

PAVEL P. KUKSA

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Education and Training

- **Postdoctoral Fellow**—University of Pennsylvania 2014-present
- **Ph.D.**—Computer Science, Rutgers University 2011
Dissertation: *Scalable Kernel Methods and Algorithms for General Sequence Analysis*
Advisor: Vladimir Pavlovic
- **M.Sc. (Honors)**—Computer Science, Bauman Moscow State Technical University, Moscow, Russia 2004
- **B.Sc. (Honors)**—Computer Engineering, Bauman Moscow State Technical University, Moscow, Russia 2002

Professional Interests

- Applied machine learning
- Modeling and analysis of sequences
- Natural language processing
- Biomedical informatics
- Kernel methods for sequences
- Pattern recognition
- Large-scale algorithms and inference

Research and Industry Experience

- **Associate Fellow**—Institute for Biomedical Informatics, University of Pennsylvania 2014-present
 - Large-scale machine learning methods for next-generation sequencing data (RNA-seq, smRNA-seq, Hi-C, DMS-seq, etc.)
 - Long-range enhancer-gene regulation
 - RNA structure estimation and function predictionMentor: Li-San Wang
- **Postdoctoral Scientist**—Machine Learning Department, NEC Laboratories America 2011-2014
 - Multivariate time series and sequence analysis for audio, text, and biological data
 - Immunoinformatics: high-order deep learning models and kernel methods, protein-peptide interaction prediction
 - Functional whole-genome analysis, genome-wide transcription factor prediction and annotation
 - Large-scale kernel algorithms for sequences and structured data
- **Research Assistant**—Rutgers University 2005-2011
 - Discriminative learning, string algorithms, large-scale and semi-supervised learning
 - Kernel methods and algorithms for general sequence classification: DNA barcoding, remote homology prediction, text categorization, music classification, etc.
 - Motif finding in DNA and protein sequences

- Natural language processing
- Clustering and classification of video motion sequences and audio data
- **Research Assistant**—NEC Laboratories America, Princeton, NJ *May 2009 – August 2009*
 - Semi-supervised large-scale learning for bioNLP (natural language processing for bio-medical literature), relationship extraction, etc. Supervisor: Dr. Yanjun Qi
- **Research Assistant**—NEC Laboratories America, Princeton, NJ *May 2008 – August 2008*
 - Unified Architecture for Natural Language Processing, multi-task learning with deep architectures. Supervisor: Dr. Jason Weston
- **Teaching Assistant**—Department of Computer Science, Rutgers University *09/2005-12/2010*
- **Software Engineer**—Mobile Business Systems *2003–2005*
 - Web commerce system development, customer training and support

Current research projects

1. Using high-throughput sequencing to probe RNA secondary structure. Collaborators: Brian D. Gregory (Biology), Lee E. Vandivier (Cell and Molecular Biology), University of Pennsylvania.
2. Modeling Peptide-MHC protein interactions. Collaborators: Martin Renqiang Min, NEC Laboratories America, Inc; Mark Gerstein, Yale.
3. RNA modification: Lee E. Vandivier, Brian D. Gregory, University of Pennsylvania.
4. Hi-C chromatin interaction networks and gene regulation. Collaborators: Yih-Chii Hwang (Genomics and Computational Biology), Li-San Wang (Pathology), University of Pennsylvania.
5. Identification of protein factors mediating gene-enhancer interactions. Collaborators: Yih-Chii Hwang, Li-San Wang, University of Pennsylvania.
6. Non-coding RNA function, classification and prediction. Collaborators: Yuk Yee Leung (Institute for Biomedical Informatics, Pathology), Li-San Wang, Brian D. Gregory, Lyle Ungar (Computer Science), University of Pennsylvania.
7. Modeling and prediction of intra-molecular interactions. Collaborators: Li-San Wang and Brian D. Gregory, University of Pennsylvania.
8. Prediction of Alzheimer's disease associated enhancer elements. Collaborators: Mitchell Tang, Adam Naj (Epidemiology), Li-San Wang, Gerald Schellenberg (Pathology), University of Pennsylvania.
9. Whole-genome database for human small non-coding RNA. Collaborators: Yuk Yee Leung, Li-San Wang, Brian D. Gregory
10. Machine learning for large-scale genomics data. Collaborators: Li-San Wang, Yuk Yee Leung, Alex Amlie-Wolf (Genomics and Computational Biology).

Publications

Note: In Computer Science, *conferences* and *workshops* (focused expert meetings) are primary venues for publishing original research findings. Top conferences and workshops have *lower acceptance rates* and are *highly regarded*. *Technical reports* officially document results of research projects and are often used to report original findings ahead of formal conference or journal publication.

- **Ph.D. Thesis**

1. **Pavel P. Kuksa**. Scalable Kernel Methods and Algorithms for General Sequence Analysis. Ph.D. thesis, Rutgers University, March 2011. Dissertation Committee: Vladimir Pavlovic, Casimir Kulikowski, Alexander Schliep, Christina Leslie

- **Refereed Journal Papers**

1. Yuk Yee Leung*, **Pavel P. Kuksa***, Alexandre Amlie-Wolf, Otto Valladares, Lyle H. Ungar, Sampath Kannan, Brian D. Gregory, and Li-San Wang. Dashr: database of small human noncoding rnas. *Nucleic Acids Research (Database Issue)*, 2016.
2. Lee E. Vandivier, Rafael Campos, **Pavel P. Kuksa**, Ian M. Silverman, Li-San Wang, and Brian D. Gregory. Chemical modifications mark alternatively spliced and uncapped messenger rnas in arabidopsis. *The Plant Cell*, 27(11):3024–3037, 2015.
3. **Pavel P. Kuksa**, Martin Renqiang Min, Rishabh Dugar, Mark Gerstein. High-order neural networks and kernel methods for peptide-MHC binding prediction. *Bioinformatics*, 2015.
4. Shawn W. Foley, Lee E. Vandivier, **Pavel P. Kuksa**, Brian D. Gregory. Transcriptome-wide measurement of plant RNA secondary structure. *Current Opinion in Plant Biology*, 2015.
5. Yih-Chii Hwang, Chiao-Feng Lin, Otto Valladares, John Malamon, **Pavel P. Kuksa**, Qi Zheng, Brian D. Gregory, and Li-San Wang. HIPPIE: A high-throughput identification pipeline for promoter interacting enhancer elements. *Bioinformatics*, 2014.
6. **Pavel P. Kuksa**. Biological sequence analysis with multivariate string kernels. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, March 2013.
7. Ronan Collobert, Jason Weston, Leon Bottou, Michael Karlen, Koray Kavukcuoglu, and **Pavel Kuksa**. Natural language processing (almost) from scratch. *Journal of Machine Learning Research (JMLR)*, 12:2493–2537, 2011.
8. **Pavel Kuksa** and Vladimir Pavlovic. Efficient motif finding algorithms for large-alphabet inputs. *BMC Bioinformatics*, 11(Suppl 8):S1, 2010.
9. **Pavel Kuksa**, Pai-Hsi Huang, and Vladimir Pavlovic. Efficient use of unlabeled data for protein sequence classification: a comparative study. *BMC Bioinformatics*, 10(Suppl 4):S2, 2009.
10. **Pavel Kuksa** and Vladimir Pavlovic. Efficient alignment-free DNA barcode analytics. *BMC Bioinformatics*, 10(Suppl 14):S9, 2009.

- **Refereed Conference Papers**

1. **Pavel P. Kuksa**, Martin Renquiang Min, Rishabh Dugar, and Mark Gerstein. High-Order Neural Networks and Kernel Methods for Peptide-MHC Binding Prediction. In *NIPS Machine Learning in Computational Biology*, 2014.
2. Y.-C. Hwang*, **P. P. Kuksa***, B. D. Gregory, and L.-S. Wang. Identifying the transcription factors mediating enhancer–target gene regulation in the human genome. In *American Society of Human Genetics Annual Meeting (ASHG)*, 2015. (**Platform talk**)
3. P. P. Kuksa, Y. Y. Leung, A. Amlie-Wolf, B. D. Gregory, and L.-S. Wang. SPAR: Sequencing-based pipeline for annotating novel small non-coding rnas. In *American Society of Human Genetics Annual Meeting (ASHG)*, 2015.
4. Y. Y. Leung*, **P. P. Kuksa***, A. Amlie-Wolf, O. Valladares, B. D. Gregory, and L.-S. Wang. Dashr - database of small human non-coding rnas. In *American Society of Human Genetics Annual Meeting (ASHG)*, 2015.
5. Mitchell Tang, Adam Naj, Li-San Wang, Gerald Schellenberg, Christian Kramer, George Xu, Michele Hawk, Yih-Chii Hwang, Chiao-Feng Lin, **Pavel P. Kuksa**, Weixin Wang, Beth Dombroski. Prediction of Late-Onset Alzheimer’s Disease Associated Enhancer Elements In *Alzheimer’s Association International Conference (AAIC)*, 2015.
6. **Pavel P. Kuksa** and Vladimir Pavlovic. Efficient evaluation of large sequence kernels. In *ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD)*, 2012. Oral presentation. Acceptance rate: 72/755 (9.5%)
7. **Pavel P. Kuksa**, Imdadullah Khan, and Vladimir Pavlovic. Generalized similarity kernels for efficient sequence classification. In *SIAM International Conference on Data Mining (SDM)*, 2012. Acceptance rate: 99/362 (27%).
8. **Pavel P. Kuksa**. Efficient sequence kernel-based genome-wide prediction of transcription factors. In *International Conference on Pattern Recognition (ICPR)*, 2012.
9. **Pavel P. Kuksa**. 2d similarity kernels for biological sequence classification. In *International Workshop on Data Mining in Bioinformatics (BIOKDD)*, 2012.
10. **Pavel Kuksa** and Yanjun Qi. Semi-supervised bio-named entity recognition with word-codebook learning. In *SIAM International Conference on Data Mining (SDM)*, 2010. Acceptance rate: 82/351 (23%)
11. **Pavel P. Kuksa**, Yanjun Qi, Bing Bai, Ronan Collobert, Jason Weston, Vladimir Pavlovic, and Xia Ning. Semi-supervised abstraction-augmented string kernel for multi-level bio-relation extraction. In *European Conference on Machine Learning (ECML)*, 2010. Acceptance rate: 106/658 (16%).
12. **Pavel P. Kuksa** and Vladimir Pavlovic. Spatial representation for efficient sequence classification. In *International Conference on Pattern Recognition (ICPR)*, 2010. Acceptance rate: 385/2140 oral (18%).
13. **Pavel Kuksa**, Pai-Hsi Huang, and Vladimir Pavlovic. Scalable algorithms for string kernels with inexact matching. In *Neural Information Processing Systems (NIPS)*, 2008. Spotlight Presentation. Acceptance rate: 123/1022 (12%)

14. **Pavel P. Kuksa** and Vladimir Pavlovic. Efficient motif finding algorithms for large-alphabet inputs. In *International Conference on Research in Computational Molecular Biology (RECOMB)*, 2010. Poster presentation.
15. **Pavel P. Kuksa** and Vladimir Pavlovic. Efficient motif finding algorithms for large-alphabet inputs. In *BIOKDD*, 2010. Acceptance rate: 7/29 regular (24%).
16. Yanjun Qi, Ronan Collobert, **Pavel Kuksa**, Koray Kavukcuoglu, and Jason Weston. Combining labeled and unlabeled data with word-class distribution learning. In *Proceeding of the 18th ACM Conference on Information and Knowledge Management (CIKM)*, pages 1737–1740, 2009. Acceptance rate: (123+171)/847 (20% short paper).
17. Yanjun Qi, **Pavel P. Kuksa**, Ronan Collobert, Kunihiro Sadamas, Koray Kavukcuoglu, and Jason Weston. Semi-supervised sequence labeling with self-learned features. In *Proc. International Conference on Data Mining (ICDM)*. IEEE, 2009. Acceptance rate: 8.9% regular (70/786).
18. **Pavel Kuksa** and Vladimir Pavlovic. Fast motif selection for biological sequences. In *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2009. Acceptance rate: (44+37)/233 (35%).
19. **Pavel Kuksa** and Vladimir Pavlovic. Efficient alignment-free barcode analytics. In *Third International Barcode of Life Conference*, 2009.
20. **Pavel Kuksa**, Pai-Hsi Huang, and Vladimir Pavlovic. Fast and accurate multi-class protein fold recognition with spatial sample kernels. In *Computational Systems Bioinformatics (CSB)*, pages 133–143, 2008. Acceptance rate: 30/135 (22%).
21. **Pavel Kuksa**, Pai-Hsi Huang, and Vladimir Pavlovic. Fast protein homology and fold detection with sparse spatial sample kernels. In *19th International Conference on Pattern Recognition (ICPR)*, 2008. Acceptance rate: 18% (oral). *Best paper nominee*.
22. **Pavel Kuksa**, Pai-Hsi Huang, and Vladimir Pavlovic. A fast, semi-supervised learning method for protein sequence classification. In *8th International Workshop on Data Mining in Bioinformatics (BIOKDD)*, pages 29–37, 2008. Acceptance rate: 8/25 (32%).
23. **Pavel Kuksa**, Pai-Hsi Huang, and Vladimir Pavlovic. On the role of local matching for efficient semi-supervised protein sequence classification. In *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2008. Acceptance rate: 38/156 (24%).
24. **Pavel Kuksa** and Vladimir Pavlovic. Fast barcode-based species identification using string kernels. In *Second International Barcode of Life Conference*, 2007. Acceptance rate: 30% (oral).
25. **Pavel Kuksa** and Vladimir Pavlovic. Fast kernel methods for SVM sequence classifiers. In *Workshop on Algorithms in Bioinformatics (WABI)*, pages 228–239, 2007. Acceptance rate: 37/131 (28%).

- **Refereed Workshop Papers**

1. **Pavel P. Kuksa**. Efficient time series classification with multivariate similarity kernels. In *NYAS Machine Learning Symposium*, 2012. *Oral presentation*. Acceptance rate: 15/62.

2. **Pavel P. Kuksa**. 2d similarity kernels and representations for sequence data. Snowbird Learning Workshop, Snowbird, Utah, April 2012, 2012.
3. **Pavel P. Kuksa**. Using string kernels to predict gene expression. Snowbird Learning Workshop, Snowbird, Utah, April 2012, 2012.
4. **Pavel Kuksa** and Vladimir Pavlovic. Efficient evaluation of large sequence kernels. In *NYAS Machine Learning Symposium*, 2011.
5. **Pavel Kuksa** and Vladimir Pavlovic. Efficient sequence classification with spatial representations. In *Snowbird Learning Workshop*, April 2010. Oral presentation [28/69].
6. Vladimir Pavlovic and **Pavel Kuksa**. Large scale sequence analytics. In *Center for Dynamic Data Analytics (CDDA) Workshop (January 25-26, 2010)*, 2010.
7. **Pavel Kuksa** and Vladimir Pavlovic. Efficient discovery of common patterns in sequences. In *Snowbird Learning Workshop*, Clearwater, Florida, April 13-16 2009, 2009.
8. Jason Weston, Ronan Collobert, Frederic Ratle, Hossein Mobahi, **Pavel Kuksa**, and Koray Kavukcuoglu. Deep learning via semi-supervised embedding. In *ICML 2009 Workshop on Learning Feature Hierarchies*, 2009.
9. **Pavel Kuksa** and Vladimir Pavlovic. String kernel-based species identification using DNA barcodes. In *Joint Molecular Biosciences Symposium*, Feb 29, 2008, 2008.
10. **Pavel Kuksa**, Pai-Hsi Huang, and Vladimir Pavlovic. High performance sequence classification with novel spatial sample embedding. In *3rd Annual Machine Learning Symposium*, NY, Oct 10, 2008, 2008.
11. **Pavel Kuksa**, Pai-Hsi Huang, and Vladimir Pavlovic. Spatially-constrained sample kernel for sequence classification. In *Snowbird Learning Workshop*, Utah, April 1-4, 2008, 2008.
12. **Pavel Kuksa** and Vladimir Pavlovic. Kernel methods for DNA barcoding. In *Snowbird Learning Workshop*, San Juan, Puerto Rico, March 2007, 2007.

- **Technical reports**

1. **Pavel P. Kuksa**. Efficient multivariate sequence classification. *CoRR abs/1409.8211*, 2013.
2. **Pavel P. Kuksa**, Imdadullah Khan, and Vladimir Pavlovic. Generalized similarity kernels for efficient sequence classification. Technical Report RU-DCS-TR684, Rutgers University, 2011.
3. Ronan Collobert, Jason Weston, Leon Bottou, Michael Karlen, Koray Kavukcuoglu, and **Pavel Kuksa**. Natural language processing (almost) from scratch. *arXiv:1103.0398v1*, 2011.
4. Robert S. Moore, Richard Howard, **Pavel Kuksa**, and Richard P. Martin. A geometric approach to device-free motion localization using signal strength. Technical Report DCS-TR-674, Rutgers University, September 2010.
5. **Pavel Kuksa** and Vladimir Pavlovic. Efficient discovery of common patterns in sequences over large alphabets. Technical Report 2009-15, DIMACS, June 2009.

6. **Pavel Kuksa**, Pai-Hsi Huang, and Vladimir Pavlovic. Kernel Methods and Algorithms for General Sequence Analysis. Technical Report DCS-TR-630, Rutgers University, 2008.
7. Pai-Hsi Huang, **Pavel Kuksa**, and Vladimir Pavlovic. Fast and accurate semi-supervised protein homology detection with large uncurated sequence databases. Technical Report RU-DCS-TR634, Rutgers University, 2008.

Patents Awarded and Patent Applications

1. Yanjun Qi, Xia Ning, **Pavel Kuksa**, Bing Bai. Systems and Methods for Semi-Supervised Relationship Extraction. US 20110270604 A1. Issued Nov 3, 2011.
2. Martin Renqiang Min, **Pavel Kuksa**, and Xia Ning. High-Order Semi-Restricted Boltzmann Machines and Deep Models for Accurate Peptide-MHC Binding Prediction and Collaborative Filtering. US Patent Application. Filed 10/10/2014.
3. **Pavel Kuksa** and Martin Renqiang Min. High-Order Sequence Kernel Methods for Peptide Analysis. US Patent Application. Filed 10/10/2014.

Awards and Honors

- DIMACS Graduate Student Award, Center for Discrete Mathematics and Theoretical Computer Science, Jan 2010
- DIMACS Graduate Student Award, Center for Discrete Mathematics and Theoretical Computer Science, Jan 2009
- Best Paper award nomination at the International Conference on Pattern Recognition in Tampa, FL, 2008
- Graduate Fellowship Award, Rutgers University, 2005-2007
- President of Russia's Award for Outstanding Young Scientists, Ministry of Education and Science, Russia, 2004 (National-level award)
- Scientific Council Scholarship Award, Bauman Moscow State Technical University (BMSTU), 2002-2003 (rare, competitive university-wide award < 1%)
- Award for Academic Excellence, Bauman Moscow State Technical University (BMSTU), 2001, 2002
- M.Sc. with Honors, 2004
- B.Sc. with Honors, 2002

Invited Lectures and Oral Presentations

1. Multivariate and generalized similarity kernels for sequence analysis. New Jersey Institute of Technology. March 7, 2013 (invited lecture)
2. String kernel-based Species Identification Using DNA Barcodes. Rutgers-UMDNJ Joint Molecular Biosciences Symposium. Feb. 29, 2008 (invited lecture)
3. Kernel Methods for DNA Barcoding. Rutgers Bioinformatics meeting, Nov. 10, 2006 (invited talk)
4. Efficient time series classification with multivariate similarity kernels. NYAS Machine Learning Symposium. New York, NY, Oct. 19, 2012 (oral presentation)
5. Efficient evaluation of large sequence kernels. KDD. Aug. 14, 2012 (oral presentation)
6. Fast and accurate multi-class protein fold recognition with spatial sample kernels. Computational Systems Bioinformatics. Stanford University, Aug. 27, 2008 (oral presentation)
7. Fast protein homology and fold detection with sparse spatial sample kernels. International Conference on Pattern Recognition. Tampa, FL, Dec. 9, 2008 (oral presentation)
8. A fast, semi-supervised learning method for protein sequence classification. International Workshop on Data Mining in Bioinformatics. Las Vegas, Aug. 24, 2008 (oral presentation)
9. On the role of local matching for efficient semi-supervised protein sequence classification. BIBM. Philadelphia, Nov. 4, 2008 (oral presentation)
10. Fast kernel methods for SVM sequence classifiers. WABI. University of Pennsylvania, Sept. 8, 2007 (oral presentation)
11. Efficient motif finding algorithms for large-alphabet inputs. BIODKDD. Washington, DC, July 25, 2010 (oral presentation)
12. Efficient sequence classification with spatial representations. Snowbird Learning Workshop, Utah, Apr. 8, 2010 (oral presentation)

Grants Awarded

- Sublinear Selection Algorithms for Motif Finding. DIMACS Award Programs, 01/2010-03/2010
- Efficient discovery of common patterns in sequences over large alphabets. DIMACS Award Programs, 12/2008-01/2009

Professional Activities

- **Journal article refereeing**

1. Nucleic Acids Research (NAR)
2. BMC Bioinformatics
3. IEEE Transactions on Computational Biology and Bioinformatics (TCBB)
4. IEEE Transactions on Language and Speech Processing (TLSP)
5. Proceedings of the Royal Society
6. Algorithmica
7. Neural Networks
8. Neural Computation
9. Machine Learning
10. IEEE Transactions on Pattern Analysis and Machine Intelligence (TPAMI)
11. Journal of Machine Learning Research (JMLR)
12. Evolutionary Bioinformatics
13. Aquatic Biosystems
14. Molecular Informatics
15. Molecular Ecology Resources
16. PLOS One
17. PLOS Computational Biology

- **Conference Referee**

- International Conference on Machine Learning (ICML)
- IEEE International conference on Pattern Recognition (ICPR)
- IEEE Conference on Computer Vision and Pattern Recognition (CVPR)
- International Conference on Computer Vision (ICCV)
- NIPS Machine Learning in Computational Biology (MLCB)
- IEEE International Conference on Bioinformatics and Biomedicine (BIBM)

- **Program committee and organizer**

- Grant proposal review panel, European Coordinated Research on Long-term Challenges in Information and Communication Sciences & Technologies ERA-Net (CHIST-ERA), 2015
- Arts and Sciences Council, The Perelman School of Medicine Art in Science Competition, 2014
- Program committee, Biomedical Postdoctoral Research Symposium, University of Pennsylvania, 2014
- Co-organizer, Yahoo Machine Learning seminar series, Rutgers University, 2010

- **Service**

- Associate Fellow, Institute for Biomedical Informatics (IBI), University of Pennsylvania, 2014-present [Elected member]
- Data Analysis Working Group (DAWG), International Consortium for Barcode of Life (CBOL), 2008-2011 [Expert panel]
- Secretary, Rutgers Compute Science Graduate Student Society, 2007–2008
- Treasurer, Rutgers Computer Science Graduate Student Society, 2006–2007
- Secretary, Rutgers Bioinformatics Club, 2006–2007
- Member of IEEE, 2005–present

Teaching Interests

- Artificial Intelligence, Data Mining, Machine Learning, Biomedical Informatics, Design and Analysis of Algorithms, Sequence Analysis, Natural Language Processing, Pattern Recognition

Teaching Experience

- **Teaching Assistant**—Introduction to Bioinformatics (CS674), Rutgers University *Fall 2010*
 - Taught lectures on selected topics
- **Teaching Assistant**—Discrete Structures II (CS206), Rutgers University *Spring 2009, 2010*
 - Taught weekly recitation classes (30-35 students)
- **Teaching Assistant**—Principles of AI (CS530), Rutgers University *Fall 2009*
 - Taught lectures on selected topics
- **Teaching Assistant**—Pattern Recognition (CS535), Rutgers University *Fall 2008*
 - Taught lectures on selected topics
- **Teaching Assistant**—Machine Learning (CS536), Rutgers University *Spring 2008*
- **Teaching Assistant**—Introduction to Artificial Intelligence (CS440), Rutgers University *Fall 2007*
 - Taught weekly recitation classes (20-25 students)
- **Teaching Assistant, Summer Co-instructor**—Computer Applications for Business (CS170), Rutgers University *Fall 2005-Fall 2006*
 - Taught recitation classes twice a week (30-35 students)
- **Instructor**—Systems modeling, Informatics and Control Systems Department, Bauman Moscow State Technical University (BMSTU) *Fall 2002*
 - Taught four-hour class and lab sessions (10-15 students)
- **Instructor Assistant**—Computer Systems Design, Informatics and Control Systems Department, Bauman Moscow State Technical University (BMSTU) *Spring 2002*
 - Conducted practical workshops on using VHDL for digital circuit design

Professional Affiliations

- The American Society of Human Genetics
- Institute for Biomedical Informatics [Elected associate member]

Appendix B. Publications in Russian

1. Kouxa, Pavel. "Applications of Associative Memory and Associative Processors in Network Devices: A Survey." (Primenenie asociativnih ZU i processorov v setevih ustroistvah) Modern Information Technologies. Moscow: BMSTU Press, 2001. 20-24. ISBN 5-7038-2083-9
2. Kouxa, Pavel. "Data Clustering with Neural Networks." (Primenenie neironnih setei dlya klasterizatsii danih) Modern Information Technologies. Moscow: BMSTU Press, 2001. 7-13. ISBN 5-7038-2083-9
3. Kouxa, Pavel. "Finding Logically Independent Operators Matrix." (Algoritm nahojdeniya matricy logicheskoi nesovmestivosti) Informatics and Control Systems in 21st century. Moscow: Eliks+ Press, 2002. 195-97. ISBN 5-93991-010-6
4. Kouxa, Pavel. "Fuzzy Systems Simulation Software at Algorithmic Level." (Sistema modelirovaniya nechetkih system na algoritmicheskom urovne) Informatics and Control Systems in 21st century. Moscow, 2002. 201-04. ISBN 5-93991-010-6
5. Kouxa, Pavel. "Finding Logically Independent Operators for Parallel Computations Scheduling." (Vychislenie matricy logicheskoi nesovmestivosti pri organizatsii parallel'nyh vychislenii) Young Scientists, Graduate and Undergraduate Students Conference. Moscow: BMSTU Press, 2003. 293-97. ISBN 5-7038-2347-1
6. Kouxa, Pavel. "Fuzzy Clustering Algorithm: Reducing Complexity." (Analiz algoritma nechetkoi klasterizatsii) Young Scientists, Graduate and Undergraduate Students Conference. Moscow: BMSTU Press, 2003. 249-53. ISBN 5-7038-2347-1
7. Kouxa, Pavel. "Fuzzy Systems Definition Language." (Yazyk opisaniya nechetkih sistem) Journal of Volzskiy Tatishev University, Information Science Series. 5 (2004): 92-97.
8. Kouxa, Pavel. "Linguistic Fuzzy Models Structure Identification and Optimization." (Strukturnaya identifikatsiya i optimizatsiya lingvisticheskikh nechetkih modelei) Modern Information Technologies. Moscow: Eliks+, 2003. 7-16. ISBN 5-93991-014-9
9. Kouxa, Pavel. "Neuro-Fuzzy Models: Analysis and Applications." (Analiz neuro-nechetkih modelei) Journal of Volzskiy Tatishev University, Information Science Series.5 (2004): 69-76.
10. Kouxa, Pavel. "Software Implementation of Fuzzy Logic Controllers." (Programmnaia realizatsiya nechetkih kontrollerov) Modern Information Technologies. Moscow: Eliks+, 2003. ISBN 5-93991-014-9
11. Kouxa, Pavel. "Type-2 Fuzzy Models." (Nechetkie lingvisticheskie modeli vtorogo roda) Journal of Volzskiy Tatishev University, Information Science Series.5 (2004): 114-20.
12. Kouxa, Pavel. "Type-2 Fuzzy Sets Algebra." (Issledovanie operacii algebry nechetkih mnojestv vtorogo porjadka) Young Scientists, Graduate and Undergraduate Students Conference, Informatics and Control Systems. Moscow: BMSTU Press, 2003. 243-48. ISBN 5-7038-2347-1
13. Kouxa, Pavel. "Approximation Accuracy of Fuzzy Systems." (Obespechenie tochnosti v nechetkih sistemah) Young Scientists, Graduate and Undergraduate Students Conference. Informatics and Control Systems in 21st century. Moscow: BMSTU Press, 2004. 152-156. ISBN 5-7038-2646-4
14. Kouxa, Pavel. "Design Optimization of Non-Local Neuro-Fuzzy Models." (Optimizatsiya i sintez nelokal'nykh lingvisticheskikh neuro-nechetkih modelei) Inter-universities Scientific and Technical Conference on Modern Information Technologies. Moscow, 2004.

15. Kouxa, P. "Fuzzy Systems: Learning and Self-Organization Methods." Young Scientists, Graduate and Undergraduate Students Conference. Informatics and Control Systems in 21st century. Moscow: BMSTU Press, 2004. 148-52. ISBN 5-7038-2646-4
16. Kouxa Pavel, Schmakov E., Yahina I., Panushkin M. "A Survey on Supercomputing: Modern State and Perspectives." (Superkomputery: sostoyanie i perspektivy) Anniversary Inter-universities Scientific and Technical Conference on "Modern Information Technologies". Moscow: BMSTU Press, 2000. 61-68. ISBN 5-7038-1752-8
17. Timofeev V.V., Kouxa P. "Design and Identification of Fuzzy Models in Control and Systems Modeling." (Postroenie i identifikatsiya nechetkih modelei v prilozheniyah upravleniya i sistemnogo modelirovaniya) First International Conference "Aerospace Technologies." Moscow: BMSTU Press, 2004. ISBN 5-7038-2517-2