

# Attila Kertész-Farkas, PhD, DSc

Laboratory Head  
Tenured Professor

Department of Data Analysis and Artificial Intelligence  
Faculty of Computer Science  
Higher School of Economics, HSE University, Moscow, Russia

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## PERSONAL

Hungarian, European Union (EU) citizen, [LinkedIn](#), [GitHub](#), [Publication List](#),

## AREA OF EXPERTISE

Computer Science, Data Science, Deep Learning, Statistics, Bioinformatics, Mass spectrometry

## ACADEMIC DEGREES AND TITLES

2024	<b>Tenured Full Professor</b> , HSE University
2022	<b>D.Sc.</b> in Computer Science, HSE University, Moscow, Russia, <a href="https://www.hse.ru/sci/diss/557729031">https://www.hse.ru/sci/diss/557729031</a> Doctor of Science: related to habilitation and to full professorships,
2021	<b>Tenured Associate Professor</b> , HSE University
2009	<b>Ph.D.</b> in Computer Science, University of Szeged, Hungary
2004	<b>M.Sc.</b> in Computer Science and Mathematics, University of Szeged, Hungary

## WORK EXPERIENCE

2024-present	<b>Full Professor</b> at the Department of Data Analysis and Artificial Intelligence, HSE University,
2020-present	<b>Laboratory Head</b> , <a href="#">Laboratory on AI for Computational Biology</a> , HSE University,
2015-2024	Associate Professor at the Department of Data Analysis and Artificial Intelligence, HSE University,
2013-2015	Postdoctoral Fellow, Noble Lab, <b>University of Washington, Seattle WA, USA</b>
2009-2013	Postdoctoral Fellow, Bioinformatics Group, International Centre of Genetic Engineering and Biotechnology (ICGEB), <b>Trieste, Italy</b>
2008-2009	Research Fellow, Division of Imaging and Applied Mathematics, CDRH, <b>U.S. Food and Drug Administration (U.S. FDA)</b> , Silver Spring MD, USA. Joint affiliation with Department of Biology, University of Maryland Baltimore County (UMBC), Catonsville MD, USA
2004-2008	Ph.D. Student, University of Szeged, Hungary
2000-2004	Undergraduate Research Assistant, Research Group on Artificial Intelligence, Hungarian Academy of Sciences, Szeged, Hungary

## SCHOLARSHIPS AND AWARDS

2021,2022	High Quality Performance awards by the HSE University
Occasionally	Best paper/talk awards
2007-2008	Predoctoral scholarship granted by the Foundation for Research and Teaching of Informatics, Hungary
2006-2007	Erasmus scholarship (student exchange), <b>Technische Universität Dresden, Germany</b>
2003-2008	Honors College (Eötvös Collegium) for outstanding students at University of Szeged, Hungary
2004	1 <sup>st</sup> prize at a Scientific Conference of Students, University of Szeged, Hungary
2002	1 <sup>st</sup> prize at a Scientific Conference of Students, University of Szeged, Hungary

**ADVISING**

**MSc, BSc, International Interns:** many, approx. 70+

**PhD students:**

- Roman Chereshev (2015-2019): Dissertation title: Human gait controlling system using machine learning methods suitable for robotic prostheses for patients suffering from double transfemoral amputation. The thesis bases on one article in Q2 journal, two articles in Q3 journals.  
Date of Defense: 10 October 2019, <https://www.hse.ru/sci/diss/290226447>
- Pavel Sulimov (2016-2020): Dissertation title: Learning generative probabilistic models for mass spectrometry data identification. The thesis bases on three articles in Q1 journals and one article in a Q3 venue.  
Date of Defense: 9 September 2020, <https://www.hse.ru/sci/diss/377487862>  
Now, Pavel is a senior researcher at *Zurich University of Applied Sciences in Switzerland*.
- Nikita Moshkov (2017-2022): Dissertation title: Application of deep learning algorithms to single-cell segmentation and phenotypic profiling. The thesis is based on three articles published in Q1 journals.  
Date of Defense: 27<sup>th</sup> of October 2022, <https://www.hse.ru/sci/diss/664946503>  
Now, Nikita is a senior researcher at *Helmholtz Munich in Germany*
- Seungmin Jin (2021-2023): Dissertation title: A visual analytics system for explaining and improving attention-based traffic forecasting models. The thesis is based on three articles all published in Q1 and A\* venues.  
Date of Defense: 27<sup>th</sup> of June 2024. <https://www.hse.ru/sci/diss/903157911>
- Frank Lawrence Nii Adoquaye Acquaye (2021-2024): Dissertation title: Computationally efficient methods for tandem mass spectrometry data analysis. Expected in Sept 2025
- Kishankumar Bhimani (2021-2024): Dissertation title: Exact p-value calculation for high resolution Tandem Mass Spectrometry data. Expected in Sept 2025

**TEACHING EXPERIENCES**

2023-present	Machine Learning, (in English), HSE, Moscow, Russia
2017-2023	Discriminative Methods in Machine Learning, (in English), HSE, Moscow, Russia
2017-2023	Generative Methods in Machine Learning, (in English), HSE, Moscow, Russia
2016-present	Lecturer of Computational Mass Spectrometry (in English), HSE, Moscow, Russia
2015-2017	Lecturer of Advanced Topics in Machine Learning (Eng.), HSE, Moscow, Russia
2015	Lecturer at Bioinformatics Tools for Life Sciences Workshop (Eng.), Quito, Ecuador
2012	Lecturer at Theoretical and Practical Course on Advanced Bioinformatics (Eng.), ICGEB, Italy
2010-2013	Teaching assistant, Theoretical and Practical Course on Bioinformatics (Eng.), ICGEB, Italy
2007	Teaching assistant, Operational Research (in Hungarian), University of Szeged
2006	Teaching assistant, Algorithms and Data Structures (Hun), University of Szeged
2004-2005	Teaching assistant Introduction to Pascal, C and Java Programming (Hun), University of Szeged

**MEMBERSHIPS**

2018, 2019	PC member, Intl' Conference on Analysis of Images, Social networks and Texts (AIST'18)
2017	PC member, Bioinformatics and Artificial Intelligence at International Joint Conference on Artificial Intelligence, (bai@IJCAI2017)
2014-2018	Industrial/Research Chair, Biotechno conference series
2012-2019	Editorial board of International Journal on Advances in Life Sciences
2006-2014	John von Neumann Computer Science Society, Hungary
2005-2007	PhD student representative on the Board of Doctoral Schools, Faculty of Sci., Univ of Szeged
2005-2007	PhD student representative on the Board of the Institute of Informatics, University of Szeged

## COLLABORATIONS

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2015-2017	Huawei Research Center, Moscow, Russia
2017-2022	Biological Research Center, Szeged, Hungary
2021-	Noble Lab, University of Washington, <b>Seattle, WA, USA</b>
2021-	Szilagyi Lab, University of Szeged, Hungary,

## LIST OF PUBLICATIONS

## THESES

1. D.Sc.: *Computational Methods for Tandem Mass Spectrometry Data Annotation*, HSE University, Moscow, 2022
2. Ph.D.: *Protein Classification in a Machine Learning Framework*, SZTE University, Szeged, Hungary, 2010
3. M.Sc.: *Compact Representation of Finite Languages with Nondeterministic Finite Automata*, SZTE University, Szeged, Hungary, 2004

## PEER-REVIEWED JOURNAL PAPERS (\*equally contributed authors; †corresponding author; Q1 journal)

4. Andrey Borevsky, Attila Kertesz-Farkas†: Toward reliable false discovery rate control in classification problems under distribution shift, 2025, under review
5. Muhammad Sufiyan, Andrey Borevskiy, Attila Kertesz-Farkas†: Target-decoy approaches result in biased false discovery rates in database-searching-based MS/MS spectrum annotation in large scale experiments, under revision to *Journal of Mass Spectrometry*, 2025, Q2 journal
6. Kishankumar Bhimani, Arina Peresadina, Karina Burmak, Kartik Joshi, Attila Kertesz-Farkas†: Single amino acid variation identification in high resolution tandem mass spectrometry data in bottom up proteomics, under review in *International Journal of Mass Spectrometry*, Q2 journal
7. Frank Lawrence Nii Adoquaye Acquaye, Bo Wen, Charles Ernest Grant, William Stafford Noble, Attila Kertesz-Farkas: Label-free quantification in the Crux toolkit, 2025, under revision to **Journal of Proteome Research**. Q1 journal,
8. Attila Kertesz-Farkas, Frank Lawrence Nii Adoquaye Acquaye, Vladislav Ostapenko, Rufino Haroldo Locon, Yang Lu, Charles E Grant, William Stafford Noble: Fast and memory efficient searching of large-scale mass spectrometry data using Tide, 2025, under review in **Journal of Proteome Research**. Q1 journal,
9. Insan-Aleksandr Latipov, Andrey Borevskiy, Attila Kertesz-Farkas†: CLEVR-BT-DB: A Benchmark Dataset to Evaluate the Reasoning Abilities of Deep Neural Models in Visual Question Answering Problems, *Proc. SPIE 13169, Fifth International Conference on Computer Vision and Computational Intelligence (CVCI)*, 13169, 74—81, 2024, Q4 venue, <https://doi.org/10.1117/12.3027602>
10. Frank Lawrence Nii Adoquaye Acquaye, Insan-Aleksandr Latipov, Attila Kertesz-Farkas†: Hypernym Information and Sentiment Bias Probing in Distributed Data Representation, *Proceedings of International Conference on Machine Learning and Computing (ICMLC)*, ACM, Q4 venue, 2023. <https://doi.org/10.1145/3587716.3587753>
11. Kishankumar Bhimani, Arina Peresadina, Dmitrii Vozniuk, Attila Kertesz-Farkas†: Exact p-value calculation for XCorr scoring of high resolution MS/MS data, **Proteomics**, Q1 journal, IF: 3.4, <https://doi.org/10.1002/pmic.202300145>
12. Muhammad Sufiyan, Attila Kertesz-Farkas†: Peptide-shuffling decoy generation results in biased false discovery rate estimation in database-searching-based MS/MS spectrum annotation, **submitted**
13. Attila Kertesz-Farkas, Frank Lawrence Nii Adoquaye Acquaye, Kishankumar Bimani, Jimmy Eng, William E Fondrie, Charles Ernest Grant, Michael R Hoopmann, Andy Lin, Yang Lu, Robert L Moritz, Michael J MacCoss, William Stafford Noble: The Crux toolkit for analysis of bottom-up tandem mass spectrometry proteomics data, **Journal of Proteome Research**, 22(2), 561-569, 2023, Q1 Journal, Impact Factor: 4.466, <https://doi.org/10.1021/acs.jproteome.2c00615>
14. Frank Lawrence Nii Adoquaye Acquaye, Attila Kertesz-Farkas, William Stafford Noble: Efficient indexing of peptides for database search using Tide, **Journal of Proteome Research**, 22(2), 577-584, 2023, Q1 Journal, IF4.466, <https://doi.org/10.1021/acs.jproteome.2c00617>
15. Polina Kudryavtseva, Matvey Kashkinov, and Attila Kertesz-Farkas†: *Deep convolutional neural networks help scoring tandem mass spectrometry data in database-searching approaches*, **Journal of Proteome Research**, 20 (10), 4708-4717, 2021, Q1 Journal, Impact Factor: 5.370 <https://doi.org/10.1021/acs.jproteome.1c00315>
16. Nikita Moshkov, Botond Mate, Attila Kertesz-Farkas, Reka Hollandi, and Peter Horvath, *Test-time augmentation for deep learning-based cell segmentation on microscopy images*, **Scientific Reports**, 10, 5068, 2020, Q1 Journal,

Impact Factor: 3.998 (JCR SCI 2020), <https://doi.org/10.1038/s41598-020-61808-3>

17. Pavel Sulimov, Anastasia Voronkova, and Attila Kertész-Farkas<sup>†</sup>: *Annotation of tandem mass spectrometry data using stochastic neural networks in shotgun proteomics*, **Bioinformatics**, 36(12), 3781–3787, 2020, Q1 Journal, Impact Factor: 5.61 (JCR SCI 2020) <https://doi.org/10.1093/bioinformatics/btaa206>
18. Pavel Sulimov and Attila Kertész-Farkas<sup>†</sup>: *Tailor: A Nonparametric and Rapid Score Calibration Method for Database Search-Based Peptide Identification in Shotgun Proteomics*, **Journal of Proteome Research**, 19(4), 1481–1490, 2020, Q1 Journal, Imp. Factor: 4.074 (JCR SCI 2020) <https://doi.org/10.1021/acs.jproteome.9b00736>
19. Roman Chereshevnev, Attila Kertész-Farkas<sup>†</sup>: *GaIn: Human Gait Inference for Lower Limbic Prostheses for Patients Suffering from Double Trans-Femoral Amputation*, **Sensors**, 18(12), 4146, 2018, Q1 Journal, Impact Factor: 3.275(JCR SCI 2020) <https://doi.org/10.1021/acs.jproteome.9b00736>
20. Pavel Sulimov, Elena Sukmanova, Roman Chereshevnev, and Attila Kertész-Farkas<sup>†</sup>: *Guided Layer-wise Learning for Deep Models using Side Information*, *Communication in Computer and Information Science*, 1086, 2020, Q3 Journal, SJR Score: 0.168 (SJR 2018), [https://doi.org/10.1007/978-3-030-39575-9\\_6](https://doi.org/10.1007/978-3-030-39575-9_6)
21. Yulia Danilova, Anastasia Voronkova, Pavel Sulimov, Attila Kertész-Farkas<sup>†</sup>: *Bias in false discovery rate estimation in mass-spectrometry-based peptide identification*, **Journal of Proteome Research**, 18(5), 2354–2358, 2019, Q1 Journal, Impact Factor: 3.780 (JCR SCI 2019) <https://doi.org/10.1021/acs.jproteome.8b00991>
22. Gleb Filatov, Bruno B. Bauwens, and Attila Kertész-Farkas<sup>†</sup>: *LZW-Kernel: fast kernel utilizing variable length code blocks from LZW compressors for protein sequence classification*, **Bioinformatics**, 34(19), 3281–3288, 2018, Q1 Journal, Impact Factor: 5.481 (JCR SCI 2018), <https://doi.org/10.1093/bioinformatics/bty349>
23. Roman Chereshevnev, Attila Kertész-Farkas<sup>†</sup>: *RapidHARE: An Energy-Efficient Method for Real-Time Human Activity Recognition from Wearable Sensors*; *Journal of Ambient Intelligence and Smart Environments*, 10(5), 377–391, 2018, Q3 Journal, SJR-Score: 0.273 (SJR), Impact Factor: 0.878 (JCR SCI 2018), <https://doi.org/10.3233/AIS-180497>
24. Andrey Shestakov, Danila Doroshin, Dmitri Shmelkin, and Attila Kertész-Farkas<sup>†</sup>: *Lookup Lateration: Non-linear Received Signal Strength to Distance Mapping for Non-Line-of-Sight Geo-localization in Outdoor Urban Areas*; 7th International Conference on Analysis of Images, Social Networks and Texts (AIST) 2018, *Lecture Notes in Computer Science, Revised Selected Papers*, 2018 – **Best paper award**, Q2 Journal, SJR score: 0.283 (SJR 2018) [https://doi.org/10.1007/978-3-030-11027-7\\_23](https://doi.org/10.1007/978-3-030-11027-7_23)
25. Marina L. Mokrishcheva, Attila Kertész-Farkas, and Dmitri V. Nikitin: *New bifunctional restriction-modification enzyme AolI isoschizomer (PcoI): bioinformatics analysis, purification and activity confirmation*; *Gene*, 660, 6–12, 2018, Q2 Journal, Impact Factor: 2.497 (JCR SCI 2018), <https://doi.org/10.1016/j.gene.2018.03.069>
26. Roman Chereshevnev, Attila Kertész-Farkas<sup>†</sup>: *HuGaDB: Database for Human Gait Analysis from Wearable Inertial Sensor Networks*; 6th International Conference on Analysis of Images, Social Networks and Texts (AIST) 2017, *Lecture Notes in Computer Science, Revised Selected Papers*, 124–134, 2017, Q2 Journal, SJR score: 0.295 (SJR 2017) [https://doi.org/10.1007/978-3-319-73013-4\\_12](https://doi.org/10.1007/978-3-319-73013-4_12)
27. Uri Keich, Attila Kertész-Farkas, and William Stafford Noble: *Mix-Max: an improved false discovery rate estimation procedure for shotgun proteomics*, **Journal of Proteome Research**, 14(8) 3148–3161, 2015
28. Attila Kertész-Farkas, Uri Keich, and William Stafford Noble: *Tandem mass spectrum identification via Cascaded search*; **Journal of Proteome Research**, 14(8) 3027–3038, 2015, Q1 journal, Impact Factor: 4.268
29. Bruna Marini, Attila Kertész-Farkas, Hashim Ali, Bojana Lucic, Kamil Lisek, Lara Manganaro, Sándor Pongor, Roberto Luzzati, Alessandra Recchia, Fulvio Mavilio, Mauro Giacca, and Marina Lusica: *Nuclear architecture dictates HIV-1 integration site selection*; **Nature** 521, 227–231, 2015, Q1, Impact Factor: 40.137 <https://doi.org/10.1038/nature14226>
30. Sean McIlwain, Kaipo Tamura, Attila Kertész-Farkas, Charles E. Grant, Benjamin Diamant, Barbara Frewen, J. Jeffry Howbert, Michael R. Hoopmann, Lukas Käll, Jimmy K. Eng, Michael J. MacCoss, and William Stafford Noble: *Crux: rapid open source protein tandem mass spectrometry analysis*; **Journal of Proteome Research** 13(10) 4488–4491, 2014
31. Attila Kertész-Farkas, Beáta Reiz, Roberto Vera, Michael P. Myers, and Sándor Pongor: *PTMTTreeSearch: a Novel Two-Stage Tree Search Algorithm with Pruning Rules for the Identification of Post-Translational Modification of Proteins in MS/MS Spectra*; **Bioinformatics** 30(2): 234–241, 2014
32. János Juhász\*, Attila Kertész-Farkas\*, Dóra Szabo, and Sándor Pongor: *Emergence of Collective Territorial Defense in Bacterial Communities: Horizontal Gene Transfer Can Stabilize Microbiomes*; **PLoS One** 9(4), 2014
33. Roberto Vera, Yasset Perez-Riverol, Sonia Perez, Balázs Ligeti, Attila Kertész-Farkas, and Sándor Pongor: *JBioWH: an open-source Java framework for bioinformatics data integration*; **Database**, 2013

34. Beáta Reiz, Michael P. Myers, Sándor Pongor, and Attila Kertész-Farkas<sup>†</sup>: *Precursor Mass Dependent filtering of Mass Spectra for Proteomics Analysis*; Protein and Peptide Letters 21(8) 858-863, 2013
35. Beáta Reiz, Attila Kertész-Farkas, Somdutta Dhir, Sándor Pongor, and Michael P. Myers: *Chemical rule-based filtering of MS/MS spectra*; **Bioinformatics** 29(7) 925-932, 2013
36. Attila Kertész-Farkas, Beáta Reiz, Michael P. Myers, and Sándor Pongor: *Database searching in mass spectrometry based proteomics*; Current Bioinformatics 7(2) 221-230, 2012
37. Dóra Bihary, Ádám Kerényi, Zsolt Gelencsér, Sergiu Netotea, Attila Kertész-Farkas, Vittorio Venturi, and Sándor Pongor: *Simulation of communication and cooperation in multispecies bacterial communities with an agent based model*; Scalable Computing: Practice and Experience 13(1) 21–28, 2012
38. Beáta Reiz, Attila Kertész-Farkas, Sándor Pongor, and Michael P. Myers: *Data preprocessing and filtering in mass spectrometry based proteomics*; Current Bioinformatics 7(2) 212-220, 2012
39. Attila Kertész-Farkas, Beáta Reiz, Michael P. Myres, and Sándor Pongor: *PTMSearch: A Greedy Tree Traversal Algorithm for Finding Protein Post-Translational Modifications in Tandem Mass Spectra*; In: European Conference on Machine Learning and Principles and Practical Knowledge Discovery in Databases 2, Vol. 6912 Springer, 162–176, 2011
40. Emily Doughty\*, Attila Kertész-Farkas\*, Olivier Bodenreider, Gary Thompson, Asa Adadey, Thomas Peterson, and Maricel G. Kann: *Toward an automatic method for extracting cancer- and other disease-related point mutations from the biomedical literature*; **Bioinformatics** 27(3) 408-415, 2011
41. Somdutta Dhir, Mircea Pacurar, Dino Franklin, Zoltán Gáspári, Attila Kertész-Farkas, András Kocsor, Frank Eisenhaber and Sándor Pongor: *Detecting atypical examples of known domain types by sequence similarity searching: The SBASE domain library approach*; Current Protein Peptide Science 11(7) 538-549, 2010
42. József Dombi and Attila Kertész-Farkas<sup>†</sup>: *Applying Fuzzy Technologies to Equivalence Learning in Protein Classification*; **Journal of Computational Biology** 16(4) 611-623, 2009
43. Róbert Busa-Fekete, Attila Kertész-Farkas, András Kocsor, and Sándor Pongor: *Balanced ROC analysis (BAROC) protocol for the evaluation of protein similarities*; Journal of Biochemical and Biophysical Methods 70(6) 1210-1214, 2008
44. Attila Kertész-Farkas, Somdutta Dhir, Paolo Sonogo, Mircea Pacurar, Sergiu Netoteia, Harm Nijveen, Arnold Kuzniar, Jack A.M. Leunissen, András Kocsor, and Sándor Pongor: *Benchmarking protein classification algorithms via supervised cross-validation*; Journal of Biochemical and Biophysical Methods 70(6) 1215-1223, 2008
45. Attila Kertész-Farkas, András Kocsor, and Sándor Pongor: *Equivalence Learning in Protein Classification*; In: P. Perner (Ed.) Machine Learning and Data Mining in Pattern Recognition, Springer Verlag, Heidelberg, LNAI (4571) 824-837, 2007
46. János Z. Kelemen, Attila Kertész-Farkas, András Kocsor, and László G. Puskás: *Kalman Filtering for Disease-State Estimation from Microarray Data*; **Bioinformatics** 22(24) 3047-3053, 2006
47. László Kaján, Attila Kertész-Farkas, Dino Franklin, Nelly Ivanova, András Kocsor, and Sándor Pongor: *Application of a simple log likelihood ratio approximant to protein sequence classification*; **Bioinformatics** 22(23) 2865-2869, 2006
48. Paolo Sonogo, Mircea Pacurar, Somdutta Dhir, Attila Kertész-Farkas, András Kocsor, Zoltán Gáspári, Jack A.M. Leunissen, and Sándor Pongor: *A Protein Classification Benchmark collection for Machine Learning*; **Nucleic Acids Research** 35 232-236, 2006
49. András Kocsor, Attila Kertész-Farkas, László Kaján, and Sándor Pongor: *Application of compression-based distance measures to protein sequence-classification: a methodological study*; **Bioinformatics** 22(4) 407-412, 2006
50. Attila Kertész-Farkas and András Kocsor: *Kernel-based Classification of Tissues using Feature Weightings*; Applied Ecology and Environmental Research 4(2) 63-71, 2006
51. Attila Kertész-Farkas, Zoltán Fülöp, and András Kocsor: *Compact Representation of Hungarian Corpora*; (in Hungarian), Hungarian Journal of Applied Linguistics (1-2) 63-70, 2005

#### BOOK CHAPTERS

52. Attila Kertész-Farkas, András Kocsor, and Sándor Pongor: *The application of Data Compression-based Distance to Biological Sequences*; In: Frank Emmert-Streib. (Ed.) Information Theory and Statistical Learning, 73-88, 2008
53. Dmitry V. Nikitin, Attila Kertész-Farkas, Alexander S. Solonin, and Marina L. Mokrishcheva: *Bifunctional prokaryotic DNA-methyltransferases*; In: Dr. Anica Dricu (Ed.) Methylation (ISBN 980-953-307-146-1), 2012

## CONFERENCES

54. *CLEVR-BT-DB: A Benchmark Dataset to Evaluate the Reasoning Abilities of Deep Neural Models in Visual Question Answering Problems*, Fifth International Conference on Computer Vision and Computational Intelligence (CVCI 2024), Bangkok, Thailand, January 30-31, 2024,
55. *Hypernym Information and Sentiment Bias Probing in Distributed Data Representation*, International Conference on Machine Learning and Computing (ICMLC), Zhuhai, China, February 17-20, 2023, **Best Talk Award**
56. *Generative probabilistic modelling of peptide-spectrum matching in tandem mass spectrometry*; International Congress on Biotechnology: State and Prospects of Development, Moscow Russia, February 25-27, 2019
57. *Bias in false discovery rate estimation in mass-spectrometry-based peptide identification*; International Congress on Biotechnology: State and Prospects of Development, Moscow Russia, February 25-27, 2019
58. *Lookup Latent: Non-linear Received Signal Strength to Distance Mapping for Non-Line-of-Sight Geolocalization in Outdoor Urban Areas*; 7th International Conference on Analysis of Images, Social Networks and Texts (AIST), Moscow Russia, 5-7 July 2018 – **Best Talk Award**
59. *High-dimensional generative probabilistic models for peptide-spectrum-matching in tandem mass spectrometry*; Proteomics-2017, Valencia Spain, 8-11 November 2017
60. *PTMTreeSearch: a new algorithm for post-translational modification identification in tandem mass spectrometry data*; Proteomics-2017, Valencia Spain, 8-11 November 2017
61. *Cascaded false discovery rate control tandem mass spectrometry (MS/MS) data for peptide identification*; Proteomics-2017, Valencia Spain, 8-11 November 2017
62. *HuGaDB: Database for Human Gait Analysis from Wearable Inertial Sensor Networks*; International Conference on Analysis of Images, Social Networks, and Texts (AIST), Moscow Russia, 2017 – **Best Talk Award**
63. *Peptide identification in tandem mass spectrometry data via cascade search*; US HUPO; Seattle USA, 6-9 April 2014
64. *PTMSearch: A Greedy Tree Traversal Algorithm for Finding Protein Post-Translational Modifications in Tandem Mass Spectra*; European Conference on Machine Learning and Principles and Practice of knowledge discovery in databases; Athens Greece, 5-9 September 2011
65. *Equivalence Learning in Protein Classification*; International Conference on Machine Learning and Data Mining in Pattern Recognition; Leipzig Germany, 18-20 July 2007
66. *Classification of Tissues using Feature Weightings*; VII. Hungarian Conference on Biometrics and Biomathematics; Budapest Hungary, 5-6 July 2005.
67. *Kernel-based learning with dimension weighting*; Scientific Conference of Students, University of Szeged; April 2004,
68. *Compact Representation of Hungarian Vocabulary with Nondeterministic Finite Automata*; I. Conference on Hungarian Computational Linguistic; Szeged Hungary, 10-11 December 2003
69. *Compact representation of finite languages with nondeterministic automata*; Scientific Conference of Students, University of Szeged; October 2002,
70. *EMU: A tool for the Extraction of Mutations with disease associations from literature*; Growth Factor and Signal Transduction Conferences: System Biology, Integrative, Comparative and Multiscale Modeling, Iowa USA, 11-14 June 2009

## TALKS

71. AI in computational mass spectrometry, 2024 China-Eastern European Experts Cooperation and Exchange Activity, Harbin, China, May 2024
72. *Statistics in Tandem Mass Spectrometry Data Annotation*, Omics Seminar, Moscow State University, Moscow, December 2021.
73. *Large-scale localization method for urban area*, The 3<sup>rd</sup> Professor Day Academic Conference by Huawei Russian Research Centre, Moscow Russia, December 2016
74. *Cascade search for identification of heterogeneous tandem mass spectrometry data*, HSE International Laboratory of Algorithms and Technologies for Network Analysis, Nizhny Novgorod Russia, November 2016
75. *False discovery rate control for database search methods over heterogeneous biological data*, Keynote talk at Analysis of Images, Social Networks, and Texts (AIST'2016), Yekaterinburg Russia, April 2016
76. *Statistical methods in MS/MS spectrum identification*, Universidad San Francisco de Quito, Ecuador, Oct. 2015

77. *Algorithmic identification of post-translational modifications of proteins in tandem mass spectra*, Luxembourg Centre for Systems Biomedicine, Université du Luxembourg, Luxembourg, April 2013
78. *Noise filtering and compression of mass spectra for proteomics*; Symposium at International Centre for Genetic Engineering and Biotechnology; Trieste Italy, June 2012
79. *A new algorithm for identification of post-translational modification in tandem mass spectrometry data*; Symposium at International Centre for Genetic Engineering and Biotechnology; Trieste Italy, June 2011
80. *Equivalence Learning in Protein Classification*; Young Researcher Symposium on Intelligent Systems at the John von Neumann Computer Society; Budapest Hungary, November 2007
81. *Protein databases and similarity measures for protein classification*; Bioinformatics seminar at Rényi Mathematical Institute; Budapest Hungary, October 2007