Meena Choi

College of Science and College of Computer and Information Science
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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

Current appointment

04/2016 - current	**Postdoctoral Research Associate** College of Science and College of Computer and Information Science Northeastern University, Boston, MA, USA Mentor : Dr. Olga Vitek

Education

2016	**Ph.D in Statistics** Department of Statistics, Purdue University, West Lafayette, IN, USA *Supervisor:* Dr. Olga Vitek, Department of Statistics and Computer Science *Dissertation title* : 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.S. in Applied Statistics** Department of Statistics, Purdue University, West Lafayette, IN, USA
2008	**B.S. in Management, Honors with Distinction** Krannert school of management, Purdue University, West Lafayette, IN, USA
2002	**B.S. in Biology** Department of Biological Sciences Korea Advanced Institute of Science and Technology, Daejon, South Korea

Professional experience

04/2016 - current	**Postdoctoral Research Associate**. College of Science and College of Computer and Information Science, Northeastern University, Boston, MA, USA • Statistical protein quantification in mass spectrometry-based proteomic experiments • Development of educational program, materials and case studies
08/2016 - 12/2016	**Statistical consultant**. Alkahest, Inc., San Carlos, CA • Statistical analysis for somalogic data, mass spectrometric-based proteomic data • Consulting about statistical design of experiment

09/2010 - 12/2015	**Research Assistant**. Department of Statistics, Purdue University, West Lafayette, IN

- Statistical protein quantification in mass spectrometry-based proteomic experiments
- Statistical selection and evaluation of candidate protein biomarkers of disease.
  In collaboration with the Aebersold lab, Institute of Molecular Systems Biology, ETH Zürich, Switzerland.
- Analysis of bacterial detection for classification.
  In collaboration with Advanced Bioimaging System, West Lafayette, IN, USA

01/2010 - 12/2011	**Teaching Assistant**. Department of Statistics, Purdue University, West Lafayette, IN

- Lecturer: *"Elementary Statistical Methods"*
- Recitations and grading: *"Elementary Statistical Methods"*
- Grading: *"Applied Regression Analysis"*, *"Design of Experiments"*, *"Intermediate Statistical Methodology"*, *"Advanced Statistical Methodology"*, *"Statistical Methods For Bioinformatics and Computational Biology"*

Awards

1. ThinkSwiss Research Scholarship from Embassy of Switzerland in the United States of America, 2013.

Publications

1. **M. Choi**, N. Shulman, C. Chiva, M. Pavlou, E. Verschueren, E. Sabidó, B. Wollscheid, B. MacLean, O. Vitek, "Relative protein quantification in mass spectrometry-based proteomics: a split plot approach", *In preparation.*

2. R. Hüttenhain*, **M. Choi***, P. Wild, A.K. Zimmermann, L. M. Fuente, C. Chang, S. Surinova, L. Reiter, T. Clough, D. Dinulescu, E. Niméus-Malmström, O. Vitek, and R. Aebersold, "Improved sensitivity in detecting Type 1 ovarian cancer using a type-specific protein biomarker discovery strategy", *In preparation.*

3. E. Caron, R. Roncagalli, T. Hase, W. Wolski, T. Hase, **M. Choi**, M. G. Menoita, S. Durand, A. Garcia-Blesa, I. Fierro-Monti, T. Sajic, M. Heusel, T. Weiss, M. Malissen, R. Schlapbach, B. Collins, S. Ghosh, H. Kitano, R. Aebersold, B. Malissen, M. Gstaiger, "Precise temporal profiling of GRB2 protein complexes in primary T cells using SWATH mass spectrometry", *Cell Reports*, DOI: http://dx.doi.org/10.1016/j.celrep.2017.03.019, 2017

4. S.E. Abbatiello, B.L. Ackermann, C.H. Borchers, R.A. Bradshaw, S.A. Carr, R.J. Chalkley, **M. Choi**, E.W. Deutsch, B. Domon, A.N. Hoofnagle, H. Keshishian, E. Kuhn, D.C. Liebler, M.J. MacCoss, B. MacLean, D.R. Mani, H. Neubert, D. Smith, O. Vitek, L. Zimmerman, "New Guidelines for Publication of Manuscripts Describing Development and Application of Targeted Mass Spectrometry Measurements of Peptides and Proteins", *Molecular & Cellular Proteomics*, doi: 10.1074/mcp.E117.067801, 2017

5. **M. Choi***, Z. F. Eren-Dogu*, C. Colangelo, J. Cottrell, M. R. Hoopmann, E. A. Kapp, S. Kim, H. Lam, T. A. Neubert, M. Palmblad, B. S. Phinney, S. T. Weintraub, B. MacLean, O. Vitek, "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*, doi:10.1021/acs.jproteome.6b00881, 2017

6. C. Terfve, E. Sabidó, Y. Wu, E.Gonçalves, **M. Choi**, S. Vaga, O. Vitek, J. Saez-Rodriguez, R. Aebersold, "System-wide quantitative proteomics of the metabolic syndrome in mice: genotypic and dietary effects", *Journal of Proteome Research* , doi:10.1021/acs.jproteome.6b00815, 2016

7. E. Borràs, E. Cantó, **M. Choi**, L. M. Villar, J.C. Álvarez-Cermeño, C. Chiva, X. Montalban, O. Vitek, M. Coma-bella, E. Sabido, "Protein-based classifier to predict conversion from Clinically Isolated Syndrome to Multiple Sclerosis", *Molecular & Cellular Proteomics* , doi:10.1074/mcp.M115.053256, 2015

8. S. Surinova, **M. Choi**, S. Tao, P. Schüffler, C. Chang, T. Clough, K. Vysloužil, M. Khoylou, J. Srovnal, Y. Liu, M. Matondo, R. Hüttenhain, H. Weisser, J. M. Buhmann, M. Hajdúch, H. Brenner, O.Vitek, R. Aebersold, "Prediction of colorectal cancer diagnosis based on circulating plasma proteins", *EMBO Molecular Medicine*, **7**(9), 1166-1178, 2015

9. S. Surinova, L. Radová, **M. Choi**, J. Srovnal, H. Brenner, O. Vitek, M. Hajdúch, R. Aebersold, "Non-invasive prognostic protein biomarker signatures associated with colorectal cancer", *EMBO Molecular Medicine*, **7**(9), 1153-1165, 2015

10. **M. Choi**, C. Chang, T. Clough, D. Broudy, T. Killeen, B. MacLean, O. Vitek, "MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments", *Bioinformatics*. 30:2524-2536, 2014.

11. D. Broudy, T. Killeen, **M. Choi**, N. Shulman, D. Mani, S. Abbatiello, D. Mani, R. Ahmad, A. Sahu, B. Schilling, K.Tamura, Y. Boss, V. Sharma, B. Gibson, S. Carr, O. Vitek, M. MacCoss, B. MacLean, "A framework for installable external tools in Skyline", *Bioinformatics*. 30:2521-2523, 2014.

12. F. Cerciello, **M. Choi**, A. Nicastri, D. Bausch-Fluck, A. Ziegler, O. Vitek, E. Felley-Bosco, R. Stahel, R. Aebersold, B. Wollscheid, "Identification of a seven glycopeptide signature for malignant pleural mesothelioma in human serum by selected reaction monitoring", *Clinical Proteomics*. 10:16, 2013.

 * Equal contribution

Invited talks

1. "Statistical analysis with MSstats". Session : Proteomics in the Era of large datasets, Northeast Rigional Life Sciences Core Directors (NERLSCD), Boston, USA, October 2016.

2. "Computational and statistics for quantitative proteomics", Workshop, Annual Conference of the US Human Proteome Organization (US HUPO). Boston, USA, March 2016.

3. "Experimental design and statistics, Statistical analysis with MSstats". Bioinformatics seminar, Seoul National University, College of Medicine. Seoul, Korea, October 2014.

4. "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). Baltimore, USA, June 2014.

Poster presentations

1. "Detection of differentially abundant proteins with MSstats 3.6 improves reproducibility between data processing tools". Annual Conference of American Society for Mass Spectrometry (ASMS). Indianapolis, USA, 2017.

2. "New developments in MSstats: statistical process control, LoD/LoQ, and relative protein quantification with split plot approach". Annual Conference of American Society for Mass Spectrometry (ASMS). San Antonio, USA, 2016.

3. "Relative protein quantification in mass spectrometry-based proteomics: a split plot approach". Annual Conference of the US Human Proteome Organization (US HUPO). Boston, USA, 2016.

4. "MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments". Annual Conference of the US Human Proteome Organization (US HUPO). Seattle, USA, 2014.

5. "Statistical protein quantification and interpretation in label-free and label-based LC-MS and SRM workflows". World Congress of the Human Proteome Organization (HUPO). Boston, USA, 2012.

6. "SRMstats: An Open-Source Software Suite for Protein Quantification in SRM Experiments". World Congress of the Human Proteome Organization (HUPO). Geneva, Switzerland, 2011.

SOFTWARE

1. `MSstats`: **Lead developer and maintainer**
   - `www.msstats.org`
   - Open-source, R-based software
   - Statistical protein quantification in DDA, SRM, and DDA experiments using a flexible family of linear mixed models.
   - 9886 lines of R code (version 3.2.3)
   - Top 20% most downloaded packages in Bioconductor (as of October 20, 2016)
     - 1808 distinct IPs, 3891 downloads in 2016
     - 1825 distinct IPs, 3877 downloads in 2015
     - 1976 distinct IPs, 3745 downloads in 2014
     - 366 distinct IPs, 697 downloads from unique IP since October 2013.
   - Most downloaded external tool in mass spectrometry signal processing software, Skyline, 9724 downloads (March 29, 2017) from unique IP since February 2013.

2. `SRMstats`: **Co-developer**
   - The open-source, R-based software is available at `www.stat.purdue.edu/~ovitek/Software.html`
   - Statistical protein quantification in SRM experiments

PROGRAMMING SKILLS

1. Most experienced with R and Git
2. Some experience with Python, C++, SAS, SPSS and Matlab

ORGANIZER OR INSTRUCTOR OF SHORT COURSES

1. **Co-instructor**, two-day short course, "Summer Short course #21 : Case Studies in Quantitative Proteomics", Annual Conference of American Society for Mass Spectrometry (ASMS), Indianapolis, USA, June 2017.

2. **Organizer and instructor**, two-week course, "May Institute - Computation and statistics for mass spectrometry and proteomics", Northeastern University, Boston, USA, May 2017.
   - It is supported by the 1R25EB023929-01 award from the National Institutes of Health(NIH), and by German Network for Bioinformatics infrastructure.

3. **Co-instructor**, one-day satellite workshop, "Introduction to statistical methods for life scientists", Annual meeting of the Association of Biomolecular Resource Facilities (ABRF), San Diego, USA, March 2017.

4. **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", Annual Conference of the US Human Proteome Organization (US HUPO), San Diego, USA, March 2017.

5. **Speaker**, one-week course "Targeted proteomics : Experimental design and data analysis - Data interpretation and statistical analysis", EMBO practical course on targeted proteomics, Barcelona, Spain, November 2016.

6. **Co-instructor**, one-week course "Design and analysis of quantitative proteomic experiments". EMBO advanced proteomics workshop, Varna, Italy, August 2016.

7. **Co-instructor**, one-week course "Computation and statistics for targeted proteomics", Northeastern University, Boston, May 2016.

8. **Co-instructor**, one-day course "Design and analysis of quantitative proteomic experiments : Introduction to statistical methods and practical examples using Skyline", Annual Conference of the US Human Proteome Organization (US HUPO), Boston, March 2016.

9. **Co-instructor**, one-week course "Targeted Proteomics", Buck Institute, San Francisco, March 2016.

10. **Co-instructor**, one-week course "Mass spectrometry-based proteomics: computation and statistics for discovery and targeted analysis", Northeastern University, Boston, May 2015.

11. **Co-instructor**, one-day course "Design and analysis of quantitative proteomic experiments : Introduction to statistical methods and practical examples using Skyline", Annual Conference of the US Human Proteome Organization (US HUPO), Tempe, March 2015.

12. **Co-instructor**, one-week course "Targeted quantitative proteomics course", University of Washington, Seattle, March 2015.

13. **Co-instructor**, two-day workshop "Statistical considerations for experimental design and data analysis", 6th Annual Meeting of Proteomics Society, India (PSI), Mumbai, India, December 2014.

14. **Co-instructor**, two-day workshop "Using MSstats for statistical analysis of targeted proteomic data", The 1st SNU International Computational Bioinformatics workshop, Seoul, Korea, October 2014.

15. **Speaker**, one-week course "Targeted proteomics : Experimental design and data analysis - Data interpretation and statistical analysis", EMBO practical course on targeted proteomics, Barcelona, Spain, September 2014.

16. **Co-instructor**, one-week course "Design and analysis of quantitative proteomic experiments". 8th European Summer School in Proteomics, Brixen/Bressanone, Italy, August 2014.

17. **Co-instructor**, one-day course "Design and analysis of quantitative proteomic experiments : Introduction to statistical methods and practical examples using Skyline". Annual Conference of the US Human Proteome Organization (US HUPO), Seattle, April 2014.

18. **Co-instructor**, one-week course "Targeted quantitative proteomics course". University of Washington, Seattle, March 2014.

19. **Co-instructor**, one-week course "Selected Reaction Monitoring". ETH Zürich, Switzerland, February 2014.

20. **Co-instructor**, one-week course "Selected Reaction Monitoring". ETH Zürich, Switzerland, July 2013.

21. **Co-instructor**, one-day course "Statistical methods for quantitative proteomics: design of experiments and interpretation of results". Annual Conference of the US Human Proteome Organization (US HUPO), Baltimore, March 2013.

Other professional activities

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

Journal referee / Reviewer

1. *Proteomics*, December 2014 and July 2015
2. *Scientific Reports*, September 2016

PROFESSIONAL MEMBERSHIPS

1. Member, American Society of Mass Spectrometry (ASMS)
2. Member, US Human Proteome Organization (US HUPO)