

CONTACT INFORMATION	<p>Department of Software Engineering Faculty of Mathematics and Physics Charles University in Prague</p> <p style="text-align: right;"><i>Phone:</i> +420-951-554-406 <i>Fax:</i> +420-221-914-323 <i>E-mail:</i> hoksza@ksi.mff.cuni.cz <i>WWW:</i> http://siret.ms.mff.cuni.cz/hoksza</p> <p>Malostranské nám. 25 118 00 Prague, Czech Republic</p>																				
EDUCATION	<p>Charles University in Prague, Czech Republic Faculty of Mathematics and Physics, School of Computer Science</p> <p>Ph.D., Software Systems, September 2010</p> <ul style="list-style-type: none"> • Thesis: <i>Similarity Search in Protein Databases</i> • Advisor: Tomáš Skopal, PhD. <p>RNDr., Software Systems, September 2008</p> <p>M.Sc., Data Engineering, August 2006</p> <ul style="list-style-type: none"> • Thesis: <i>Multidimensional Indexing in Relational Databases</i> • Advisor: Tomáš Skopal, PhD. 																				
RESEARCH INTERESTS	<p>bioinformatics : structural bioinformatics, protein sequence and structure databases, rna sequence and structure databases, visualization</p> <p>cheminformatics : chemical space exploration and visualization, virtual screening</p> <p>databases : indexing, metric indexing, non-metric indexing</p>																				
ACADEMIC APPOINTMENTS	<table border="0" style="width: 100%;"> <tr> <td style="width: 70%;">Assistant Professor</td> <td style="text-align: right;">June 2012 – present</td> </tr> <tr> <td colspan="2">Department of Software Engineering, School of Computer Science, FMP, Charles University in Prague</td> </tr> <tr> <td>Researcher</td> <td style="text-align: right;">September 2010 – June 2012</td> </tr> <tr> <td colspan="2">Department of Software Engineering, School of Computer Science, FMP, Charles University in Prague</td> </tr> <tr> <td>Lecturer</td> <td style="text-align: right;">September 2010 – February 2015</td> </tr> <tr> <td colspan="2">Laboratory of Informatics and Chemistry, Faculty of Chemical Technology, Institute of Chemical Technology Prague</td> </tr> <tr> <td>Lecturer</td> <td style="text-align: right;">September 2009 – September 2011</td> </tr> <tr> <td colspan="2">Department of Software Engineering, Faculty of Information Technology, Czech Technical University in Prague</td> </tr> <tr> <td>Lecturer</td> <td style="text-align: right;">September 2006 – August 2008</td> </tr> <tr> <td colspan="2">Department of Computer Science and Mathematics, The University of Finance and Administration</td> </tr> </table>	Assistant Professor	June 2012 – present	Department of Software Engineering, School of Computer Science, FMP, Charles University in Prague		Researcher	September 2010 – June 2012	Department of Software Engineering, School of Computer Science, FMP, Charles University in Prague		Lecturer	September 2010 – February 2015	Laboratory of Informatics and Chemistry, Faculty of Chemical Technology, Institute of Chemical Technology Prague		Lecturer	September 2009 – September 2011	Department of Software Engineering, Faculty of Information Technology, Czech Technical University in Prague		Lecturer	September 2006 – August 2008	Department of Computer Science and Mathematics, The University of Finance and Administration	
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RESEARCH STAYS	<table border="0" style="width: 100%;"> <tr> <td style="width: 70%;">Georg-August-Universität Göttingen</td> <td style="text-align: right;">January 2015</td> </tr> <tr> <td colspan="2">Institut für Informatik</td> </tr> <tr> <td colspan="2">Knowledge-based modification of conditional random fields protein-protein identification method</td> </tr> <tr> <td>Helmholtz Zentrum München</td> <td style="text-align: right;">January 2012 – April 2012</td> </tr> </table>	Georg-August-Universität Göttingen	January 2015	Institut für Informatik		Knowledge-based modification of conditional random fields protein-protein identification method		Helmholtz Zentrum München	January 2012 – April 2012												
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Institute of Bioinformatics and Systems Biology, Chemoinformatics & Chemical Biology group

Application of similarity search in protein active sites databases to the drug side effects prediction

SELECTED
PUBLICATIONS

- J. Velkoborsky, D. Hoksza. Scaffold analysis of PubChem database as background for hierarchical scaffold-based visualization. *Journal of Cheminformatics*, 8(74), 2016
- R. Eliáš, D. Hoksza. RNA secondary structure visualization using tree edit distance. *International Journal of Bioscience, Biochemistry and Bioinformatics*, 6(1), 2016
- R. Galvanek, D. Hoksza. Template-based prediction of RNA tertiary structure. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2016
- D. Hoksza, P. Škoda. Using Bayesian Modeling on Molecular Fragments Features for Virtual Screening. *International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB)*, 2016
- R. Krivák, D. Hoksza. P2RANK: knowledge-based ligand binding site prediction using aggregated local features. In *AlcoB 2015*, Mexico City, Mexico, pp.: 41 - 52, Springer, 2015, ISBN: 978-3-319-21232-6
- R. Krivák, D. Hoksza. Improving protein-ligand binding site prediction accuracy by classification of inner pocket points using local features. *Journal of Cheminformatics*, 7(1), 2015
- P. Čech, D. Hoksza, D. Svozil. MultiSETTER: web server for multiple RNA structure comparison. *BMC Bioinformatics*, 16(253), 2015
- D. Hoksza, D. Svozil. Multiple 3D RNA Structure Superposition Using Neighbor Joining. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2014, PP(99)
- D. Hoksza, P. Škoda, P. Voršilák, D. Svozil. Molpher: a software framework for systematic chemical space exploration. *Journal of Cheminformatics*, 6(7), 2014
- D. Hoksza, P. Škoda. 2D Pharmacophore Query Generation. In *ISBRA'14*, Zhangjiajie, China, Springer, 2014
- D. Hoksza, P. Szepe, D. Svozil. MultiSETTER - Multiple RNA Structure Similarity Algorithm. In *BSB'13, Brazilian Symposium on Bioinformatics*, Recife, Brazil, pp.: 59-70, Springer, 2013, ISBN: 978-3-319-02623-7
- P. Škoda, D. Hoksza. Chemical Space Visualization Using ViFrame. In *ICIS 2013*, Niigata, Japan, pp.: 541 - 546, IEEE, 2013, ISBN: 978-147990174-6

- D. Hoksza, P. Szepe, D. Svozil. MultiSETTER - Multiple RNA Structure Similarity Algorithm. In *ICIS 2013, International Conference on Computer and Information Science*, in press, *IEEE*, 2013
- J. Galgonek, T. Skopal, D. Hoksza. P3S: Protein Structure Similarity Search. In *3rd International Workshop on High Performance Bioinformatics and Biomedicine (HiBB)*, Rhodes Island, Greece, pp.: 228-23, *Lecture Notes in Computer Science, Springer*, ISSN: 0302-9743, 2013
- J. Novák, T. Sachsenberg, D. Hoksza, T. Skopal, O. Kohlbacher. A Statistical Comparison of SimTandem with State-of-the-Art Peptide Identification Tools. In *7th International Conference on Practical Applications of Computational Biology & Bioinformatics (PACBB)*, Salamanca, Spain, pp.: 1001-109, *Advances in Intelligent and Soft-Computing, Springer*, ISSN: 0302-9743, 2013
- P. Čech, D. Svozil, D. Hoksza. SETTER: web server for RNA structure comparison. *Nucleic Acids Res.* 2012, 40(Web Server issue):W42-8
- D. Hoksza, D. Svozil. Efficient RNA pairwise structure comparison by SETTER method. *Bioinformatics* 2012, 28(14):1858-64
- J. Galgonek, D. Hoksza, T. Skopal. SProt: sphere-based protein structure similarity algorithm. *Proteome Science* 2011, 9(Suppl 1):S20
- J. Novák, J. Galgonek, D. Hoksza, T. Skopal. SimTandem: Similarity Search in Tandem Mass Spectra. In *Similarity Search and Applications (SISAP)*, Toronto, Ontario, Canada, pp.: 242-43, *Lecture Notes in Computer Science 7404, Springer*, ISSN: 0302-9743, 2012
- D. Hoksza, D.Svozil, Exploration of Chemical Space by Molecular Morphing. *IEEE International Conference on Bioinformatics & Bioengineering 2011*, Taiwan, ISBN 978-0-7695-4391-8, pp. 201-208, *IEEE*, 2011
- D. Hoksza, D.Svozil, SETTER - RNA SEcondary sTructure-based TERtiary Structure Similarity Algorithm. In *ISBRA'11, International Symposium on Bioinformatics Research and Applications*, pp. 37-49, *Springer*, 2011
- J. Galgonek, D. Hoksza, SProt - From Local to Global Protein Structure Similarity. In *IEEE BIBM'10, Bioinformatics and Biomedicine Workshops*, pp. 124-129, *IEEE Press*, 2010
- J. Novák, D. Hoksza, Similarity Search and Posttranslational Modifications in Tandem Mass Spectra. In *IEEE BIBM'10, Bioinformatics and Biomedicine Workshops*, pp. 845-846, *IEEE Press*, 2010
- D. Hoksza, J. Galgonek, Alignment-Based Extension to DDPI Feature Extraction. In *International Journal of Computational Bioscience*, 1(1), pp. 79-87, *ACTA Press*,

2010

- D. Hoksza, DDPIIn - Distance and Density Based Protein Indexing. In *CIBCB'09: Proceedings of the 6th Annual IEEE conference on Computational Intelligence in Bioinformatics and Computational Biology*, pp. 263–270, *IEEE Press*, 2009
- J. Novák, D. Hoksza, An Application of the Metric Access Methods to the Mass Spectrometry Data. In *CIBCB'09: Proceedings of the 6th Annual IEEE conference on Computational Intelligence in Bioinformatics and Computational Biology*, pp. 220–227, *IEEE Press*, 2009
- D. Hoksza, T. Skopal, Native Multidimensional Indexing in Relational Databases. In *COMAD 2008, Proceedings of the 14th International Conference on Management of Data*, pp. 251–260, *IIT Bombay*, 2008
- D. Hoksza, Improved Alignment of Protein Sequences Based on Common Parts. In *ISBRA*, volume 4983 of *Lecture Notes in Computer Science*, pp. 87–99. *Springer*, 2008.
- T. Skopal, D. Hoksza, Improving the Performance of M-tree Family by Nearest-Neighbor Graphs In *ADBIS*, volume 4690 of *Lecture Notes in Computer Science*, pp. 172-188. *Springer*, 2007.
- T. Skopal, D. Hoksza, J. Pokorný, Construction of Tree-based Indexes for Level-Contiguous Buffering Support. In *Database System for Advanced Applications (DASFAA)*, volume 4443 of *Lecture Notes in Computer Science*, pp. 361–373, *Springer*, 2007.

REVIEWING AND ORGANIZATION SERVICE

Reviewing:

- *Nucleic Acids Research* , *Journal of Chemical Information and Modeling* , *Journal of Cheminformatics* , *DKE Journal* , *Journal of Computer Mathematics* , *Journal of Molecular Graphics and Modelling* , *Current Bioinformatics* , *SISAP (2008, 2009, 2010, 2012, 2013)* , *ADBIS (2011)* , *DATESO (2008, 2012)* , *PACBB (2014, 2015, 2016, 2017)*

Organization:

- Founding bioinformatics study program at Charles University
- *ENBIK 2012, 2014* — National Bioinformatics Conference
- *CSPUG seminars 2011* — co-organizing seminars of the Czech and Slovak PostgreSQL Group
- *DATESO 2007*

MEMBERSHIP

Founding member of SIRET Research Group

Member of CSBMB (Czech Society For Biochemistry and Molecular Biology)

Member of FOBIA (Czech Free & Open BioInformatic Association)

Member of CSCH (Czech Chemical Society)

GRANTS

- Czech Science Foundation* **2015–2018**
- Project ID: 15-00885S
 - Topic: *Novel methods for computational prediction and visualization of secondary structures of ribosomal ribonucleic acids - an integrated solution*
 - Role: *Co-Investigator*
- Czech Science Foundation* **2014–2016**
- Project ID: 14-29032P
 - Topic: *Efficient chemical space exploration using multi-objective optimization*
 - Role: *Principal Investigator*
- Technology Agency of Czech Republic* **2012–2015**
- Project ID: TA02010212
 - Topic: *ReceptorX: Integrated Platform for Identification and Development of new Drugs*
 - Role: *Team Member*
- Czech Science Foundation* **2011–2014**
- Project ID: P202/11/0968
 - Topic: *Large-scale Nonmetric Similarity Search in Complex Domains*
 - Role: *Team Member*
- Czech Science Foundation* **2009–2011**
- Project ID: 201/09/0683
 - Topic: *Similarity Searching in Very Large Multimedia Databases*
 - Role: *Team Member*
- Grant Agency of Charles University* **2007–2008**
- Project ID: 57907
 - Topic: *Similarity Search in Biological Databases*
 - Role: *Principal Investigator*

PROFESSIONAL
EXPERIENCE

- ASP a.s.**, Prague, Czech Republic
- Analyst of Information Systems, Database Expert* **2004–2010**
- Design of information system (conceptual modeling)
 - SQL programming (Microsoft SQL Server — TSQL, Oracle — PL/SQL)
 - SQL optimization (Microsoft SQL Server, Oracle)
 - Database administration (MSSQL, Oracle)
 - Web programming (ASP.NET, C#)

TEACHING
EXPERIENCE

- Charles University in Prague**, Prague, Czech Republic
- Teaching Assistant* **September 2006 – present**
- Data visualization
 - Data organization and processing
 - Administration of MS SQL Server
 - Database Systems
 - Database Applications

Institute of Chemical Technology, Prague, Czech Republic

Teaching Assistant

September 2011 – February 2015

- Bioinformatics Algorithms
- Database Systems

Czech Technical University in Prague, Prague, Czech Republic

Teaching Assistant

September 2009 – September 2011

- Database Systems
- Retrieval of Multimedia Content on the Web
- Searching Web and Multimedia Databases

The University of Finance and Administration, Prague, Czech Republic

Lecturer

September 2006 – August 2008

- Introduction to Unix

AWARDS

Bernard Bolzano Foundation in Computer science Award

- Awarded for the paper *Density-Based Classification of Protein Structures Using Iterative TM-score*, 2010

Werner Von Siemens Excellence Award

- Honorable mention for the PhD thesis *Similarity Search in Protein Databases*, 2010

SOFTWARE SKILLS

Programming Languages:

- C, C++, C#, ASP.NET, Java, JavaScript, PHP, UNIX shell scripting, SQL

Databases:

- Microsoft SQL Server (TSQL programming, administration), Oracle(PL/SQL programming, administration), PostgreSQL (PG/SQL programming), Firebird (SQL programming), MySQL (SQL programming)