Ting Huang
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PERSONAL INFORMATION

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EDUCATION

PhD candidate, Computer Science. Advisor: Olga Vitek   05/2015-now
Khoury College of Computer Sciences
Northeastern University, USA

PhD program, Statistics. Advisor: Olga Vitek   08/2014-05/2015
Department of Statistics
Purdue University, USA

MS, Computer Applied Technology. Advisor: Zengyou He   09/2011-06/2014
School of Software
Dalian University of Technology, P.R. China

Bachelor in Software Engineering   09/2007-06/2011
School of Software
Dalian University of Technology, P.R. China

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 pacakge MSstatsTMT.

EXPERIENCE

Summer intern:

Research and development team, Biognosys AG, Switzerland   05/2017-08/2017
- Design benchmarking experiments for relative protein quantification in data-independent acquisition (DIA).
- Combine precursor and fragment information for improved detection of differential abundance in data independent acquisition (DIA).

Graduate Research Assistant:

Olga Vitek's Lab, Northeastern University   05/2015-present
- 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).
- Develop simulation-based methods and open-source software for sample size estimation and optimal design of mass spectrometry-based proteomic experiments.

Olga Vitek's Lab, Purdue University   05/2017-08/2017
- Develop, evaluate and implement a statistical approach for identifying multivariate but robust, interpretable and accurate panels of gene biomarkers of drug therapy response.

Zengyou He's Lab, Dalian University of Technology   09/2011-06/2014
- Develop a linear programming model for protein inference problem in shotgun proteomics (DDA).

- 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. Verschueren, 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. Verschueren, 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.

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*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.*

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]

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.

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.