

CONTACT INFORMATION	College of Science and College of Computer and Information Science Northeastern University 360 Huntington Ave Boston, MA, USA 02115	email: <a href="mailto:m.choi@northeastern.edu">m.choi@northeastern.edu</a> twitter: <a href="https://twitter.com/MeenaChoi">@MeenaChoi</a> github: <a href="https://github.com/MeenaChoi">MeenaChoi</a> website: <a href="https://meenachoi.github.io">meenachoi.github.io</a>
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RESEARCH INTERESTS Development of statistical methods, tools and software for the analysis of mass spectrometry-based proteomics and metabolomic data, Integrative analyses of genomic, proteomic and metabolomic experiments, Interdisciplinary research for biomarker discovery of disease, Statistical consulting for design and analysis of experiments

## EDUCATION

- 2016 **PhD., Statistics**, Department of Statistics, Purdue University, West Lafayette, IN USA  
*Ph.D. Advisors: Olga Vitek, Ph.D. (Statistics - Purdue University)*  
*Dissertation: A flexible framework for statistical design and analysis of quantitative mass spectrometry-based proteomics: a split plot approach, and its implementation in MSstats*
- 2011 **M.A., Applied Statistics**, Department of Statistics, Purdue University, West Lafayette, IN USA
- 2008 **B.S., Management**, Krannert school of management, Purdue University, West Lafayette, IN USA  
*Honors with Distinction*
- 2002 **B.S., Biology**, Department of Biological Sciences, Korea Advanced Institute of Science and Technology, Daejeon, South Korea

## PROFESSIONAL POSITIONS

- Sep 2018 - Present **Associate Research Scientist**  
Khoury College of Computer and Information Sciences, Northeastern University, Boston, MA
- Apr 2016 - Aug 2018 **Postdoctoral Research Associate**  
College of Science and College of Computer and Information Science, Northeastern University, Boston, MA  
*Mentor: Olga Vitek, Ph.D.*
- Aug 2016 - Dec 2016 **Statistical consultant**  
Alkahest, Inc., San Carlos, CA  
*Statistical analysis for somalogic data, mass spectrometric-based proteomic data, Consulting about statistical design of experiment*
- Sep 2010 - Dec 2015 **Research Assistant**  
Department of Statistics, Purdue University, West Lafayette, IN  
*Ph.D. Advisors: Olga Vitek*
- Jan 2010 - Dec 2011 **Teaching Assistant**  
Department of Statistics, Purdue University, West Lafayette, IN  
*Elementary Statistical Methods, Applied Regression Analysis, Design of Experiments, Intermediate Statistical Methodology, Advanced Statistical Methodology, Statistical Methods For Bioinformatics and Computational Biology*

## Professional Societies

- 2014 - Present Member, American Society of Mass Spectrometry (ASMS)
- 2013 - Present US Human Proteome Organization (US HUPO)

## HONORS &amp; AWARDS

- 2013 ThinkSwiss Research Scholarship from Embassy of Switzerland in the United States of America

## Peer-reviewed Journal Articles

- [1] Caron E, Roncagalli R, Hase T, Wolski W, Hase T, **Choi M**, Menoita MG, Durand S, Garcia-Blesa A, Fierro-Monti I, Sajic T, Heusel M, Weiss T, Malissen M, Schlapbach R, Collins B, Ghosh S, Kitano H, Aebersold R, Malissen B, Gstaiger M. (2017). Precise temporal profiling of GRB2 protein complexes in primary T cells using SWATH mass spectrometry, *Cell Reports* **18**(13):3219-3226. doi:<http://dx.doi.org/10.1016/j.celrep.2017.03.019>. PMID: 28355572. PMCID: PMC5382234.
- [2] Abbatiello SE, Ackermann BL, Borchers CH, Bradshaw RA, Carr SA, Chalkley RJ, **Choi M**, Deutsch EW, Domon B, Hoofnagle AN, Keshishian H, Kuhn E, Liebler DC, MacCoss MJ, MacLean B, Mani DR, Neubert H, Smith S, Vitek O, Zimmerman L. (2017). New Guidelines for Publication of Manuscripts Describing Development and Application of Targeted Mass Spectrometry Measurements of Peptides and Proteins. *Molecular & Cellular Proteomics* **16**(3):327-328. doi:[10.1074/mcp.E117.067801](https://doi.org/10.1074/mcp.E117.067801). PMID: 28183812. PMCID: PMC5340997.
- [3] **Choi M\***, Eren-Dogu ZF\*, Colangelo C, Cottrell J, Hoopmann MR, Kapp EA, Kim S, Lam H, Neubert TA, Palmblad M, Phinney BS, Weintraub ST, MacLean B, Vitek O. (2017) ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of differentially abundant proteins in label-free quantitative LC-MS/MS experiments. *Journal of Proteome Research* **16**(2):945-957. doi:[10.1021/acs.jproteome.6b00881](https://doi.org/10.1021/acs.jproteome.6b00881). PMID: 27990823.
- [4] Terfve C, Sabidó E, Wu Y, Gonçalves E, **Choi M**, Vaga S, Vitek O, Saez-Rodriguez J, Aebersold R. (2016). System-wide quantitative proteomics of the metabolic syndrome in mice: genotypic and dietary effects. *Journal of Proteome Research* **16**(2):831-841. doi:[10.1021/acs.jproteome.6b00815](https://doi.org/10.1021/acs.jproteome.6b00815). PMID: 27936760.
- [5] Borràs E, Cantó E, **Choi M**, Maria Villar L, Álvarez-Cermeño JC, Chiva C, Montalban X, Vitek O, Comabella M, Sabidó E. (2015). Protein-based classifier to predict conversion from Clinically Isolated Syndrome to Multiple Sclerosis. *Molecular & Cellular Proteomics* **15**(1):318-28. doi:[10.1074/mcp.M115.053256](https://doi.org/10.1074/mcp.M115.053256). PMID: 26552840. PMCID: PMC4762525.
- [6] Surinova S, **Choi M**, Tao S, Schöffler PJ, Chang C, Clough T, Vysloužil K, Khoylou M, Srovnal J, Liu Y, Matondo M, Hüttenhain R, Weisser H, Buhmann JM, Hajdúch M, Brenner H, Vitek O, Aebersold R. (2015). Prediction of colorectal cancer diagnosis based on circulating plasma proteins. *EMBO Molecular Medicine* **7**(9):1166-1178. doi:[10.15252/emmm.201404873](https://doi.org/10.15252/emmm.201404873). PMID: 26253081. PMCID: PMC4568950.
- [7] Surinova S, Radová L, **Choi M**, Srovnal J, Brenner H, Vitek O, Hajdúch M, Aebersold R. (2015). Non-invasive prognostic protein biomarker signatures associated with colorectal cancer. *EMBO Molecular Medicine* **7**(9):1153-1165. doi:[10.15252/emmm.201404874](https://doi.org/10.15252/emmm.201404874). PMID: 26253080. PMCID: PMC4568949.
- [8] **Choi M**, Chang CY, Clough T, Broudy D, Killeen T, MacLean B, Vitek O. (2014). MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments. *Bioinformatics* **30**:2524-2536. doi:[10.1093/bioinformatics/btu305](https://doi.org/10.1093/bioinformatics/btu305). PMID: 24794931
- [9] Broudy D, Killeen T, **Choi M**, Shulman N, Mani DR, Abbatiello SE, Mani E, Ahmad R, Sahu AK, Schilling B, Tamura K, Boss Y, Sharma V, Gibson BW, Carr SA, Vitek O, MacCoss MJ, MacLean B. (2014). A framework for installable external tools in Skyline. *Bioinformatics* **30**(17):2521-2523. doi:[10.1093/bioinformatics/btu148](https://doi.org/10.1093/bioinformatics/btu148). PMID: 24713211. PMCID:PMC4147880.
- [10] Cerciello F, **Choi M**, Nicastri A, Bausch-Fluck D, Ziegler A, Vitek O, Felley-Bosco E, Stahel R, Aebersold R, Wollscheid B. (2013). Identification of a seven glycopeptide signature for malignant pleural mesothelioma in human serum by selected reaction monitoring. *Clinical Proteomics* **10**(1):16. doi:[10.1186/1559-0275-10-16](https://doi.org/10.1186/1559-0275-10-16). PMID: 24207061. PMCID: PMC3827840.
- [11] Tarca AL, Lauria M, Unger M, Bilal E, Boue S, Kumar Dey K, Hoeng J, Koeppl H, Martin F, Meyer P, Nandy P, Norel R, Peitsch M, Rice JJ, Romero R, Stolovitzky G, Talikka M, Xiang Y, Zechner C, IMPROVER DS Collaborators: Veliz-Cuba A, Song J, Nguyen H, Zeller M, Sadowski P, Klamt S, Heise S, Gustafsson M, Malovini A, Mulas F, Barbarini N, Unger M, Nandy P, Kumar Dey K, Zechner C,

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\*Equal contribution

Koepl H, Cristea N, Petty T, Liu Y, Ting Liu T, Zhao C, Felici G, Lauria M, Provero P, Tabak EG, Haibe-Kains B, Papillion-Cavanagh S, De Jay N, Dreos R, Zhou F, Zhang W, Chen Z, Yuxuan H, Chau K, de Almeida RM, da Silva SR, Perrone GC, Rossell D, Aloy P, Ong ML, Voichita C, Haidarian S, Tagett R, Hopp L, Li B, Bhattacharjee M, Gu JL, **Choi M**, Poirel C, Badger D, Rahman A, Rodrigues R, Balov N, Chikina M, Zaslavsky E, Tarca AL, Romero R, Ren X, Horvath S, Song L, Efroni S, Ben-Hamo R, Suarez-Farinas M, Tian S, Lee S, Lim WK, Liu X, Chen L, Zeng T, Huang D, Haibe-Kains B, Hu I, Sinan Sarac AM, Ayoubi T, Wang K, Cho JH, Lin A, Ye C, Li J, Cui H, Salzman P, Sysi-Aho M, Castillo Priego S, Oresic M, Peddinti G, Di Camillo B, Maier Z, Wen Z, Zhang XD. (2013). Strengths and limitations of microarray-based phenotype prediction: lessons learned from the IMPROVER Diagnostic Signature Challenge. *Bioinformatics* **29**(22):2892-9. doi:[10.1093/bioinformatics/btt492](https://doi.org/10.1093/bioinformatics/btt492). PMID: 23966112. PMCID: PMC3810846.

## Submitted

- [1] Hüttenhain R\*, **Choi M\***, Fuente LM, Oehl K, Chang C, Zimmermann AK, Malander S, Olsson H, Surinova S, Clough T, Dinulescu D, Wild P, Niméus-Malmström E, Vitek O, and R. Aebersold R. A targeted mass spectrometry strategy for developing proteomic biomarkers: a case study of epithelial ovarian cancer. *Submitted*.
- [2] Cerciello F, **Choi M**, Lomeo K, Amann JN, Felley-Bosco E, Stahel RA, Robinson B, Creaney J, Pass HI, Vitek O, Carbone DP. Multiplexed targeted proteomics signature for serum diagnostic of malignant pleural mesothelioma. *Submitted*.

## PRESENTATIONS

### Invited Talks

- [1] [Quantitative approaches in discovery proteomics: How do they measure up?](#) nature.com webcasts. 2018 Nov 7.
- [2] Statistical design and analysis for reproducible quantitative mass spectrometry-based experiments. The Association of Biomolecular Resource Facilities (ABRF) Annual Meeting. 2018 Apr 25. Myrtle Beach, SC, USA.
- [3] Statistical design and analysis for reproducible quantitative mass spectrometry-based experiments. The Ohio State University and Waters Corporation joint core facilities event: Past, Present and Future direction. 2018 Mar 16. Columbus, OH, USA.
- [4] Experimental design and data analysis - Data interpretation and statistical analysis. EMBO practical course on targeted proteomics. 2016 Nov 17. Barcelona, Spain.
- [5] Statistical analysis with MSstats. Session : Proteomics in the Era of large datasets, Northeast Regional Life Sciences Core Directors (NERLSCD). 2016 Oct 14. Boston, MA, USA.
- [6] Computational and statistics for quantitative proteomics. Workshop, Annual Conference of the US Human Proteome Organization (US HUPO). 2016 Mar 14. Boston, MA, USA.
- [7] [Experimental design and data analysis - Data interpretation and statistical analysis](#). EMBO practical course on targeted proteomics. 2014 Sep 19. Barcelona, Spain
- [8] Experimental design and statistics, Statistical analysis with MSstat. Bioinformatics seminar, Seoul National University, College of Medicine. 2014 Oct 21. Seoul, Korea.
- [9] MSstats as an external tool in Skyline - an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments. Third annual Skyline user group meeting at American society for Mass Spectrometry (ASMS). 2014 Jun 15. Baltimore, USA.

### Selected Poster Presentations

- [1] Cerciello F, **Choi M**, Katie L, Joseph A, Emanuela FB, Rolf S, Robinson B, Creaney J, Harvey P, Vitek O, David C. Diagnosis of malignant pleural mesothelioma cancer relying on targeted proteomics in blood. Poster presented at *World Congress of the Human Proteome Organization (HUPO)*. 2018 Sep 30-Oct 3. Orlando, FL, USA.

- [2] Huang H, **Choi M**, Tzouros M, Pandya N, Banfai B, Dunkley T, Vitek O. Statistical model for detecting differentially abundant proteins in isobaric labeling-based protein quantification experiments. Poster presented at *Annual Conference of the US Human Proteome Organization (US HUPO)*. 2018 Mar 12-13. Minneapolis, USA.
- [3] Cerciello F, **Choi M**, Katie L, Joseph A, Emanuela FB, Rolf S, Robinson B, Creaney J, Harvey P, Vitek O, David C. Multiplexed targeted proteomics signature for serum diagnostic of malignant pleural mesothelioma. Poster presented at *European Society for Medical Oncology (ESMO 2017 Congress)*. 2017 Sep 8-12. Madrid, Spain.
- [4] **Choi M**, Sabidó E, Bernhardt O, Shulman N, MacLean B, Vitek O. Detection of differentially abundant proteins with MSstats 3.6 improves reproducibility between data processing tools. Poster presented at *Annual Conference of American Society for Mass Spectrometry (ASMS)*. 2017 Jun 6. Indianapolis, USA.
- [5] Cerciello F, **Choi M**, Katie L, Joseph A, Emanuela FB, Rolf S, Robinson B, Creaney J, Harvey P, Vitek O, David C. Targeted proteomics based clinical investigation of serum early detection biomarkers for malignant pleural mesothelioma cancer. Poster presented at *World Congress of the Human Proteome Organization (HUPO)*. 2016 Sep 10. Taipei, Taiwan.
- [6] **Choi M**, Dogu E, Galitzine C, Vitek O. New developments in MSstats: statistical process control, LoD/LoQ, and relative protein quantification with split plot approach. Poster presented at *Annual Conference of American Society for Mass Spectrometry (ASMS)*. 2016 Jun 9. San Antonio, USA.
- [7] **Choi M**, Chang L, Shulman N, Pavlou M, Chiva C, Verschueren E, Wollscheid B, Sabidó E, MacLean B, Vitek O. Relative protein quantification in mass spectrometry-based proteomics: a split plot approach. Poster presented at *Annual Conference of the US Human Proteome Organization (US HUPO)*. 2016 Mar 14-15. Boston.
- [8] **Choi M**, Chang L, Clough T, Broudy D, Killen T, MacLean B, Vitek O. MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments. Poster presented at *Annual Conference of the US Human Proteome Organization (US HUPO)*. 2014 Apr 7-8. Seattle, USA.
- [9] **Choi M**, Clough T, Vitek O. Statistical protein quantification and interpretation in label-free and label-based LC-MS and SRM workflows. Poster presented at *World Congress of the Human Proteome Organization (HUPO)*. 2012 Sep. Boston, USA.
- [10] Chang C, **Choi M**, Picotti P, Hüttenhain R, Heinzelmann-Schwarz V, Jovanovic M, Aebersold R, Vitek O. SRMstats: An Open-Source Software Suite for Protein Quantification in SRM Experiments. Poster presented at *World Congress of the Human Proteome Organization (HUPO)*. 2011 Sep. Geneva, Switzerland.

#### EDITORIAL ACTIVITIES

**Peer Review Activities:** ([Publons Profile](#))

*Journal Referee* for

- [1] *Journal of Proteome Research*, September 2018
- [2] *Scientific Reports*, September 2016
- [3] *Proteomics*, December 2014 and July 2015

#### SERVICE

##### Conferences

2016 - 2017 **Coordinator** for the American Society for Mass Spectrometry (ASMS), Bioinformatics for MS Interest Group for the 2016 and 2017 meetings.

- Open Source Software Packages : Using and Making your contribution. 2017 Jun 5. Workshop for Bioinformatics Interest group
- Challenge & opportunities in Proteogenomics. 2016 Jun 6. Workshop for Bioinformatics Interest group

**Bioconductor and Github**

- [1] *MSstats*: An R-package for statistical protein quantification in DDA, SRM, and DDA experiments using a flexible family of linear mixed models [Available on [Bioconductor](#) and [GitHub](#)]
  - website : [msstats.org](http://msstats.org)
  - rank : 230/1649 in Bioconductor (as of 2018 Nov 2.)
  - Most downloaded external tool in mass spectrometry signal processing software, Skyline, 14360 downloads (2018 Nov 2.) from unique IP since February 2013.
- [2] *MSstatsTMT*: An R-package for protein significance analysis in shotgun mass spectrometry-based proteomic experiments with tandem mass tag (TMT) labeling [Available on [Bioconductor](#) and [GitHub](#)]
- [3] *MSstatsBioData*: An R-experiment package for Datasets of published biological studies with DDA or SRM experiments [Available on [Bioconductor](#)]
- [4] *SRMstats*: An R-package for Statistical protein quantification in SRM experiments. [Available on [web-page](#)]

**Classroom Instruction**

2010 Summer **Lecturer**, Elementary Statistical Methods (Purdue - STAT 301) Taught lectures and labs for summer semester.

2010 Spring **Lab Instructor**, Elementary Statistical Methods (Purdue - STAT 301)  
Hold labs 3 hrs/week to teach student to use SPSS.

**Organizer or instructor of short courses**

- 2018 **Co-instructor**, two-day short course: Summer Short course #14 : Case Studies in Quantitative Proteomics. 2018 Jun 2-3. Annual Conference of American Society for Mass Spectrometry (ASMS), Indianapolis, USA.
- 2018 **Organizer and instructor**, two-week course: May Institute - Computation and statistics for mass spectrometry and proteomics. 2018 Apr 30 - May 11, Northeastern University, Boston, USA.
  - It is supported by the 1R25EB023929-01 award from the National Institutes of Health(NIH), and by German Network for Bioinformatics infrastructure.
  - [Webpage](#), [Materials on GitHub](#), [Videos on YouTube](#)
- 2018 **Co-instructor**, two-day short course: [Design and analysis of quantitative proteomic experiments - Introduction to statistical methods and practical examples using Skyline, R, and MSstats](#). 2018 Mar 10-11. Annual Conference of the US Human Proteome Organization (US HUPO), Minneapolis, USA.
- 2017 **Co-instructor**, two-day short course: Summer Short course #21 : Case Studies in Quantitative Proteomics. 2017 Jun 3-4. Annual Conference of American Society for Mass Spectrometry (ASMS), Indianapolis, USA.
- 2017 **Organizer and instructor**, two-week course: May Institute - Computation and statistics for mass spectrometry and proteomics. 2017 May 1-10. Northeastern University, Boston, USA.
  - It is supported by the 1R25EB023929-01 award from the National Institutes of Health(NIH), and by German Network for Bioinformatics infrastructure.
  - [Materials on GitHub](#), [Videos on YouTube](#)
- 2017 **Co-instructor**, one-day satellite workshop: [Introduction to statistical methods for life scientists](#). 2017 Mar 24-25. Annual meeting of the Association of Biomolecular Resource Facilities (ABRF), San Diego, USA.

- 2017 **Co-instructor**, two-day short course: [Design and analysis of quantitative proteomic experiments: Introduction to statistical methods and practical examples using Skyline, R, and MSstats](#). 2017 Mar 18-19. Annual Conference of the US Human Proteome Organization (US HUPO), San Diego, USA.
- 2016 **Co-instructor**, one-week course: Design and analysis of quantitative proteomic experiments. 2016 Aug 1-5. EMBO advanced proteomics workshop, Varna, Italy.
- 2016 **Co-instructor**, one-week course: Computation and statistics for targeted proteomics. 2016 May 2-6. Northeastern University, Boston, USA.
- 2016 **Co-instructor**, one-day course: Design and analysis of quantitative proteomic experiments : Introduction to statistical methods and practical examples using Skyline. 2016 Mar 13. Annual Conference of the US Human Proteome Organization (US HUPO), Boston, USA.
- 2016 **Co-instructor**, one-week course: Targeted Proteomics. 2016 Mar 7-11. Buck Institute, San Francisco, USA.
- 2015 **Co-instructor**, one-week course: Mass spectrometry-based proteomics - computation and statistics for discovery and targeted analysis. 2015 May 18-22. Northeastern University, Boston, USA.
- 2015 **Co-instructor**, one-day course: Design and analysis of quantitative proteomic experiments - Introduction to statistical methods and practical examples using Skyline. 2015 Mar 15. Annual Conference of the US Human Proteome Organization (US HUPO), Tempe, Arizona, USA.
- 2015 **Co-instructor**, one-week course: Targeted quantitative proteomics course. 2015 Mar 23-27, University of Washington, Seattle, USA.
- 2014 **Co-instructor**, two-day workshop: Statistical considerations for experimental design and data analysis. 2014 Dec 10-11. 6th Annual Meeting of Proteomics Society, India (PSI), Mumbai, India.
- 2014 **Co-instructor**, two-day workshop: Using MSstats for statistical analysis of targeted proteomic data. 2014 Oct 13-14. The 1st SNU International Computational Bioinformatics workshop, Seoul, South Korea.
- 2014 **Co-instructor**, one-week course: Design and analysis of quantitative proteomic experiments. 2014 Aug 3-9. 8th European Summer School in Proteomics, Brixen/Bressanone, Italy.
- 2014 **Co-instructor**, one-day course: Design and analysis of quantitative proteomic experiments - Introduction to statistical methods and practical examples using Skyline. 2014 Apr 6. Annual Conference of the US Human Proteome Organization (US HUPO), Seattle, USA.
- 2014 **Co-instructor**, one-week course: Targeted quantitative proteomics course. 2014 Mar 31-Apr 4. University of Washington, Seattle.
- 2014 **Co-instructor**, one-week course: Selected Reaction Monitoring. 2014 Feb 10-14. ETH Zürich, Switzerland.
- 2014 **Co-instructor**, one-week course: Selected Reaction Monitoring. 2013 Jul 15-19. ETH Zürich, Switzerland.
- 2013 **Co-instructor**, one-day course: Statistical methods for quantitative proteomics - design of experiments and interpretation of results. 2013 Mar 10. Annual Conference of the US Human Proteome Organization (US HUPO), Baltimore, Maryland, USA.

#### COMMUNITY PROJECTS

- Nov 2018 **Boston R/Bioconductor for Genomics** ([Creating a Bioconductor Package - Part 1](#)), Boston, MA, USA  
Present the session 2 : Coding style, creating, building and checking a package and introduce the best practice.
- Sep 2016 **Boston R/Bioconductor for Genomics** ([Networking, Seminar from Rafa Irizarry & Lightning talks](#)), Boston, MA, USA  
Present lightning talk.