all the graduate students to award their excellent research work.

## PUBLICATIONS

#### Peer-reviewed publications

- [1] T. Maculins, E. Verschuere, T. Hinkle, P. Chang, C. Chalouni, J. Lim, A. Katakam, R. Kunz, B. Erickson, **T. Huang**, M. Choi, T. Tsai, O. Vitek, M. Reichelt, J. Rohde, I. Dikic, D. Kirkpatrick and A. Murthy. Proteomics of autophagy deficient macrophages reveals enhanced antimicrobial immunity via the oxidative stress response. *eLife*, 2021.
- [2] **T. Huang\***, M. Choi\*, M. Tzouros, S. Golling, N. Pandya, B. Banfai, T. Dunkley and O. Vitek. MSstatsTMT: Statistical detection of differentially abundant proteins in experiments with isobaric labeling and multiple mixtures. *Molecular & Cellular Proteomics*, 19:1706, 2020.
- [3] **T. Huang\***, R. Bruderer\*, J. Muntel, Y. Xuan, O. Vitek and L. Reiter. Combining precursor and fragment information for improved detection of differential abundance in data independent acquisition. *Molecular & Cellular Proteomics*, 19:421, 2020.
- [4] M. Choi, J. Carver, C. Chiva, M. Tzouros, **T. Huang**, T. Tsai, B. Pullman, O. M. Bernhardt, R. Hüttenhain, G. Ci Teo, Y. Perez-Riverol, J. Muntel, M. Müller, S. Goetze, M. Pavlou, E. Verschuere, B. Wollscheid, A. I. Nesvizhskii, L. Reiter, T. Dunkley, E. Sabidó, N. Bandeira and O. Vitek. MassIVE.quant: A community resource of curated quantitative mass spectrometry-based proteomics datasets. *Nature Methods*, 17:981, 2020.
- [5] J. Muntel, J. Kirkpatrick, R. Bruderer, **T. Huang**, O. Vitek, A. Ori and L. Reiter. Comparison of protein quantification in a complex background by DIA and TMT workflows with fixed instrument time. *Journal of Proteome Research*, 18:1340, 2019.
- [6] Z. He, **T. Huang**, X. Liu, P. Zhu, B. Teng and S. Deng. Protein inference: A protein quantification perspective. *Computational Biology and Chemistry*, 63:21, 2016.

\*Equal contribution

- [7] Z. He, **T. Huang**, C. Zhao, B. Teng. Protein Inference. *Modern Proteomics–Sample Preparation, Analysis and Practical Applications*, 237-42, 2016.
- [8] B. Teng, **T. Huang** and Z. He. Decoy-free protein-level false discovery rate estimation. *Bioinformatics*, 30:675, 2013.
- [9] **T. Huang**, H. Gong, C. Yang and Z. He. ProteinLasso: a Lasso regression approach to protein inference problem in shotgun proteomics. *Computational Biology and Chemistry*, 43:46, 2013.
- [10] **T. Huang** and Z. He. A linear programming model for protein inference problem in shotgun proteomics. *Bioinformatics*, 28:2956, 2012.
- [11] **T. Huang**, J. Wang, W. Yu and Z. He. Protein inference: A review. *Briefings in Bioinformatics*, 13:586, 2012.

#### Submitted

- [1] M. Choi, T. Tsai, **T. Huang**, N. Shulman, O. M. Bernhardt, A. I. Nesvizhskii, L. Reiter, E. Sabidó, B. X. MacLean and O. Vitek. MSstats maximizes the producibility of detecting differentially abundant proteins across tools that process raw mass spectra. *Under revision*.

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#### SOFTWARE

- [1] *MSstatsTMT*: An R-package for protein significance analysis in shotgun mass spectrometry-based proteomic experiments with tandem mass tag (TMT) labeling [Bioconductor and GitHub]
  - 3,960 downloads from 1,684 unique IPs in Bioconductor since October 2018.
- [2] *MSstatsSampleSize*: An R-package for optimal design of high-dimensional MS-based proteomics experiments [Bioconductor and GitHub]

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#### PRESENTATIONS

- 2020 MSstatsTMT: Statistical detection of differentially abundant proteins in experiments with isobaric labeling and multiple mixtures.  
*Contributed talk, Bioconductor Conference, Boston MA.*
- 2019 MSstatsTMT: Statistical detection of differentially abundant proteins in experiments with isobaric labeling and multiple mixtures.  
*Poster, Annual Conference of American Society for Mass Spectrometry (ASMS), Atlanta GA.*
- 2019 Combining precursor and fragment information for improved detection of differential abundance in data independent acquisition.  
*Lightning talk and poster, Annual Conference of the US Human Proteome Organization (USHUPO), Rockville MD.*
- 2018 MSstatsTMT: Statistical detection of differentially abundant proteins in mass spectrometry experiments with isobaric labeling.  
*Promoted talk, World Congress of the Human Proteome Organization (HUPO), Orlando FL.*
- 2018 MSstatsTMT: Statistical detection of differentially abundant proteins in mass spectrometry experiments with isobaric labeling.  
*Lightning talk and poster, Annual Conference of the US Human Proteome Organization (USHUPO), Minneapolis MN.*
- 2017 Optimization of the number of proteins and biological replicates in large-scale proteomics.  
*Lightning talk and poster, Annual Conference of the US Human Proteome Organization (USHUPO), San Diego CA.*

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#### REFEREE

- 2020 *Journal of the American Society for Mass Spectrometry, PLOS One, Bioinformatics*
- 2019 *Journal of Proteome Research, Bioinformatics, Molecular & Cellular Proteomics*

## **SHORT COURSE INSTRUCTOR**

- 2020 May Institute - Computation and statistics for mass spectrometry and proteomics. 2 weeks, Northeastern University, Boston MA.
- 2019 Short course - Quantitative proteomics: case Studies. 2 days, Annual Conference of American Society for Mass Spectrometry (ASMS), Atlanta GA.
- 2019 May Institute - Computation and statistics for mass spectrometry and proteomics. 2 weeks, Northeastern University, Boston MA.
- 2018 May Institute - Computation and statistics for mass spectrometry and proteomics. 2 weeks, Northeastern University, Boston MA.
- 2017 May Institute - Computation and statistics for mass spectrometry and proteomics. 2 weeks, Northeastern University, Boston MA.
- 2017 Workshop - Introduction to statistical methods for life scientists. 1 day, Annual meeting of the Association of Biomolecular Resource Facilities (ABRF), San Diego CA.