I. GENERAL INFORMATION

Olga Vitek

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A Education

Postdoc, 2006	Proteomics, Institute for Systems Biology, Seattle WA Supervisor: R. Aebersold
PhD, 2005	Statistics, Purdue University, West Lafayette IN Co-advisors: B. A. Craig, Statistics, Purdue University and C. Bailey-Kellogg, Computer Science, Dartmouth College. Dissertation: *"An inferential approach to protein backbone nuclear magnetic resonance assignment"*
M.S., 2001	Mathematical Statistics, Purdue University, West Lafayette IN
M.S., 1997	Econometrics and Statistics, University of Geneva, Switzerland Advisor: E. Ronchetti, University of Geneva Dissertation: *"Tree-based classifiers with application to medical data"*
B.S., 1995	Econometrics and Statistics, University of Geneva, Switzerland

B Previous Positions

2014 - 2018	Sy and Laurie Sternberg Interdisciplinary Chair and Associate Professor, Khoury College of Computer Sciences and College of Science, Northeastern University
2011 - 2014	Associate Professor, Statistics (90%) and Computer Science (10%), Purdue University
2012 - 2013	Visiting Associate Professor, Department of Radiology, Stanford University
2006 - 2011	Assistant Professor, Statistics (90%) and Computer Science (10%), Purdue University
2004 - 2004	Intern in Proteomics, Eli Lilly and Company, Indianapolis IN
2001 - 2005	Research assistant, Purdue University, West Lafayette IN
2000 - 2000	Member, Statistical Consulting Service, Purdue University, West Lafayette IN
1996 - 1999	Teaching assistant, University of Geneva, Switzerland
1997 - 1998	Statistician, University Hospitals, Geneva, Switzerland
1996 - 1997	Member, Laboratory of Applied Economics, University of Geneva, Switzerland

C Present Position

2019 - now	Professor, Khoury College of Computer Sciences, Northeastern University
2014 - now	Faculty Fellow, Barnett Institute for Chemical and Biological Analysis, Northeastern University
2014 - now	Adjunct Associate Professor, Department of Statistics, Purdue University
2015 - now	Faculty Affiliate, Tufts Clinical and Translational Sciences Institute

D Awards and Honors

2014	Sy and Laurie Sternberg Interdisciplinary Chair, Northeastern University
2013	University Faculty Scholar, Purdue University
2011	National Science Foundation CAREER Award
2010	Outstanding Assistant Professor Teaching Award, Department of Statistics, Purdue University
2010	Graduate Student Mentoring Award, College of Science, Purdue University
2008	Teaching for Tomorrow Award, Office of the Provost, Purdue University
2008	Member, Sigma Xi
2005	Laha Travel Award, Institute of Mathematical Statistics
2004	Graduate School Dissertation Fellowship, Purdue University
2003	Charlie Sampson Best Poster Award, Midwest Biopharmaceutical Statistics Workshop, IN
1997	Prize of the Industrial Services of Geneva, Geneva, Switzerland

E Professional and Scholarly Associations

American Society for Mass Spectrometry (ASMS)
American Statistical Association (ASA)
The Association of Biomolecular Resource Facilities (ABRF)
International Society for Computational Biology (ISCB)
United States Human Proteome Organization (US HUPO)
World Human Proteome Organization (HUPO)

II. TEACHING

A Teaching at Northeastern University

Semester	Title	Type	Course questions*	Learning questions*	Instructor questions*	Instructor effectiveness*	Respond / enroll
Fall 2019	Topics in Statistical Inference	Grad	/	/	/	/	/ 17
Spring 2019	Supervised Machine Learning	Grad	4.2 / 4.0	4.3 / 5.0	4.2 / 4.0	4.1 / 4.0	23 / 35
Fall 2018	Supervised Machine Learning	Grad	3.8 / 4.0	3.7 / 4.0	3.9 / 4.0	3.7 / 4.0	21 / 38
Spring 2018	Topics in Statistical Inference	Grad	4.3 / 5.0	4.4 / 4.0	4.5 / 5.0	4.2 / 4.0	11 / 22
Fall 2017	Supervised Machine Learning	Grad	3.9 / 4.0	3.9 / 4.0	3.9 / 4.0	3.9 / 4.0	16 / 19
Fall 2017	Machine Learning	Grad	3.5 / 3.0	3.4 / 4.0	3.7 / 4.0	3.2 / 3.0	10 / 13
Spring 2017	Supervised Machine Learning	Grad	3.9 / 4.0	4.0 / 4.0	4.4 / 5.0	4.3 / 4.5	6 / 8
Spring 2017	Machine Learning	Grad	3.8 / 4.0	4.0 / 4.0	4.0 / 5.0	3.8 / 4.0	18 / 32
Fall 2016	Topics in Statistics & Data	Grad	4.0 / 4.0	4.0 / 5.0	4.2 / 5.0	4.2 / 5.0	10 / 18
Spring 2016	Topics in Statistics & Data	Grad	4.7 / 5.0	4.6 / 5.0	4.8 / 5.0	4.8 / 5.0	9 / 14
Fall 2015	Data Mining Techniques	Grad	4.0 / 4.0	4.1 / 4.0	4.2 / 4.0	4.1 / 4.0	20 / 35
Spring 2015	Statistics for Big Data	Grad	4.4 / 4.0	-	-	4.9 / 5.0	8 / 13

* Mean / median of ratings in a series of questions. Student evaluation on a scale from 1="Very poor" to 5="Excellent".

B Teaching at Purdue

Semester	Title	Type	Course evaluation*	Instructor evaluation*	Respond/ / enroll
Spring 2014	Advanced Stat. Methodology	Grad	4.6	4.6	23 / 32
Fall 2013	Stat. Methods for Bioinformatics	Grad	4.3	4.3	8 / 12
Spring 2012	Advanced Stat. Methodology	Grad	4.3	4.7	14 / 27
Fall 2011	Stat. Methods for Bioinformatics	Grad	4.6	4.8	11 / 19
Spring 2011	Advanced Stat. Methodology	Grad	4.7	4.6	19 / 29
Fall 2010	Intermediate Stat. Methodology	Grad	4.9	4.9	21 / 34
Spring 2010	Advanced Stat. Methodology	Grad	4.5	4.5	12 / 16
Fall 2009	Stat. Methods for Bioinformatics	Grad	5.0	5.0	13 / 14
Spring 2009	Intermediate Stat. Methodology	Grad	4.6	4.6	9 / 14
Fall 2008	Intermediate Stat. Methodology	Grad	4.2	4.0	25 / 28
Spring 2008	Intermediate Stat. Methodology	Grad	4.7	4.7	9 / 11
Fall 2007	Stat. Methods for Bioinformatics	Grad	4.7	4.8	11 / 11
Spring 2007	Stat. Methods for Biology	So.-Gr.	4.2	4.6	27 / 36
Fall 2006	Stat. Methods for Biology	So.-Gr.	4.1	4.5	31 / 38

* Median student evaluation on a scale from 1="Very poor" to 5="Excellent".

C External Tutorials and Short Courses

2020 American Society for Mass Spectrometry (ASMS) Fall workshop, Boston, MA.
“R for mass spectrometry”. 2 days, co-organizer.

2020 Annual conference of the American Society for Mass Spectrometry (ASMS), Houston, TX.
“Case studies in quantitative proteomics”. 2 days, co-organizer.

2020 University of Washington, Seattle WA.
“Targeted proteomics course”. 1 week, lecturer.

2020 EMBL Heidelberg, Germany.
“Quantitative proteomics: Strategies and tools to probe biology”. 1 week, instructor.

2020 Northeastern University, Boston, MA.
“May Institute: Computation & statistics for mass spectrometry and proteomics”. 2 weeks, lead organizer.

2020 Annual Conference of the US Human Proteome Organization (US HUPO), Seattle, WA.
“Design and analysis of quantitative proteomic experiments”. 2 days, co-organizer.

2019 Annual conference of the American Society for Mass Spectrometry (ASMS), Atlanta, GA.
“Case studies in quantitative proteomics”. 2 days, co-instructor.

2019 Northeastern University, Boston, MA.
“May Institute: Computation & statistics for mass spectrometry and proteomics”. 2 weeks, lead organizer.

2019 Annual Conference of the US Human Proteome Organization (US HUPO), Bethesda, MD.
“Design and analysis of quantitative proteomic experiments”. 2 days, co-organizer.

2018 University of Wisconsin, Madison, WI.
“1st Annual North American Mass Spectrometry Summer School”. 1 week, co-instructor.

2018 University of Washington, Seattle WA.
“Targeted proteomics course”. 1 week, lecturer.

2018 ETH Zürich, Switzerland
“Targeted proteomics course”. 1 week, lecturer.

2018 Annual conference of the American Society for Mass Spectrometry (ASMS), San Diego, CA.
“Case studies in quantitative proteomics”. 2 days, co-instructor.

2018 Northeastern University, Boston, MA.
“May Institute: Computation & statistics for mass spectrometry and proteomics”. 2 weeks, lead organizer.

2018 Annual Conference of the US Human Proteome Organization (US HUPO), San Diego CA.
“Design and analysis of quantitative proteomic experiments”. 2 days, co-organizer.

2017 University of Washington, Seattle WA.
“Targeted proteomics course”. 1 week, lecturer.

2017 ETH Zürich, Switzerland
“Targeted proteomics course”. 1 week, lecturer.

2017 Annual conference of the American Society for Mass Spectrometry (ASMS), Indianapolis, IN.
“Case studies in quantitative proteomics.”. 2 days, co-instructor.

2017 Northeastern University, Boston, MA.
“May Institute: Computation & statistics for mass spectrometry and proteomics”. 2 weeks, lead organizer.

2017 Annual Conference of the US Human Proteome Organization (US HUPO), San Diego CA.
“Design and analysis of quantitative proteomic experiments”. 2 days, co-organizer.

2017 Annual Conference of the Association of Biomedical Resource Facilities (ABRF), San Diego CA.
“Introduction to statistical methods for life scientists”. 2 days, co-organizer.

2016 PRBB, Barcelona, Spain
“EMBO targeted proteomics course”. 1 week, lecturer.

2016 Varna, Italy.
“EMBO advanced proteomics workshop”. 1 week, lecturer.

2016 University of Washington, Seattle WA.
“Targeted proteomics course”. 1 week, lecturer.

2016 Northeastern University, Boston, MA.
“Computation & statistics for targeted proteomics”. 1 week, co-organizer.

2016 Annual Conference of the US Human Proteome Organization (US HUPO), Boston MA.
“Design and analysis of quantitative proteomic experiments”. 1 day, co-instructor.

2016 Buck Institute, North San Francisco, CA.
“Targeted proteomics course”. 1 week, lecturer.

2016 ETH Zürich, Switzerland
“Targeted proteomics course”. 1 week, lecturer.

2015 PRBB, Barcelona, Spain
“EMBO targeted proteomics course: experimental design and data analysis”. 1 week, lecturer.

2015 Cold Spring Harbor, NY.
“Targeted quantitative proteomics”. 1 week, lecturer.

2015 ETH Zürich, Switzerland.
“Targeted proteomics”. 1 week, co-instructor.

2015 Northeastern University, Boston MA.
“Mass spectrometry-based proteomics: computation and statistics for discovery and targeted analysis”.
1 week, co-organizer and co-instructor.

2015 University of Washington, Seattle WA.
“Targeted quantitative proteomics”. 1 week, co-instructor.

2015 Annual Conference of the US Human Proteome Organization (US HUPO).
“Design and analysis of quantitative proteomic experiments.”. 1 day, co-instructor.

2014 Barcelona, Spain.
“EMBO practical course on targeted proteomics”. 1 week, co-instructor.

2014 Brixen, Italy.
The FEBS Advanced Lecture Course / 8th European Summer School on Advanced Proteomics.
1 week, invited lecturer.

2014 Annual Conference of the US Human Proteome Organization (US HUPO).
“Quantitative proteomics”. 1 day, organizer and co-instructor.

2014 University of Washington, Seattle WA.
“Targeted quantitative proteomics”. 1 week, co-instructor.

2014 ETH Zürich, Switzerland.
“Targeted proteomics using selected reaction monitoring”. 1 week, co-instructor.

2013 ETH Zürich, Switzerland.
“Selected reaction monitoring”. 1 week, co-instructor.

2013 Annual Conference of the US Human Proteome Organization (US HUPO).
“Statistical methods for quantitative proteomics”. 1 day, organizer and co-instructor.

2012 Annual World Congress of the World Human Proteome Organization (HUPO).
“Quantitative bottom-up proteomics”. 1 day, co-instructor.

2012 Purdue Symposium on Statistics.
“Statistical design of experiments and linear mixed models, & applications in bioinformatics”.
2 days, co-organizer and co-instructor.

2012 Annual Conference of the US Human Proteome Organization (US HUPO).
“Quantitative bottom-up proteomics”. 1 day, co-instructor.

2011 International Conference on Intelligent Systems in Molecular Biology (ISMB).
“An insight into computational and statistical mass spectrometry-based proteomics”. 1/2 day, co-instructor.

2011 Annual Conference of the US Human Proteome Organization (US HUPO).
"Quantitative bottom-up proteomics". 1 day, co-instructor.

2011 Australasian Proteomics Society Workshop.
"Statistical design & analysis of quantitative mass spectrometry-based proteomics". 1 day, co-instructor.

2011 Indian Institute of Sciences.
"Statistical methods for high-throughput quantitative experiments in molecular biology". 1 day, co-instructor.

2010 International Conference on Intelligent Systems in Molecular Biology (ISMB).
"An insight into computational and statistical mass spectrometry-based proteomics". 1/2 day, co-instructor.

2010 Research in Computational Molecular Biology (RECOMB) Satellite Conference on Computational Proteomics.
"Statistical design & analysis of quantitative mass spectrometry-based proteomic experiments". 1/4 day, instructor.

2010 Wrocław Institute of Technology, Poland.
"Computational and statistical analysis of biomolecular networks". 1 week, instructor.

III. DISCOVERY

A Publications

A.1 Refereed Research Publications

PD: Post-doctoral associate in O. Vitek lab
GS: Graduate student in O. Vitek lab
AR: acceptance rate of the conference
IF: latest impact factor of the journal

1. R. O. Ness^{PD}, K. Paneri^{GS}, O. Vitek. “Integrating mechanistic and structural causal models enables counterfactual inference in complex systems” *In: Proceedings of the Conference on Neural Information Processing Systems (NeurIPS)*, 2019. **AR 21.1%**
2. R. Hüttenhain, M. Choi^{PD}, L. M. de la Fuente, K. Oehl, C.-Y. Chang, A.-K. Zimmermann, S. Malander, H. Olsson, S. Surinova, T. Clough, V. Heinzelmann-Schwarz, P. J. Wild, D. Dinulescu, E. Niméus, O. Vitek, R. Aebersold. “A targeted mass spectrometry strategy for developing proteomic biomarkers: a case study of epithelial ovarian cancer”. *Molecular & Cellular Proteomics*, mcp.RA118.001221, 2019. **IF 6.54**
3. D. Guo^{GS}, K. Bemis^{PD}, C. Rawlins, J. Agar, O. Vitek. “Unsupervised segmentation of mass spectrometric ion images characterizes morphology of tissues”, In: *Proceedings of International Society for Computational Biology (ISMB)*, 35:i208, 2019. **AR 18.9%**
4. E. D. Berger, C. Hollenbeck, P. Maj, O. Vitek, J. Vitek. “On the impact of programming languages on code quality”, *ACM Tansactions on Programming Languages (TOPLAS)*, 41:21, 2019. **IF 3.03**
5. M. Schwab, S. Hao^{GS}, O. Vitek, J. Tompkin, J. Huang, M. A. Borkin. “Evaluating pan and zoom timelines and sliders”, *Human-Computer Interaction (CHI)*, Paper No. 556, 2019. **AR 23.8%**
6. D. Amodei, J. Egertson, B. MacLean, R. Johnson, G. E. Merrihew, A. Keller, D. Marsh, O. Vitek, P. Mallick, M. J. MacCoss. “Improving precursor selectivity in data independent acquisition using overlapping windows”. *Journal of The American Society for Mass Spectrometry*, 30:669, 2019. **IF 2.79**
7. J. Muntel, J. Kirkpatrick, R. Bruderer, T. Huang^{GS}, O. Vitek, A. Ori, 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. **IF 4.27**
8. E. Dogu^{PD}, S. Mohammad-Taheri^{GS}, R. Olivella, F. Marty, I. Lienert, L. Reiter, E. Sabidó, O. Vitek. “MSstatsQC 2.0: R/Bioconductor package for statistical quality control of mass spectrometry-based proteomic experiments”. *Journal of Proteome Research*, 18:678, 2019. **IF 4.27**
9. K. A. Bemis^{PD}, D. Guo^{GS}, A. J. Harry^{GS}, M. Thomas, I. Lanekoff, M. P. Stenzel-Poore, S. L. Stevens, J. Laskin, O. Vitek. “Statistical detection of differentially abundant ions in mass spectrometry-based imaging experiments with complex designs”, *International Journal of Mass Spectrometry*, 437:49, 2019. **IF 1.70**
10. P. J. Beltran, K. C. Cook, Y. Hashimoto, C. Galitzine^{PD}, M. Jones, L. A. Murray, O. Vitek, I. M. Cristea. “Virus-induced peroxisome biogenesis is a metabolic strategy for viral replication”, *Cell Host & Microbe*, 24:526, 2018. **IF 17.87**
11. N. M. Atallah, O. Vitek, F. Gaiti, M. Tanurdzič, J. A. Banks.“Sex determination in *Ceratopteris richardii* is accompanied by transcriptome changes that drive epigenetic reprogramming of the young gametophyte”, *G3: Genes, Genomes, Genetics*, 8:2205, 2018. **IF 2.86**
12. C. Galitzine^{PD}, J. D. Egertson, S. Abbatiello, C. M. Henderson, A. N. Hoofnagle, M. MacCoss, O. Vitek. “Nonlinear regression improves accuracy of characterization of multiplexed mass spectrometric assays”, *Molecular & Cellular Proteomics*, RA117.000322, 2018. **IF 6.54**
13. C. Galitzine^{PD}, P. J. Beltran, I. Cristea, O. Vitek. “Statistical inference of peroxisome dynamics”. In: *Raphael B. (eds) Research in Computational Molecular Biology (RECOMB). Lecture Notes in Computer Science*, 10812:54,

2018. **AR 19%**

14. K. A. Bemis^{PD}, O. Vitek. "Matter: an R package for rapid prototyping with larger-than-memory datasets on disk", *Bioinformatics*, 19:3142, 2017. **IF 5.48**
15. T.-H. Tsai^{PD}, Z. Hao, Q. Hong, B. Moore, C. Stella, J. H. Zhang, Y. Chen, M. Kim, T. Koulis, G. A. Ryslik, E. Verschueren, F. Jacobson, W. E. Haskins, O. Vitek. "Statistical characterization of therapeutic protein modifications", *Scientific Reports*, 7: 7896, 2017. **IF 4.12**
16. E. Dogu^{PD}, S. Mohammad-Taheri^{GS}, S. E. Abbatiello, M. S. Bereman, B. MacLean, B. Schilling, O. Vitek. "MSstatsQC: Longitudinal system suitability monitoring and quality control for targeted proteomic experiments". *Molecular & Cellular Proteomics*, mcp. M116. 064774, 2017. **IF 6.54**
17. R. O. Ness^{GS}, K. Sachs, P. Mallick, O. Vitek. "A Bayesian active learning experimental design for inferring signaling networks". In: *Sahinalp S. (eds) Research in Computational Molecular Biology. RECOMB 2017. Lecture Notes in Computer Science*, 10229:134, 2017. **AR 21%**
18. M. Choi^{GS}, Z. F. Eren-Dogu, C. M. Colangelo, J. S. 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*, 16:945, 2017. **IF 4.27**
19. C. Terfve, E. Sabidó, Y. Wu, E. Gonçalves, M. Choi^{GS}, 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*, 16:831, 2017. **IF 4.27**
20. S. van de Ven, K. D. Bemis^{GS}, K. Lau, R. Adusumilli, U. Kota, M. Stolowitz, O. Vitek, P. Mallick, S. Gambhir. "Protein biomarkers on tissue as imaged via MALDI mass spectrometry: A systematic approach to study the limits of detection". *Proteomics*, 16:1660, 2016. **IF 4.04**
21. K. D. Bemis^{GS}, A. Harry^{GS}, L. S. Eberlin, C. R. Ferreira, S. M. van de Ven, P. Mallick, M. Stolowitz, O. Vitek. "Probabilistic segmentation of mass spectrometry images helps select important ions and characterize confidence in the resulting segments". *Molecular & Cellular Proteomics*, mcp.O115.053918, 2016. **IF 6.54**
22. R. Ness^{GS}, K. Sachs, O. Vitek. "From correlation to causality: statistical approaches to learning regulatory relationships in large-scale biomolecular investigations". *Journal of Proteome Research*, 4:683, 2016. **IF 4.27**
23. E. Borràs, E. Cantó, M. Choi^{GS}, L. M. Villar, J. C. Álvarez-Cermeño, C. Chiva, X. Montalban, O. Vitek, M. Comabella, E. Sabidó. "Protein-based classifier to predict conversion from clinically isolated syndrome to multiple sclerosis". *Molecular & Cellular Proteomics*, M115.053256, 2016. **IF 6.54**
24. S. Surinova, M. Choi^{GS}, S. Tao, P. J. Schüffler, C.-Y. 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*, 7:1166, 2015. **IF 9.25**
25. S. Surinova, L. Radová, M. Choi^{GS}, J. Srovnal, H. Brenner, O. Vitek, M. Hajdúch, R. Aebersold. "Non-invasive prognostic protein biomarker signatures associated with colorectal cancer". *EMBO Molecular Medicine*, 7:1153, 2015. **IF 9.25**
26. M. J. Rardin, B. Schilling, Lin.-Y. Cheng^{GS}, B. X. MacLean, D. J. Sorenson, A. K. Sahu, M. J. MacCoss, O. Vitek and B. W. Gibson. "MS1 peptide ion intensity chromatograms in MS2 (SWATH) data independent acquisitions: Improving post acquisition analysis of proteomic experiments". *Molecular & Cellular Proteomics*, O115.048181, 2015. **IF 6.54**
27. A. Palmer, E. Ovchinnikova, M. Thune, R. Lavigne, B. Guevel, A. Dyatlov, O. Vitek, C. Pineau, M. Boren, T. Alexandrov. "Using collective expert judgements to evaluate quality measures of mass spectrometry images". *Bioinformatics* 31:i375, 2015. **IF 5.48**
28. K. D. Bemis^{GS}, A. Harry^{GS}, L. S. Eberlin, C. Ferreira, S. M. van de Ven, P. Mallick, M. Stolowitz, O. Vitek. "Cardinal: an R package for statistical analysis of mass spectrometry-based imaging experiments". *Bioinformatics*, 31:2418, 2015. **IF 5.48**

29. R. Bruderer, O. M. Bernhardt, T. Gandhi, S. M. Miladinovic, L.-Y. Cheng^{GS}, S. Messner, T. Ehrenberger, V. Zanotelli, Y. Butscheid, C. Escher, O. Vitek, O. Rinner, L. Reiterd. "Extending the limits of quantitative proteome profiling with data-independent acquisition and application to acetaminophen treated 3D liver microtissues". *Molecular and Cellular Proteomics*, M114.044305, 2015. **IF 6.54**
30. Y. Liu, A. Buil, B. C. Collins, L. C. J. Gillet, L. C. Blum, L.-Y. Cheng^{GS}, O. Vitek, J. Mouritsen, G. Lachance, T. D. Spector, E. T. Dermitzakis, R. Aebersold. "Quantitative variability of 342 plasma proteins in a human twin population". *Molecular Systems Biology*, 11:786, 2015. **IF 10.87**
31. N. Selevsek, C.-Y. Chang^{GS}, L. C. Gillet, P. Navarro, O. M. Bernhardt, L. Reiter, L.-Y. Cheng^{GS}, O. Vitek, R. Aebersold. "Reproducible and consistent quantification of the Saccharomyces cerevisiae proteome by SWATH-MS". *Molecular and Cellular Proteomics*, M113.035550, 2015. **IF 6.54**
32. M. Choi^{GS}, C.-Y. Chang^{GS}, T. Clough^{GS}, D. Broudy, T. Killeen, B. MacLean, O. Vitek. "MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments". *Bioinformatics*, 30:2524-2526, 2014. **IF 5.48**
33. D. Broudy, T. Killeen, M. Choi^{GS}, N. Shulman, D. R. Mani, S. E. Abbatiello, D. Mani, R. Ahmad, A. K. Sahu, B. Schilling, K. Tamura, Y. Boss, V. Sharma, B. W. Gibson, S. A. Carr, O. Vitek, M. J. MacCoss, B. MacLean. "A framework for installable external tools in Skyline". *Bioinformatics*, 30:2521-2523, 2014. **IF 5.48**
34. C.-Y. Chang^{GS}, E. Sabidó, R. Aebersold, O. Vitek. "Targeted protein quantification using sparse reference labeling". *Nature Methods*, 11:301-304, 2014. **IF 25.06**
35. S. Carr, S. E. Abbatiello. B. L. Ackermann, C. Borchers, B. Domon, E. W. Deutsch, R. P. Grant, A. N. Hoofnagle, R. Hüttenhain, J. M. Koomen, D. C. Liebler, T. Liu, B. MacLean, D. R. Mani, E. Mansfield, H. Neubert, A. G. Paulovich, L. Reiter, O. Vitek, R. Aebersold, L. Anderson, R. Bethem, J. Blonder, E. Boja, J. Botelho, M. Boyne, R. A. Bradshaw, A. L. Burlingame, D. Chan, H. Keshishian, E. Kuhn, C. Kinsinger, J. Lee, S.-W. Lee, R. Moritz, J. Oses-Prieto, N. Rifai, J. Ritchie, H. Rodriguez, P. R. Srinivas, R.R. Townsend, J. Van Eyk, G. Whiteley, A. Wiita, S. Weintraub. "Targeted peptide measurements in biology and medicine: best practices for mass spectrometry-based assay development using a fit-for-purpose approach". *Molecular and Cellular Proteomics*, Article M113.036095, 2014. **IF 6.54**
36. F. Cerciello, M. Choi^{GS}, 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. **IF 3.48**
37. S. Surinova, R. Hüttenhain, C.-Y. Chang^{GS}, O. Vitek, R. Aebersold. "Automated SRM data analysis workflow for large scale targeted proteomic studies". *Nature Protocols*, 8:1602-1619, 2013. **IF 15.27**
38. E. Sabidó, Y. Wu, L. Bautista, T. Porstmann, C.-Y. Chang^{GS}, O. Vitek, M. Stoffel, R. Aebersold. "Targeted proteomics reveals strain-specific changes in the mouse insulin and central metabolic pathways after sustained high-fat diet", *Molecular Systems Biology*, 9, article 681, 2013. **IF 10.88**
39. D. Yu^{GS}, W. Huber, O. Vitek. "Shrinkage estimation of dispersion in Negative Binomial models for RNA-seq experiments with small sample size". *Bioinformatics*, 29:1275-1282, 2013. **IF 5.48**
40. D. Yu^{GS}, J. M. C Danku, I. Baxter, S. Kim, O. K. Vatamaniuk, O. Vitek, D. E. Salt. "High-resolution genome-wide scan of genes, gene-networks and cellular systems impacting the yeast ionome". *BMC Genomics*, 13:623, 2012. **IF 3.73**
41. T. Clough^{GS}, S. Thaminy, S. Ragg, R. Aebersold, O. Vitek. "Statistical protein quantification and significance analysis in label-free LC-MS experiments with complex designs". *BMC Bioinformatics*, 13:S16, 2012. **IF 2.45**
42. K. Ma^{GS}, O. Vitek, A. I. Nesvizhskii. "A statistical model-building perspective to identification of MS/MS spectra with PeptideProphet". *BMC Bioinformatics*, 13:S16, 2012. **IF 2.45**
43. J. K. Muhlemann, H. Maeda, C.-Y. Chang^{GS}, P. San Miguel, I. Baxter, B. Cooper, M. A. Perera, B. J. Nikolau, O. Vitek, J. A. Morgan, N. Dudareva. "Developmental changes in the metabolic network of snapdragon flowers". *PLoS One*, 7(7): e40381, 2012. **IF 4.41**
44. E. Sabidó, O. Quehenberger, Q. Shen, C.-Y. Chang^{GS}, I. Shah, A. M. Armando, A. Andreyev, O. Vitek, E. A.

Dennis, R. Aebersold. “Targeted proteomics of the Eicosanoid biosynthetic pathway completes an integrated genomics-proteomics-metabolomics picture of cellular metabolism. *Molecular and Cellular Proteomics*, Article M111.014746, 2012. **IF 6.54**

45. C.-Y. Chang^{GS}, P. Picotti, R. Hüttenhain, V. Heinzelmann-Schwarz, M. Jovanovic, R. Aebersold, O. Vitek. “Protein significance analysis in selected reaction monitoring (SRM) measurements”. *Molecular and Cellular Proteomics*, Article M111.014662, 2012. **IF 6.54**
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52. A. L. Dill, L. S. Eberlin, A. B. Costa, C. Zheng^{GS}, D. R. Ifa, L. Cheng, T. A. Masterson, M. O. Koch, O. Vitek, R. G. Cooks. “Multivariate statistical identification of human bladder carcinomas using ambient ionization imaging mass spectrometry”, *Chemistry: A European Journal*, 17, p. 2897-2902, 2011. **IF 5.16**
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60. A. L. Oberg, O. Vitek. “Statistical design of quantitative mass spectrometry-based proteomic experiments”.

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66. L. N. Mueller, O. Rinner, A. Schmidt, S. Letarte, B. Bodenmiller, O. Vitek, R. Aebersold, M. Muller. “SuperHirn - a novel tool for high resolution LC-MS based peptide/protein profiling”. *Proteomics*, 19, p.3470-3480, 2007. **IF 4.04**
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68. Z. Yi, O. Vitek, M. A. Qasim, S. M. Lu, W. Lu, M. Ranjbar, J. Li, M. C. Laskowski, C. Bailey-Kellogg, M. Laskowski. “Functional evolution within protein superfamilies”. *Proteins: Structure, Function and Bioinformatics*, 63, p.697-708, 2006. **IF 2.50**
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70. L. S. Riter, O. Vitek, K. M. Gooding, B. D. Hodge, R. K. Julian, Jr. “Statistical design of experiments as a tool in mass spectrometry”. *Journal of Mass Spectrometry*, 40, p.565-579, 2005. **IF 2.38**
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72. J. C. Fleet, L. Wang, O. Vitek, B. A. Craig, H. J. Edenberg. “Gene expression profiling of Caco-2 BBe cells suggests a role for sSpecific signaling pathways during intestinal differentiation”, *Physiological Genomics*, 13, p.57-68, 2003. **IF 2.95**
73. T. V. Perneger, A.-C. Raë, J.-M. Gaspoz, F. Borst, O. Vitek, C. Héliot. “Screening for pressure ulcer risk in an acute care hospital: Development of a brief bedside scale”. *Journal of Clinical Epidemiology*, 55, p.498-504, 2002. **IF 2.17**
74. B. A. Craig, O. Vitek, M. A. Black, M. Tanurdzic, R. W. Doerge. “Designing microarrays.” In *Proceedings of Applied Statistics in Agriculture, Kansas State University*, edited by George Milliken, p.159-182, 2001.
75. S. Beer-Borst, A. Morabia, S. Hercberg, O. Vitek, M. S. Bernstein, P. Galan, R. Galasso, S. Giampaoli, S. Houterman, E. McCrum, S. Panico, F. Pannozzo, P. Preziosi, L. Ribas, L. Serra-Majem, W. M. M. Verschuren, J. Yarnell, M. E. Northridge. “Obesity and other health determinants across Europe: The Euralim Project”. *Journal of Epidemiology and Community Health*, 54, p.424-430, 2000. **IF 3.19**
76. S. Beer-Borst, S. Hercberg, A. Morabia, M. S. Bernstein, P. Galan, R. Galasso, S. Giampaoli, E. McCrum, S. Panico, P. Preziosi, L. Ribas, L. Serra-Majem, M. F. Vescio, O. Vitek, J. Yarnell, M. E. Northridge. “Dietary patterns in six European populations: results from Euralim, a collaborative European data harmonization and information campaign”. *European Journal of Clinical Nutrition*, 54, p.253-262, 2000. **IF 3.06**

A.2 Other Publications

1. F. Cerciello, M. Choi^{PD}, K. Lomeo, J. M. Amann, E. Felley-Bosco, R. A. Stahel, B. Robinson, J. Creaney, H. I. Pass, O. Vitek, D. P. Carbone. "Multiplexed targeted proteomics signature for serum diagnostic of malignant pleural mesothelioma", *Annals of Oncology*, 28:supp5, 2017.
2. S. Abbatiello, B. L. Ackermann, C. Borchers, R. A. Bradshaw, S. A. Carr, R. Chalkley, M. Choi^{PD}, E. Deutsch, B. Domon, A. N. Hoofnagle, H. Keshishian, E. Kuhn, D. C. Liebler, M. 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*, E117.067801, 2017
3. O. Kohlbacher, O. Vitek, S. T. Weintraub "Challenges in large-scale computational mass spectrometry and multi-omics". In *Journal of Proteome Research*, 15:681, 2016.
4. R. Aebersbold, O. Kohlbacher, O. Vitek. "Computational Mass Spectrometry (Dagstuhl Seminar 15351)". In *Dagstuhl Reports*, 8:9, 2016.
5. R. Aebersbold, O. Kohlbacher, O. Vitek. "Computational Mass Spectrometry (Dagstuhl Seminar 13491)". In *Dagstuhl Reports*, 3:1, 2014.
6. O. Vitek. "Leading a statistical bioinformatics lab: it's all about finding balance". In *PLoS Computational Biology*, 9:e1003333, 2013.
7. M. Key^{GS}, O. Vitek. "Designing experiments for sound statistical inference". In *Encyclopedia of Systems Biology*, W. Dubitzky, O. Wolkenhauer, H. Yokota, K.-H. Cho (Eds.), 2012.
8. O. Vitek. "An inferential approach to protein backbone nuclear magnetic resonance assignment". *Ph.D. dissertation.* Purdue University, USA, 2005.
9. O. Vitek, B. A. Craig, R. Becker. "Statistical sampling plan for monitoring egg quality in an egg breaking plant". *Technical Assistance Program*, Purdue University, 2000.
10. O. Vitek, B. A. Craig, R. Becker. "Statistical sampling plan for monitoring the quality of seed lots". *Technical Assistance Program*, Purdue University, 2000.
11. G. Antille Gaillard, N. Chavaz, E. El May, E. Ronchetti and O. Ryndina[1], "Evaluation of postoperative improvement in functional autonomy in Treatment and Rehabilitation Centers of Canton Vaud, Switzerland" (in French). *Laboratory of Applied Economics.* University of Geneva, Switzerland, 1998.
12. S. Beer-Borst, A. Morabia, S. Hercberg, O. Vitek, M. S. Bernstein, P. Galan, R. Galasso, S. Giampaoli, S. Houterman, E. McCrum, S. Panico, F. Pannozzo, P. Preziosi, L. Ribas, L. Serra-Majem, W. M. M. Verschuren, J. Yarnell, M. E. Northridge. "Nutrition and Heart". *Information brochures for general public and for health professionals.* University Hospital, Geneva, Switzerland, 1998.

A.3 Software

All software is open-source, most is implemented in R.

<u>*Current:*</u>

1. **Matter:** Memory-efficient reading, writing, and manipulation of structured binary data on disk.
2. **Cardinal:** Signal processing and statistical analysis of mass spectrometry-based imaging experiments.
   - John M. Chambers Statistical Software Award of the American Statistical Association, 2015
   - 10K+ downloads, 660 monthly average downloads in 2019
3. **MSstats:** Protein quantification in label-free and label-based LC-MS and SRM experiments.
   - 50K+ downloads, 1030 monthly average downloads in 2019

<u>*Past:*</u>

4. **sparseQuant:** Protein quantification in Selected Reaction Monitoring (SRM) experiments with stable isotope labeled reference peptides, which utilize a reduced subset of the references.
5. **SRMstats:** Protein quantification in Selected Reaction Monitoring (SRM) experiments.
6. **sSeq:** Finding differentially expressed genes in RNA-seq experiments with a small sample size.
7. **HTSmix:** Interpretation of high-throughput perturbation screens measuring low-dimensional quantitative phenotypes.
8. **BQuant:** Fully automated, probabilistic database-based identification and quantification of metabolites in local regions of Nuclear Magnetic Resonance (NMR) spectra.
9. **MBA (Model-Based Assignment)**: A software for inferential assignment of protein backbone nuclear magnetic resonances. Implemented in Java.

B Invited Lectures

1. Keystone Symposia on Proteomics in Cell Biology and Disease, Santa Fe, NM, 2020.
   TBA.
2. Mass Spectrometry Applications in Clinical Laboratory (MSCL), Palm Springs, CA, 2020.
   TBA.
3. Applied Bioinformatics in Life Sciences, Leuven, Belgium, 2020.
   TBA.
4. The European Bioinformatics Community (EuBIC) Developers' Meeting, Nyborg, Denmark, 2020.
   TBA.
5. Asilomar Conference of the American Society for Mass Spectrometry, Pacific Grove, CA, 2019.
   Statistical Methods and Software for Mass Spectrometry Imaging.
6. Pfizer, Boston, 2019.
   Components of reproducible quantitative mass spectrometry-based research.
7. Copenhagen Bioscience Snapshots, The University of Copenhagen and The Technical University of Denmark, Denmark, 2019.
   Components of reproducible quantitative mass spectrometry-based research.
8. Lorne Proteomics Symposium, Lorne, VIC, Australia, 2019.
   Components of reproducible quantitative mass spectrometry-based research.
9. Women In Statistics And Data Science Conference, Cincinnati, OH, 2018.
   Building a community of competent statistical practitioners in proteomics.
10. Causal inference workshop, AI Research Week, IBM Research, Cambridge, MA 2018.
    A Bayesian active learning experimental design for inferring signaling networks.
11. Human Proteome Organization Annual World Congress, Orlando, FL, 2018.
    Components of reproducible quantitative mass spectrometry-based research: a statistician's perspective.
12. Cedars-Sinai Medical Center, Loa Angeles, CA, 2018.
    Statistical design and analysis for reproducible quantitative mass spectrometry-based experiments.
13. EMBL-EBI Industry workshop on Proteomics and Proteogenomics, Pfizer, Cambridge, MA, 2018.
    Statistical analysis of proteomic data.
14. R in Pharma conference, Harvard University, Boston, MA, 2018.
    Building a community of competent developers and users of R-based tools in mass spectrometry-based research.

15. The Broad Institute, Boston, MA, 2018.
Statistical design and analysis of mass spectrometry-based experiments with Tandem Mass Tag labeling.
16. MIT Math & CSAIL Bioinformatics Seminar, Cambridge MA, 2018.
Statistical design and analysis for reproducible quantitative mass spectrometry-based experiments.
17. Frontiers in Bioinformatics and Systems Biology Seminar Series, UC San Diego, 2018.
Statistical design and analysis for reproducible quantitative mass spectrometry-based experiments.
18. UCL Cancer Institute, London, UK, 2017.
Statistical design and analysis of reproducible quantitative mass spectrometry-based experiments.
19. Institut Pasteur, Paris, France, 2017.
Statistical design and analysis of reproducible quantitative mass spectrometry-based experiments.
20. Danish Proteomics Society Symposium, Odense, Denmark, 2017.
Statistical design and analysis of reproducible quantitative mass spectrometry-based experiments.
21. Delaware Valley Mass Spectrometry Discussion Group, Philadelphia, 2017.
MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments.
22. OurCon: Imaging Mass Spectrometry Conference, Doorn, the Netherlands 2017.
Statistical methods for mass spectrometry imaging experiments (Plenary presentation).
23. Pfizer, Cambridge, MA 2017.
Statistical methods and tools for quantitative mass spectrometry-based proteomics.
24. Annual Symposium "Biomedical Computation at Stanford (BCATS)", Stanford University, CA 2017.
Statistical methods for quantitative mass spectrometry-based proteomics (Keynote presentation).
25. Keystone Symposium on Molecular and Cellular Biology, Breckenridge, CO, 2017.
Statistical methods for quantitative proteomics.
26. Frontiers of Science Invited Lecture Series, Turku, Finland, 2016.
From proteomics to biological insights using statistics.
27. Northeast Regional Life Sciences Core Directors Meeting, Boston, MA 2016.
iPRG (proteome informatics research group) study 2014.
28. Genentech, South San Fransisco, 2016.
Statistical methods for quantitative mass spectrometry-based proteomics.
29. New York University (NYU), 2016.
MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments.
30. Mass Spectrometry: Applications to the Clinical Lab (MSACL), Palm Springs, 2016.
Statistical inference for mass spectrometry imaging.
31. The Pennsylvania State University, University Park, PA 2016.
Statistical methods and tools for quantitative mass spectrometry-based proteomics.
32. Proteomics Workshop, Brazilian Biosciences National Laboratory (LNBio) at the Brazilian Center for Research in Energy and Materials (CNPEM), Campinas, Brazil 2015.
Statistical methods for quantitative proteomics.
33. The Royal Society, Theo Murphy International Scientific Meeting, Chichley Hall, UK 2015.
Statistical inference for mass spectrometry imaging.
34. OurCon: Imaging Mass Spectrometry Conference, Pisa, Italy 2015.
Statistical inference for mass spectrometry imaging.
35. Meeting of the Association of Biomolecular Resource Facilities (ABRF), St. Louis 2015.
iPRG 2015 Study: Differential abundance analysis in label-free quantitative proteomics.
36. International Quantitative and Computational Biology (QCB) seminar series, Princeton University, 2014.

Statistical methods and tools for quantitative mass spectrometry-based proteomics.

37. Research seminar, Research Center for Statistics, University of Geneva, Switzerland, 2014.
Statistical methods and tools for quantitative mass spectrometry-based proteomics.
38. International Mass Spectrometry Conference (IMSC), Geneva, Switzerland 2014.
Statistical methods and tools for mass spectrometry-based proteomics.
39. UCSF, San Francisco, 2014.
Statistical methods and tools for mass spectrometry-based proteomics.
40. Bioconductor conference, Boston 2014.
Statistical methods and tools for mass spectrometry-based proteomics.
41. Mass Spectrometry Special Interest Group (MS-SIG), International Conference on Intelligent Systems for Molecular Biology (ISMB), Boston 2014.
Nonlinear regression improves the accuracy of estimation and calibration in quantitative proteomics.
42. Genentech, South San Fransisco, 2014.
MSstats: an R package for quantitative mass spectrometry-based proteomics.
43. Annual Symposium of Canadian National Proteomics Network, 2014.
MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments.
44. Annual Conference of the Association of the Biomedical Resource Facilities (ABRF), 2014.
Report of the Proteome Informatics Research Group.
45. Annual Conference of the Association of the Biomedical Resource Facilities (ABRF), 2014.
Statistical methods for biomedical resource facilities.
46. Annual Conference of the US Human Proteome Organization (US HUPO) 2014.
MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments.
47. Department of Mathematics, Northeastern University, Boston 2014.
Statistical methods and tools for quantitative mass spectrometry-based proteomics.
48. The Indo-USA workshop on Statistical Methods for Bioinformatics, Bangalore 2013.
Protein significance analysis in quantitative mass spectrometry-based proteomics.
49. Mass Spectrometry Research Center, Vanderbilt University, 2013.
Statistical methods and software for mass spectrometry-based imaging.
50. Mass Spectrometry Special Interest Group (MS-SIG), International Conference on Intelligent Systems for Molecular Biology (ISMB), Berlin, Germany 2013.
Statistical selection of informative features for protein quantification in DIA experiments.
51. F. Hoffmann-La Roche Ltd, Basel Switzerland, 2013.
Statistical protein quantification from mass spectra.
52. Statistics Seminar, Stanford University 2013.
Statistical methods and tools for quantitative mass spectrometry-based proteomics.
53. Workshop on Targeted Peptide Measurements in Biology and Medicine, NIH 2013.
Statistical methods for analysis of targeted proteomic experiments.
54. Statistics and Genomics Seminar, UC Berkeley 2013.
Statistical methods and tools for quantitative mass spectrometry-based proteomics.
55. Proteomics Group Seminar, UCSF 2013.
Statistical methods and tools for quantitative mass spectrometry-based proteomics.
56. Qatar Computing Research Institute, 2013.
Statistical proteomics and bioinformatics.
57. Department of Statistics, UC Irvine, 2013.

Statistical methods and tools for quantitative mass spectrometry-based proteomics.

58. Department of Electrical and Computer Engineering, UT at San Antonio, 2012.
Statistical methods and tools for quantitative mass spectrometry-based proteomics.
59. Samuel Lunenfeld Research Institute, Toronto, Canada, 2012.
Statistical methods and tools for quantitative mass spectrometry-based proteomics.
60. Department of Biostatistics, University of Washington, Seattle, 2012.
Statistical mass spectrometry-based proteomics.
61. Department of Biostatistics, Stanford University, 2012.
Statistical mass spectrometry-based proteomics.
62. Information Sciences in Imaging, Stanford University, 2012.
Statistical design and analysis of experiments for quantitative and imaging mass spectrometry-based proteomics.
63. Mass Spectrometry Special Interest Group (MS-SIG), International Conference on Intelligent Systems for Molecular Biology (ISMB), Long Beach, 2012.
Statistical analysis can account for sparsity and redundancy in protein quantifications to save cost and gain deeper biological insight.
64. ISMB, Swiss Federal Institute of Technology (ETH), Zürich Switzerland, 2012.
Protein quantification from mass spectra.
65. F. Hoffmann-La Roche Ltd, Basel Switzerland, 2012.
Protein quantification from mass spectra.
66. Department of Statistics, University of British Columbia, Vancouver Canada, 2012.
Protein quantification from mass spectra: statistical methods and tools for overcoming variation and sparsity.
67. Annual meeting of the Center for Algorithmic and Systems Biology, UCSD, San Diego, 2012.
Statistical analysis can account for sparsity and redundancy in protein quantifications to save cost and gain deeper biological insight.
68. Training Program in Biostatistics, Bioinformatics, Nutrition and Cancer, Texas A& M, 2012.
Protein quantification from mass spectra: statistical methods and tools for overcoming variation and sparsity.
69. Joint meeting of the French Mass Spectrometry Society and the French Proteomics Society, Avignon, France 2011.
Statistical methods for quantitative proteomics.
70. Qatar Computing Research Institute, Doha, Qatar, 2011.
An insight into computational and statistical mass spectrometry-based proteomics.
71. The George Institute, University of Sydney, Australia, 2011.
Statistical framework for protein quantification with mass spectrometry-based proteomic experiments.
72. Annual meeting of the Australasian Proteomics Society, Lorne, Australia, 2011.
Statistical Analysis of Quantitative Mass Spectrometry-Based Proteomic Experiments.
73. Department of Bioinformatics and Biostatistics, University of Louisville, KY, 2010.
Mixed-effect models for high-throughput mass spectrometry-based proteomic profiling experiments.
74. Commissariat à l'Energie Atomique et aux Energies Alternatives (CEA), Grenoble, France, 2010.
Statistical protein quantification in label-free LC-MS experiments: methods, software & case studies.
75. Research and Training Center on Bioinformatics, Russian Academy of Sciences, Moscow, 2010.
An insight into computational and statistical mass spectrometry-based proteomics.
76. The US Human Proteome Organization (US HUPO), Denver, CO, 2010.
Statistical experimental design and protein quantification in LC-MS experiments: methods, software and case study.

77. Center for Bioinformatics Research, Indiana University at Bloomington, 2010.
Mixed-effect models for high-throughput mass spectrometry-based molecular profiling experiments.
78. Training Program in Bioinformatics, Texas A& M, 2009.
Protein Quantification in Label-free LC-MS experiments.
79. The US Human Proteome Organization (US HUPO), San Diego, CA, 2009.
Introduction to Statistical Principles in Designing Proteomics Experiments.
80. Keystone Symposium "Omics Meets Cell Biology", Breckenridge, CO, 2009.
Experimental Design from a Statistics Point of View.
81. Swiss Federal Institute of Technology (ETH), Zürich, Switzerland, 2008.
Statistical design and analysis of LC-MS profiling experiments.
82. Swiss Institute of Bioinformatics, Geneva, Switzerland, 2008.
Statistical design and analysis of LC-MS profiling experiments.
83. Indiana University Purdue University, Indianapolis, IN, 2007.
Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.
84. IBM T. J. Watson, Yorktown Heights, NY, 2007.
Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.
85. New York University, New York, 2007.
Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.
86. International Chinese Statistical Association Applied Statistics Symposium, Raleigh, NC, 2007.
Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.
87. University of Illinois-Urbana Champain, IL, 2007.
Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.
88. Monsanto Company, St. Louis, MO, 2006.
A combined LC-MS and LC-MS/MS framework for quantitative peptide and protein profiling.
89. Bioinformatics and statistical genetics seminar series, Purdue University, 2005.
A scalable inferential approach to protein backbone nuclear magnetic resonance assignment.
90. Swiss Federal Institute of Technology (ETH), Zürich, Switzerland, 2005.
Inferential analysis of protein Nuclear Magnetic Resonance (NMR) spectra.

C Other Selected Presentations

1. Annual conference of the American Society for Mass Spectrometry, Minneapolis, MN, 2013.
Oral presentation: *Statistical selection of informative features for protein quantification in data-independent spectral acquisition.*
2. Annual conference of the American Society for Mass Spectrometry, Vancouver, Canada, 2012.
Oral presentation: *A statistical framework for protein significance analysis in SRM experiments with sparse labeled references.*
3. Keystone Symposium "Omics Meets Cell Biology", Alpbach, Austria 2011.
Oral presentation: *Statistical Methods and Tools for Protein Quantification in MS-based Proteomics.*
4. Joint Statistical Meetings, Vancouver, CA, 2010.
Oral presentation: *Mixed-effect models for high-throughput mass spectrometry-based proteomic profiling experiments.*
5. Joint Statistical Meeting, Denver CO, 2008.
Oral presentation: *Introducing bioinformatics as part of statistics curriculum at Purdue.*

6. Bioinformatics and statistical genetics seminar series, Purdue University, 2008.
   Oral presentation: *False discovery rates in database-based identification of tandem mass spectra*.
7. Bioinformatics and statistical genetics seminar series, Purdue University, 2006.
   Oral presentation: *Inferential approaches to peptide sequence identification and quantitative protein profiling in MS-based proteomics*.
8. Joint Statistical Meeting, Seattle, 2006.
   Oral presentation: *Determination of differentially abundant peptides and proteins in a combined LC-MS and LC-MS/MS proteomics workflow*.
9. New Researchers Conference, Seattle, 2006.
   Oral presentation: *Determination of differentially abundant peptides and proteins in a combined LC-MS and LC-MS/MS proteomics workflow*.
10. Joint Statistical Meeting, Minneapolis, 2005.
    Oral presentation: *Model search in highly dimensional constrained graphical models with application to protein backbone NMR assignment*.
11. Eastern North American Region (ENAR) meeting of the International Biometric Society, 2004.
    Oral presentation: *Inferential analysis of protein Nuclear Magnetic Resonance (NMR) spectra*.
12. Joint Statistical Meeting, San Francisco, 2003.
    Oral presentation: *Model-based analysis of protein backbone NMR*.
13. Bioinformatics and statistical genetics seminar series, Purdue University, 2002.
    Oral presentation: *Statistical issues in protein structure determination by nuclear magnetic resonance spectroscopy (NMR)*.
14. Bioinformatics and statistical genetics seminar series, Purdue University, 2002.
    Oral presentation: *Gene expression profiling of intestinal cell differentiation: biological and statistical issues*.
15. Bioinformatics and statistical genetics seminar series, Purdue University, 2000.
    Oral presentation: *Designing microarray experiments: chips, dips, flips, and skips*.

D Other Professional Activities

D.1 Editorial Positions

1. Editorial Board Member, *Genome Biology*, since 2019.
2. Guest co-editor, special issue on "Benchmarking of bioinformatic tools" in *Genome Biology*, 2019.
3. Editorial advisory board member, *Journal of Proteome Research*, since 2015.
4. Editorial board member, *Molecular and Cellular Proteomics*, since 2012.
5. Guest co-editor, special issue on "Large-scale computational mass spectrometry and multi-omics" in *Journal of Proteome Research*, 2015-2016.
6. Associate Editor. *Journal of Statistical Planning and Inference*, 2012-2014.
7. Co-editor. *"Statistical methods for MS-based proteomics"*, BMC Bioinformatics Supplement, 2012.

E Funding

E.1 External funding

Current

1. *MassIVE.quant: a curated and scalable community resource for quantitative proteomics*

NIH-NLM-R01.
06/01/2019 - 05/31/2023.
PI: N. Bandeira.

2. *ENS: Collaborative research: Enhancing R for scalability and deployment*
NSF-CISE/CCRI.
10/01/2019 - 10/01/2022.
PI: J. Vitek.
3. *ABI Innovation: Scalable and agile analysis of mass spectrometry experiments*
NSF-BIO/DBI
08/01/2018-07/31/2021
PI: O. Vitek.
4. *Summer school: Big Data and statistics for bench scientists*
NIH-BD2K-R25
09/20/2016-05/31/2019
PI: O. Vitek

Past

1. *Statistical framework for design and analysis of mass spectrometry-based proteomics experiments with isobaric labeling.*
Genentech.
01/01/2019 - 12/31/2019.
PI: O. Vitek.
2. *Deep knowledge: Accelerating knowledge extraction from large-scale multi-data resources by incorporating prior knowledge with deep learning*
DARPA; subcontract to Stanford University
05/01/2017-05/01/2019
PI: O. Vitek.
3. *Statistical design and analysis of quantitative, mass spectrometry-based experiments utilizing TMT labeling*
NIH Intramural subcontract
04/01/2018-12/31/2018
PI: O. Vitek.
4. *Causal inference of biomolecular networks from multi-platform experiments*
GNS Healthcare
01/08/2018-04/30/2018
PI: O. Vitek.
5. *Statistical methods for relative quantification of post-translational modifications in global proteomics experiments.*
Genentech.
03/01/2017-12/31/2018.
PI: O. Vitek.
6. *Statistical methods for mass spectrometry-based proteomic experiments with tandem mass tag (TMT) labeling*
Hoffman LaRoche, Basel, Switzerland
09/01/2016-08/31/2017
PI: O. Vitek
7. *gMODs: A computational tool to accelerate the characterization of therapeutic protein modifications*
Genentech
07/09/2015-12/31/2016
PI: O. Vitek

8. *Statistical methods for Selected Reaction Monitoring of proteins*
   Hoffman LaRoche, Basel, Switzerland
   10/01/2014-09/31/2016
   PI: O. Vitek
9. *CAREER: Sparse-sampling inference for functional proteomics, metabolomics and ionomics*
   NSF-BIO/DBI
   07/01/2011-07/01/2016
   PI: O. Vitek
10. *Quantification of signal transduction pathways in Bayesian network to facilitate tailored cancer therapy research*
    Eli Lilly and Co
    08/01/2014-12/01/2015
    PI: O. Vitek.
11. *Desorption Electrospray Ionization mass spectrometry imaging in clinical diagnostics*
    NIH-NCI-R21
    04/01/2013 - 03/31/2015
    PI: G. Cooks, Purdue.
12. *Pheromonal control of gamete determination and differentiation in Ceratopteris*
    NSF-BIO
    05/01/2013-04/30/2015
    PI: J. A. Banks, Purdue.
13. *New proteomic technologies for the analysis of tyrosine kinase signaling pathways*
    NIH-NIGMS-R01
    07/01/2010-07/01/2015
    PI: W. A. Tao, Purdue.
14. *SI2: Conceptualization: Dynamic languages for scalable data analytics*
    NSF-SI2
    10/01/2012 - 03/31/2014
    PI: J. Vitek, Purdue.
15. *Computational imaging mass spectrometry*
    Canary Center at Stanford for Cancer Early detection
    01/01/2013-12/30/2013.
    PI: O. Vitek.
16. *A tracing virtual machine for statistical computing*
    NSF-SI2-SSE
    12/01/2010-11/31/2013
    PI: J. Vitek, Purdue.
17. *Statistical methods and computing for functional interpretation of high-throughput experiments in molecular systems biology*
    Qatar Research Foundation
    08/15/2012-08/14/2013
    PI: O. Vitek.
18. *Statistical validation of the G-Series RayBiotech arrays for biomarker screening*
    RayBiotech Biomarker Discovery Research Pilot Grant
    04/30/2010-04/30/2012
    PI: O. Vitek.
19. *Classification of multiple bacterial pathogens using light-scattering sensor imaging*
    Advanced BioImaging Systems

05/30/2010-05/30/2011.
PI: O. Vitek.

20. *Development of workflows for integration of high throughput data and clinical variables: Additional Indiana CTSI support.*
IU School of Medicine/NIH
05/01/2009-04/30/2010.
PI: C. Weaver, Purdue.
21. *Accurate quantification of protein abundance for clinical applications of mass spectrometry-based proteomics*
IUPUI
2/1/09-01/31/2010.
PI: O. Vitek.
22. *Development of workflows for integration of high throughput data with clinical variables*
IU School of Medicine/NIH
1/1/09-05/31/2009.
PI: O. Vitek.
23. *Proteomics and metabolomics analyses to identify biomarkers in osteosarcoma*
Indiana University Cancer Center Translational Research Acceleration Collaboration (ITRAC),
7/15/2007-7/14/2009
PI: S. Ragg, IU School of Medicine.
24. *Proteomic and gene expression analysis to identify biomarkers in Wilms tumor*
Indiana University Cancer Center Translational Research Acceleration Collaboration (ITRAC)
5/15/08-5/14/09
PI: S. Ragg, IU School of Medicine.
25. *Interfacing biological knowledge and statistical analysis for rapid interpretation of clinical proteomics experiments*
Purdue University/IUPUI Intercampus Applied Research Program (IARP)
5/1/2008-4/30/2009.
PI: G. Schadow, IUPUI.
26. *A hypothesis testing approach to identification and assessment of statistical significance of peptides and proteins in shotgun proteomics*
Purdue University/Indiana University Collaboration in Life Sciences and Informatics Research (CLSIR)
01/01/2007-12/31/2007
PI: O. Vitek.
27. *Taking quantitative LC-MS profiling of blood samples in cardiovascular disease to a clinically relevant scale: a computational and statistical approach*
Purdue University/Indiana University School of Medicine Collaboration in Biomedical Research (CBR)
01/01/2007-12/31/2007
PI: O. Vitek.

E.2 Internal funding

Past

1. *Sy and Laurie Sternberg interdisciplinary associate professorship*
Northeastern University
09/01/2013-08/31/2018
PI: O. Vitek
2. *NSF S2I2 Scalable data analytics institute*
Northeastern University, Tier III grant

06/12/2015 - open
PI: J. Vitek, Northeastern

3. *A proteomic roadmap to the endogenous protein complexes of the endoplasmic reticulum in key plant species*
Purdue Discovery Park Seed Grant
04/01/2009-03/31/2010.
PI: D. Szymanski, Purdue.
4. *Statistical design and analysis of selected reaction monitoring (SRM) experiments for quantitative proteomics*
Purdue Research Foundation
8/17/09 - 7/31/2010.
PI: O. Vitek.

F Evidence of Involvement in the Graduate Research Program

F.1 Graduated group members

Graduated post-doctoral associates:

1. Mr. Tsung-Heng Tsai, College of Science, Northeastern University, August 2019.
First position: Assistant Professor, Kent State University
2. Mr. Cyril Galitzine, Khoury College of Computer Sciences, Northeastern University, May 2018.
    - Burrough Wellcome Collaborative Research Travel Grant, 2017.

   First position: Insight Data Science Fellow.
3. Mr. Eralp Dogu, Khoury College of Computer Sciences, Northeastern University, August 2016.
First position: Assistant Professor, Mugla University, Turkey

Graduated PhD students:

1. Mrs. April Harry, Department of Statistics, Purdue, Fall 2017.
    - George Washington Carver Fellowship, 2010
    - Purdue University StatCom Community Service Award

   Dissertation: *Design and statistical analysis of mass spectrometry imaging experiments*
   First position: Insight Data Science Fellow.
2. Mr. Robert Ness, Department of Statistics, Purdue, Fall 2016.
    - Institute of International Education Boren Fellowship, 2012

   Dissertation: *Bayesian causal inference of cell signal transduction*
   First position: Senior research scientist, Zymergen.
3. Mrs. Kylie Bemis, Department of Statistics, Purdue, Fall 2016.
    - John M. Chambers Statistical Software Award of the American Statistical Association, 2015
    - NSF Graduate Research Dissertation Fellowship, 2012

   Dissertation: *A framework for the statistical analysis of mass spectrometry imaging experiments*
   First position: Future Faculty Post-doctoral Associate, College of Science, Northeastern University.
4. Ms. Meena Choi, Department of Statistics, Purdue, Spring 2016.
    - ThinkSwiss research scholarship, 2013

   Dissertation: *A flexible and versatile framework for statistical design and analysis of quantitative mass spectrometry-based proteomic experiments*
   First position: Post-doctoral Associate, College of Science, Northeastern University.

5. Mrs. Danni Yu, Department of Statistics, Fall 2013, Purdue.
    - I.W. Burr Dissertation Award, 2014

   Dissertation: *Estimation of variation in high-throughput molecular biology experiments with small sample size*
   First position: Research Scientist, Eli Lilly and Company.
6. Mrs. Ching-Yun (Veavi) Chang, Department of Statistics, Summer 2013, Purdue.
   Dissertation: *Cost-effective and accurate protein quantification for large-scale targeted proteomics*
   First position: Research Scientist, Eli Lilly and Company.
7. Mr. Tim Clough, Department of Statistics, Summer 2012, Purdue.
    - StatCom leadership Award, 2011
    - ThinkSwiss research scholarship, 2010

   Dissertation: *Statistical protein quantification and prioritization in label-free shotgun LC-MS/MS proteomics*
   First position: Senior Biometrician, Novartis.
8. Mr. Cheng Zheng, PhD. Department of Statistics, Fall 2010, Purdue.
    - I.W. Burr Dissertation Award, 2010
    - Bilsland Fellowship 2009-2010.

   Dissertation: *Model-based identification and quantification of metabolites in* ^1H *NMR spectra*
   First position: Senior Biostatistician, Novartis.

Graduated MS students:

1. Mr. Kaushal Paneri, MS in Data Science, Northeastern University. August 2019.
   Dissertation: *Integrating Markov Process and structural causal models enables counterfactual inference in complex systems*

F.2 Current group members

Current senior group members:

1. Mrs. Kylie Bemis, Lecturer, Khoury College of Computer Sciences, Northeastern University.
    - Burrough Wellcome Postdoctoral Enrichment Award, 2018
2. Mrs. Meena Choi, Research Scientist, Khoury College of Computer Sciences, Northeastern University.

Current PhD students:

1. Mrs. Dan Guo, CCIS, Northeastern University, 01/2018-now.
2. Mrs. Ting Huang, CCIS, Northeastern University, 05/2017-now.
    - Lucille Zanghi ’72 and Jim Dow ’72 Graduate Fellowship in Bioinformatics. 2015
    - Wolfgang Goetzinger - Amgen Memorial Graduate Scholar Award in Life Sciences, 2016.
3. Mrs. Sara Mohammad Taheri, CCIS, Northeastern University, 01/2018-now.

Current MS students:

1. Mr. Sicheng Hao, Master in Data Science, CCIS, Northeastern University. 09/2017-now

F.3 Other Activities:

Postdoctoral mentoring:

1. NIH K99/R00 mentor to Inna Smalley, H. Lee Moffitt Cancer Center, Tampa FL.

Ph.D. Committee Member:

1. Marco Hadisurya, Tao Lab, Biochemistry, Purdue University.
2. Amanda Figueroa-Navedo, Ivanov Lab, Chemistry, Northeastern University.
3. Christopher Wilson, Engen Lab, Chemistry, Northeastern University
4. Jelena Cuklina, Aebersold Lab, Systems Biology, ETH Zürich, Switzerland. Graduated Summer 2018.
5. Chinmay Shukla, Irizarry lab, Computational Biology, Harvard Medical School. Graduated Summer 2018.
6. Catherine M. Rawlins, Agar Lab, Chemistry, Northeastern University. Graduated Summer 2018.
7. Yu (Annie) Wang, Hancock Lab, Chemistry, Northeastern University. Graduated Fall 2017.
8. Yuanwei Gao, Karger Lab, Chemistry, Northeastern University. Graduated Summer 2016.
9. Michael Wleklinski, Cooks Lab, Chemistry, Purdue. Graduated Fall 2016.
10. Ms. Nadia Atallah, Banks Lab, Botany, Purdue. Graduated Spring 2015.
11. Mrs. Kelly-Ann Dixon Hamil, Zhang Lab, Statistics, Purdue. Graduated Spring 2015.
12. Mr. Ariful Azad, Pothen Lab, Computer Science, Purdue. Graduated Spring 2014.
13. Ms. Eunjung Lim, Craig Lab, Statistics, Purdue. Graduated Summer 2011.
14. Mr. Paul Livermore Auer, Doerge Lab, Statistics, Purdue. Graduated Summer 2010.
15. Mr. Shahin Mohammadi, Grama Lab, Comuputer Science, Purdue.
16. Ms. Sudeshna Paul, Craig Lab, Statistics, Purdue. Graduated Fall 2009.
17. Ms. Sandra Lövenich, Aebersold Lab, Systems Biology, ETH Zürich. Graduated Summer 2009.

M.S. Committee Member:

1. Kyungmin Ahn, Veronica Crofts, Dan Dillon, Junyan Ge, Syed Haque, Qiming Huang, Xinyan Liu, Wen Wei Loh, Chris Morgan, Xuelu Ren, Xiaosu Tong, Pu-Tai Yang, Yi Yin, Shuai Edison Yu, Catherine Withey, Noah Whitman, Yang Zhao, Jing Zhu
   Department of Statistics, Purdue University.
2. Mr. Mourad Mellal
   l'Université Joseph Fourier, Grenoble, France. Graduated Summer 2010.

Reading Courses and Coop:

1. Mr. Siddhesh Acharekar, MS in Data Science, Khoury, Northeastern University, Fall 2019.
2. Mr. Chris Botica, MS in Data Science, Khoury, Northeastern University, Fall 2019.
3. Mr. Sicheng Hao, MS in Data Science, Khoury, Northeastern University, Summer 2018-now.
4. Mrs. Rutu Nanavati, MS in Data Science, Khoury, Northeastern University, Fall 2018.
5. Mrs. Alefiya Naseem, MS in Data Science, Khoury, Northeastern University, Fall 2018.
6. Mr. Kaushal Paneri, MS in Data Science, Khoury, Northeastern University, Fall 2018.
7. Mr. Shantam Gupta, MS in Data Science, Khoury, Northeastern University, Summer 2018
8. Mr. Qiming Huang, PhD in Statistics, 06/2012-08/2012
9. Mrs. Meena Choi, MS in Statistics, 09/2010-12/2010, 01/2012-05/2012
10. Mr. Tim Clough, PhD in Statistics, 01/2008-05/2008
11. Mr. Kelvin Ma, PhD in Statistics, 01/2008-05/2008
12. Mrs. Jonna Anderson, PhD in Statistics, 01/2007-05/2007
13. Mrs. Melissa Key, PhD in Statistics, 01/2007-05/2007

IV. ENGAGEMENT

A Northeastern University

F2018-S2019:	Director, MS in Data Science, CCIS MS in Data Science Curriculum Committee, CCIS (Chair) Director Search Committee, Barnett Institute, College of Science Member, university-wide Graduate Council
F2018-S2019:	Director, MS in Data Science, CCIS MS in Data Science Curriculum Committee, CCIS (Chair) Academic Review for AI/DS area, CCIS (Chair) Governance Committee, Barnett Institute, College of Science Director Search Committee, Barnett Institute, College of Science Awards Committee, Barnett Institute, College of Science
F2017-S2018:	Hiring Committee, CCIS MS in Data Science Committee, CCIS Director Search Committee, Barnett Institute, College of Science Grievance Committee, Northeastern University Faculty Senate. Active cases: 1.
F2016-S2017:	Director Search Committee, Barnett Institute, College of Science Fellowship Committee, Barnett Institute, College of Science Mathematics Department Chair Search Committee, College of Science MS in Data Science Committee, CCIS PhD program in Statistical Science Curriculum Design Committee (Chair), Inter-College
F2015-S2016:	Dean Search Committee, College of Science Computational Faculty Search Committee, College of Science MS in Data Science Curriculum Design Committee, CCIS
F2014-S2015:	Hiring committee, CCIS

B Purdue University

F2013-S2014:	Hiring committee in computational statistics (Co-chair) Applied Methods PhD qualifying exam committee M. S. in Applied Statistics Exam committee Outstanding Assistant Professor Teaching Award committee Graduate Student Teaching Award committee Executive and Personnel committee Diversity committee College of Science Grade Appeals committee
F2011-S2012:	I.W. Burr Award committee (Chair) L. J. Cote M.S. Excellence in Statistics Award committee Strategic Planning committee Applied Methods PhD qualifying exam committee M.S. in Applied Statistics exam committee
F2010-S2011:	Applied Methods PhD qualifying exam committee (Chair) M.S. in Applied Statistics exam committee L.J. Cote award committee Strategic planning committee Hiring committee - advisory member
F2009-S2010:	Applied Methods PhD qualifying exam committee (Chair) M.S. in Applied Statistics exam committee Hiring committee Student cases committee Faculty representative at the Commencement ceremony
F2008-S2009:	Myra Samuels lecture committee (Chair) College of Science Faculty Council representative
F2007-S2008:	Computational Statistics PhD qualifying exam committee Graduate admissions committee Hiring committee
F2006-S2007:	Computational Statistics PhD qualifying exam committee Myra Samuels lecture committee

C Professional

1. Program Committee member and Community of Special Interests (COSI) representative, Intelligent Systems in Molecular Biology (ISMB), 2020.
2. Elected Member, Council of the International Human Proteome Organization (HUPO), 2019-2021.
3. Elected Officer and Program Chair, Boston Chapter of the American Statistical Association, January 2019.
4. Senior Program Committee (SPC) member and Community of Special Interests (COSI) representative, Intelligent Systems in Molecular Biology (ISMB), 2019.
5. Program Committee, OurCon VII, Saint-Malo, 2019.
6. Elected Member and Secretary, Executive Committee and Board of Directors, US Human Proteome Organization, 2015-2018.
7. Invited panelist, NHLBI-supported Biomedical Data Science Curriculum Initiative (BMDSCI), Harvard University, Boston, MA, 2018.

8. Grant proposal reviewer. NIH, Spring 2018.
9. Senior Program Committee (SPC) member, Intelligent Systems in Molecular Biology (ISMB), 2018.
10. Program Committee member, Annual International Conference on Research in Computational Molecular Biology (RECOMB), 2018.
11. Representative of the Community of Special Interests (COSI) of the International Society for Computational Biology (ISCB) on Computational Mass Spectrometry, 2018.
12. Co-organizer, Session on data analysis and quantitation. Imaging Mass Spectrometry Society Inaugural Meeting session, Boston MA 2017.
13. Grant proposal reviewer. NIH, Spring 2017.
14. Program Committee member, Annual International Conference on Research in Computational Molecular Biology (RECOMB), 2017.
15. Co-organizer, Annual Conference of the US Human Proteome Organization (US HUPO), 2016.
16. Program Committee member, Annual International Conference on Research in Computational Molecular Biology (RECOMB), 2016.
17. Program committee member, Computational Systems Biology, Application track. European Conference on Computational Biology (ECCB), 2016.
18. Co-organizer. Schloss Dagstuhl Seminar on Computational Mass Spectrometry. August 2015.
19. Invited discussant, NSF workshop "Mass Spectrometry: Big Data to Knowledge", 2015.
20. Co-organizer, Annual Conference of the US Human Proteome Organization (US HUPO), 2015.
21. Program Committee member. MS & Proteomics, Intelligent Systems in Molecular Biology (ISMB), 2015.
22. Member, founding committee. Computational mass spectrometry special interested group. Since 2014.
23. Grant proposal reviewer. NIH, Spring 2014.
24. Grant proposal reviewer. NSF, Spring 2014.
25. Organizer. Workshop on "Software and Statistics in Mass Spectrometry". International Mass Spectrometry Conference (IMSC), 2014.
26. Program committee member, Computational Systems Biology. European Conference on Computational Biology (ECCB), 2014.
27. Organizer. Workshop on Biostatistics. Annual Conference of the Association of the Biomedical Resource Facilities (ABRF), 2014.
28. Area program committee co-chair. Mass Spectrometry & Proteomics. Intelligent Systems in Molecular Biology (ISMB) 2014.
29. Education Committee member. US Human Proteome Organization (US HUPO), since 2012.
30. Co-organizer. Schloss Dagstuhl Seminar on Computational Mass Spectrometry. December 2013.
31. Grant proposal reviewer. NIH, Spring 2013.
32. Area program committee co-chair, Mass Spectrometry & Proteomics. Program committee member, Late Breaking Research. Intelligent Systems in Molecular Biology (ISMB) and European Conference on Computational Biology, 2013.
33. Proteome Informatics Research Group (iPRG), Association of Biomedical Resource Facilities 2013-2014.
34. Program Committee member. ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB) 2012.
35. Grant proposal reviewer. NIH and NSF-BIO, Spring 2012.
36. Program Committee member. Mass Spectrometry & Proteomics, Intelligent Systems in Molecular Biology (ISMB), 2012.
37. Conference co-chair. Research in Computational Molecular Biology (RECOMB) Satellite Conference on Com-

putational Proteomics, 2012.

38. Ad-hoc grant proposal reviewer, NIH and NSF-BIO, Fall 2011.
39. Program Committee member. Mass Spectrometry & Proteomics, Intelligent Systems in Molecular Biology (ISMB) and European Conference on Computational Biology, 2011.
40. Program Committee member. Workshop on Emerging Computational Methods for the Life Sciences, 2011.
41. Program Committee member. Research in Computational Molecular Biology (RECOMB) Satellite Conference on Computational Proteomics, 2011.
42. Program Committee member. Late Breaking Research program, Intelligent Systems in Molecular Biology (ISMB), 2010.
43. Program Committee member. Workshop on Algorithms in Bioinformatics (WABI), 2010.
44. Program Committee member. Research in Computational Molecular Biology (RECOMB) Satellite Conference on Computational Proteomics, 2010.
45. Program Committee member. Invited Session on Nature-Inspired Collective Intelligence, International Conference on Computational Collective Intelligence (ICCCI), 2009.
46. Grant proposal reviewer. NSF-BIO, Fall 2009.
47. Grant proposal reviewer. Qatar National Research Foundation, Fall 2009.
48. Grant proposal reviewer. NSF-DMS, Fall 2008.
49. Referee for *Bioinformatics*, *BMC Bioinformatics*, *Computational Statistics and Data Analysis*, *Genome Biology*, *IEEE Transactions on Signal Processing*, *IEEE International Workshop on Genomic Signal Processing and Statistics GENSIPS'07*, *Journal of Proteome Research*, *Molecular and Cellular Proteomics*, *Mass Spectrometry Reviews*, *Pacific Symposium of Biocomputing*, *Physiological Genomics*, *The Plant Cell*, *PloS Computational Biology*, *PloS ONE*, *Statistical Applications in Genetics and Molecular Biology*, *Nature Biotechnology*, *Nature Methods*.