Curriculum Vitae of Ján Maňuch

Personal Details

Name:	Ján Maňuch
Address:	Department of Computer Science, University of British Columbia 201-2366 Main Mall Vancouver BC, V6T 1Z4, Canada
Phone:	+1 604–724–7784
Fax:	+1 604–822–5485
Email:	jmanuch@cs.ubc.ca
Homepage:	`http://www.cs.ubc.ca/~jmanuch/`
PR Status:	permanent resident of Canada since June 19, 2005 Canadian citizen since July 15, 2009

Education & Training

1997–2002	PhD, Dept. of Mathematics, University of Turku & Turku Centre for Computer Science, Finland (rank: "laudatur")
1992–1997	MSc, Dept. of Computer Science, Comenius University, Bratislava (1st rank)
June–September 1996	Summer Student Programme in CERN, Switzerland

Specialized Courses

September 3, 2013	Developing Course Goals and Learning Objectives Workshop, University of British Columbia
August 24, 2010	Effective Classroom Communication Workshop, University of British Columbia
September 22–28, 2007	Minicourse in Quantitative Biology & Workshop on Deconstructing Biochemical Networks, CRM, University of Montreal
July 19–24, 2004	CBW Proteomics Workshop, University of Calgary
October 28–30, 2004	Instructional Skills Workshop, Simon Fraser University

Work Experience

September 2015 – present	Lecturer, Department of Computer Science, University of British Columbia
October 2014 – present	Science Researcher, Department of Computer Science, University of British Columbia
October 2013 – September 2014	Research Associate, Department of Computer Science, University of British Columbia — supervised by Arvind Gupta and Anne Condon
September 2009 – August 2013	Postdoctoral Research Fellow, Department of Computer Science, University of British Columbia — supervised by Arvind Gupta
September 2008 – August 2015	Adjunct Professor, Department of Mathematics, Simon Fraser University
September 2002 – August 2009	Postdoctoral Fellow, School of Computing Science, Simon Fraser University (supported in part by PIMS) — supervised by Arvind Gupta, Pavol Hell and Ladislav Stacho

Programming Skills

- C++, Java, Javascript, PHP, SQL, Maple, LATeX, Metapost

Teaching Experience

Instructor:

Spring 2016	UBC, Computer Science	Intermediate Algorithm Design and Analysis (CPSC 320)
Fall 2015	UBC, Computer Science	Intermediate Algorithm Design and Analysis (CPSC 320)
Spring 2015	UBC, Computer Science	Algorithms for Bioinformatics (CPSC 445)
Spring 2014	UBC, Computer Science	Algorithms for Bioinformatics (CPSC 445)
Spring 2013	UBC, Computer Science	Algorithms for Bioinformatics (CPSC 445)
Spring 2012	SFU, Mathematics	Applied Linear Algebra (MATH 232)
Fall 2010	SFU, Mathematics	Calculus for Social Sciences I (MATH 157)
Summer 2009	SFU, Mathematics	Linear optimization (MATH 308)
Summer 2008	SFU, Computer Science	Algorithms and data structures (CMPT 307)
Spring 2008	SFU, Computer Science	Object-oriented design in C++ (CMPT 212)
Summer 2006	SFU, Computer Science	Data structures and programming (CMPT 225)
Fall 2005	SFU, Computer Science	Object-oriented design in C++ (CMPT 212)
Spring 2004	SFU, Computer Science	Object-oriented design in C++ (CMPT 212)
Summer 2003	SFU, Computer Science	Algorithms and data structures (CMPT 307)

Graduate students

Name	Years Supervised	Title of Project
Evan Luo	Co-supervised 2015–	Graph traversal algorithms (MSc, Math, SFU)
Akbar Rafiey	Co-supervised 2014–	RNA secondary structure energy barrier problem (MSc, Math, SFU)
Masood Masjoody	Co-supervised 2010–	Combinatorial games on graphs (PhD, Math, SFU)
Javad Safaei	Co-supervised 2007–2015	Modelling human cell protein phosphorylation networks (PhD, CS, UBC)
Bahar Behsaz	Co-supervised 2011–2013	Computational aspects of DNA self-assembly systems at temperature 1 (MSc, Math, SFU)
Murray Patterson	Co-supervised 2006–2011	Variants of the consecutive-ones property motivated by the reconstruction of ancestral species (PhD, CS, UBC)
Christine Stoll	Co-supervised 2006–2009	Bounds on the tile complexity of shapes in self-assembly systems (MSc, Math, SFU)
Alireza Hadj Khodabakhshi	Co-supervised 2002–2008	Structure approximating IPF in 2D and 3D HPC model (PhD, CS, SFU)

Research Grants

- 2012: Primary investigator on 18-month **MITACS Accelerate Grant** "Modeling Human Cell Phosphorylation Network"; $30,000.
- 2010: Primary investigator on 5-year **NSERC Discovery Grant** "Combinatorial Models and Algorithms in Bioinformatics"; $120,000.
- 2009: Co-investigator on 2-year **NSERC Collaborative Research and Development Grant** "Mapping the Human Kineome and Phosphoproteome"; $115,000.
- 2004: 1-year PIMS Postdoctoral Fellowship; $20,000.

Publications[1]

Journal Publications

[1] Rajaraman, A., Zanetti, J.P.P., Maňuch, J., Chauve, C., Algorithms and complexity results for genome mapping problems, *Transactions on Computational Biology and Bioinformatics*, (to appear).

[2] Czyzowics, J., Dobrev, S., Joeris, B., Kranakis, E., Krizanc, D., Maňuch, J., Morales-Ponce, O., Opatrny, J., Stacho, L., Urrutia, J., Monitoring the plane with rotating radars, *Graphs & Combinatorics* **31**, No. 2, 393–405 (2015).

[3] Condon, A., Maňuch, J., Thachuk, C., The complexity of string partitioning, *J. of Discrete Algorithms* **32**, 24–43 (2015).

[1] Computer science and theoretical bioinformatics papers list authors alphabetically representing equal intellectual contributions. Some bioinformatics publications traditionally list supervisors names last, while other contributors are listed in the order of the involvement in the work on the publication.

[4] Condon, A., Kirkpatrick, B., Maňuch, J., Reachability bounds for chemical reaction networks and strand displacement systems, *Nat. Comput.* **13**, 499–516 (2014).

[5] Maňuch, J., Patterson, M., Chauve, C., Hardness results on the gapped consecutive-ones property problem, *Discrete Applied Mathematics* **160**, No. 18, 2760–2768 (2012).

[6] Condon, A., Hu, A., Maňuch, J., Thachuk, C., Less haste, less waster: on recycling and its limits in strand displacement systems, *Interface Focus* **2**, No. 4, Royal Society, 512–521 (2012).

[7] Maňuch, J., Stacho, L., Stoll, C., Step-wise tile assembly with a constant number of tile types, *Nat. Comput.* **11**, No. 3, 535–550 (2012).

[8] Gupta, A., Maňuch, J., Stacho, L., Zhao, X., Algorithm for haplotype inference via galled-tree networks with simple galls, *J. Comp. Biol.* **19**, No. 4, 439–454 (2012).

[9] Maňuch, J., Patterson, M., The complexity of the gapped consecutive-ones property problem for matrices of bounded maximum degree, *J. Comp. Biol.* **18**, No. 9, 1243–1253 (2011).

[10] Wittler, R., Maňuch, J., Patterson, M., Stoye, J., Consistency of sequence-based gene clusters, *J. Comp. Biol.* **18**, No. 9, 1023–1039 (2011).

[11] Safaei, J., Maňuch, J., Gupta, A., Stacho, L., Pelech, S., Prediction of 492 human protein kinase substrate specificities, *Proteome Science* **9**(Suppl 1):S6 (2011).

[12] Maňuch, J., Thachuk, C., Stacho, L., Condon, A., NP-completeness of the energy barrier problem without pseudoknots and temporary arcs, *Nat. Comput.* **10**, No. 1, 391–405 (2011).

[13] Gupta, A., Karimi, M., Maňuch, J., Stacho, L., Zhao, X., Haplotype inference via galled-tree networks is NP-complete, *J. Comp. Biol.* **17**, No. 10, 1435–1449 (2010).

[14] Maňuch, J., Stacho, L., Stoll, C., Two lower bounds for self-assemblies at temperature 1, *J. Comp. Biol.* **17**, No. 6, 841–852 (2010).

[15] Adams, P., Ardal, H., Maňuch, J., Hòa, V.D., Rosenfeld, M., Stacho, L., Spanning cubic graph designs, *Discrete Math.* **309**, No. 18, 5781–5788 (2009).

[16] Khodabakhshi, A.H., Maňuch, J., Rafiey, A., Gupta, A., Inverse protein folding in 3D hexagonal prism lattice under HPC model, *J. Comp. Biol.* **16**, No. 6, 769–802 (2009).

[17] Ardal, H., Maňuch, J., Rosenfeld, M., Shelah, S., Stacho, L., The odd-distance plane graph, *Discrete & Computational Geometry* **42**, No. 2, 132–141 (2009).

[18] Gupta, A., Maňuch, J., Stacho, L., Zhao, X., Haplotype inferring via galled-tree networks using a hypergraph covering problem for special genotype matrices, *Discrete Applied Mathematics* **157**, No. 10, 2310–2324 (2009).

[19] Khodabakhshi, A.H., Maňuch, J., Rafiey, A., Gupta, A., Stable structure-approximating inverse protein folding in 2D Hydrophobic-Polar-Cysteine (HPC) model, *J. Comp. Biol.* **16**, No. 1, 19–30 (2009).

[20] Gupta, A., Heuvel, J., Maňuch, J., Stacho, L., Zhao, X., On the complexity of ordered colorings, *SIAM J. Discrete Math.* **22**, No. 2, 832–847 (2008).

[21] Maňuch, J., Gaur, D.R., Fitting protein chains to cubic lattice is NP-complete, *Journal of Bioinformatics and Computational Biology* **6**, No. 1, 93–106 (2008).

[22] Gupta, A., Maňuch, J., Stacho, L., Zhao, X., Characterization of the existence of galled-tree networks, *Journal of Bioinformatics and Computational Biology* **4**:6, 1309–1328 (2006).

[23] Gupta, A., Maňuch, J., Stacho, L., Fault tolerant forwarding and optical indexes: a design theory approach, *Journal of Combinatorial Designs* **14**, No. 1, 25–40 (2006).

[24] Gupta, A., Maňuch, J., Stacho, L., Structure-approximating inverse protein folding problem in 2D HP model, *J. Comp. Biol.* **12**, No. 10, 1328–1345 (2005).

[25] Berenbrink, P., Friedetzky, T., Maňuch, J., Stacho, L., (Quasi) spanners for mobile ad hoc networks, *Journal of Interconnection Networks* **6**, No. 2, 63–84 (2005).

[26] Maňuch, J., Stacho, L., On f-wise arc forwarding index and wavelength allocations in faulty all-optical hypercubes, *Theor. Inform. Appl.* **37**, No. 3, 255–270 (2003).

[27] Ďuriš, P., Maňuch, J., On the computational complexity of infinite words, *Theoret. Comput. Sci.* **295**, No. 1–3, 141–151 (2003).

[28] Karhumäki, J., Maňuch, J., Plandowski, W., A defect theorem for bi-infinite words, *Theoret. Comput. Sci.* **292**, No. 1, 237–243 (2003).

[29] Karhumäki, J., Maňuch, J., Multiple factorizations of words and defect effect, *Theoret. Comput. Sci.* **273**, No. 1–2, 81–97 (2002).

[30] Cassaigne, J., Karhumäki, J., Maňuch, J., On conjugacy of languages, *Theor. Inform. Appl.* **35**, no. 6, 535–550 (2001).

[31] Maňuch, J., Defect effect of bi-infinite words in the two-element case, *Discrete Math. Theor. Comput. Sci.* **4**, No. 2, 273–290 (2001).

[32] Maňuch, J., Construction of very hard functions for multiparty communication complexity, *Theor. Inform. Appl.* **34**, No. 1, 61–75 (2000).

Conference publications[2]

Extended abstracts (refereed)

[1] *Haleš, J., Maňuch, J., Ponty, Y., Stacho, L., Combinatorial RNA design: Designability and structure-approximating algorithm, Proc. of *Combinatorial Pattern Matching* (CPM, Ischia, Italy, 2015), LNCS 9133, 231–246 (2015).

[2] *Chen, H-L., Doty, D., Maňuch, J., Rafiey, A., Stacho, L., Pattern overlap implies runaway growth in hierarchical tile systems, Proc. of *Annual Symposium on Computational Geometry* (SOCG, Eindhoven, Netherlands, 2015), LIPIcs **34**, 360–373 (2015).

[3] *Safaei, J., Maňuch, J., Stacho, L., Learning polytrees with constant number of roots from data, Proc. of *Australasian Joint Conference on Artificial Intelligence* (AI, Dunedin, New Zealand, 2013), LNCS **8272**, 447–452 (2013).

[2]The talks or posters presented by me are marked with *.

[4] Maňuch, J., Patterson, M., Wittler, R., Chauve, C., Tannier, E., Linearization of ancestral multichromosomal genomes, Proc. of *Annual RECOMB Satellite Workshop on Comparative Genomics* (RECOMB-CG, Niterói, Brazil, 2012), BMC Bioinformatics **13**(Suppl 19):S11 (2012).

[5] Condon, A., Kirkpatrick, B., Maňuch, J., Reachability bounds for chemical reaction networks and strand displacement systems, Proc. of *International Meeting on DNA Computing and Molecular Programming* (DNA, Aarhus, Denmark, 2012), LNCS **7433**, 43–57 (2012).

[6] Behsaz, B., Maňuch, J., Stacho, L., Turing universality of step-wise and stage assembly at temperature 1, Proc. of *International Meeting on DNA Computing and Molecular Programming* (DNA, Aarhus, Denmark, 2012), LNCS **7433**, 1–11 (2012).

[7] *Condon, A., Maňuch, J., Thachuk, C., The complexity of string partitioning, Proc. of *Combinatorial Pattern Matching* (CPM, Helsinki, Finland, 2012), LNCS **7354**, 159–172 (2012).

[8] Safaei, J., Maňuch, J., Gupta, A., Stacho, L., Pelech, S., Evolutionary conservation of human phosphorylation sites, Proc. of *IEEE International Conference of Bioinformatics and Biomedicine* (BIBM, Atlanta, Georgia, USA, 2011), IEEE Computer Society, 222–227 (2011).

[9] Condon, A., Hu, A., Maňuch, J., Thachuk, C., Less haste, less waster: On recycling and its limits in strand displacement systems, Proc. of *International Meeting on DNA Computing and Molecular Programming* (DNA, Pasadena, California, USA, 2011), LNCS **6937**, 84–99 (2011).

[10] Chauve, C., Maňuch, J., Patterson, M., Wittler, R., Tractability results for the consecutive-ones property with multiplicity, Proc. of *Combinatorial Pattern Matching* (CPM, Palermo, Italy, 2011), LNCS **6661**, 90–103 (2011).

[11] *Maňuch, J., Patterson, M., A. Gupta, Towards a characterisation of the generalised character compatibility problem for non-branching character trees, Proc. of *International Symposium on Bioinformatics Research and Applications* (ISBRA, Changsha, China, 2011), LNBI **6674**, 440–451 (2011).

[12] Safaei, J., Maňuch, J., Gupta, A., Stacho, L., Pelech, S., Prediction of human protein kinase substrate specificities, Proc. of *IEEE International Conference of Bioinformatics and Biomedicine* (BIBM, Hong Kong, 2010), IEEE Computer Society, 259–264 (2010).

[13] *Maňuch, J., Patterson, M., The complexity of the gapped consecutive-ones property problem for matrices of bounded maximum degree, Proc. of *Annual RECOMB Satellite Workshop on Comparative Genomics* (RECOMB-CG, Ottawa, Ontario, Canada, 2010), LNBI **6398**, 278–289 (2010).

[14] Maňuch, J., Patterson, M., Poon S.-H., Thachuk, C., Complexity of finding non-planar rectilinear drawings of graphs, Proc. of *International Symposium on Graph Drawing* (GD, Konstanz, Germany, 2010), LNCS **6502**, 305–316 (2011).

[15] Thachuk, C., Maňuch, J., Rafiey, A., Mathieson, L-A., Stacho, L., Condon, A., An algorithm for the energy barrier problem without pseudoknots and temporary arcs, Proc. of *Pacific Symposium on Biocomputing* (PSB, Big Island, Hawaii, USA, 2010), World Scientific Publishing, 108–119 (2010).

[16] *Maňuch, J., Stacho, L., Stoll, C., Step-assembly with a constant number of tile types, Proc. of *International Symposium on Algorithms and Computation* (ISAAC, Honolulu, Hawaii, USA, 2009), LNCS **5878**, 954–963 (2009).

[17] Chauve, C., Maňuch, J., Patterson, M., On the gapped consecutive-ones property, Proc. of *European Conference on Combinatorics, Graph Theory and Applications* (EUROCOMB, Bordeaux, France, 2009), ENDM **34**, 121–125 (2009).

[18] Maňuch, J., Thachuk, C., Stacho, L., Condon, A., NP-completeness of the direct energy barrier problem without pseudoknots, Proc. of *International Meeting on DNA Computing and Molecular Programming* (DNA, Fayetteville, Arkansas, USA, 2009), LNCS **5877**, 106–115 (2009).

[19] Maňuch, J., Patterson, M., Gupta, A., On the generalized character compatibility problem for non-branching character trees, Proc. of *Annual International Computing and Combinatorics Conference* (COCOON, Niagara Falls, New York, USA, 2009), LNCS **5609**, 268–276 (2009).

[20] *Maňuch, J., Stacho, L., Stoll, C., Two lower bounds for self-assemblies at temperature 1, Proc. of *International Conference on Bioinformatics and Biomedical Engineering* (iCBBE, Beijing, China, 2009), 1–4 [DOI: 10.1109/ICBBE.2009.5163719] (2009).

[21] Khodabakhshi, A.H., Maňuch, J., Rafiey, A., Gupta, A., Inverse protein folding in 3D hexagonal prism lattice under HP model, Proc. of *International Conference on Bioinformatics & Computational Biology* (BIOCOMP, Las Vegas, Nevada, USA, 2008), CSREA Press, 619–625 (2008).

[22] Khodabakhshi, A.H., Maňuch, J., Rafiey, A., Gupta, A., A robust class of stable proteins in the 2D HPC model, Proc. of *Bioinformatics Research and Development* (BIRD, Vienna, Austria, 2008), Communications in Computer and Information Science **13**, 180-192 (2008).

[23] *Gupta, A., Maňuch, J., Stacho, L., Zhao, X., Haplotype inferring via galled-tree networks is NP-complete, Proc. of *Annual International Computing and Combinatorics Conference* (COCOON, Dalian, China, 2008), LNCS **5092**, 287–298 (2008).

[24] Condon, A., Maňuch, J., Thachuk, C., Complexity of a collision-aware string partition problem and its relation to oligo design for gene synthesis, Proc. of *Annual International Computing and Combinatorics Conference* (COCOON, Dalian, China, 2008), LNCS **5092**, 265–275 (2008).

[25] *Khodabakhshi, A.H., Maňuch, J., Rafiey, A., Gupta, A., Structure-approximating design of stable proteins in 2D HP model fortified by cysteine monomers, Proc. of *Asia Pacific Bioinformatics Conference* (APBC, Kyoto, Japan, 2008), Advances in Bioinformatics and Computational Biology **6**, 49–58 (2008).

[26] *Gupta, A., Karimi, M., Khodabakhshi, A.H., Maňuch, J., Rafiey, A., Design of artificial protein structures in 3D hexagonal prism lattice under HP model, Proc. of *International Conference on Bioinformatics & Computational Biology* (BIOCOMP, Las Vegas, Nevada, USA, 2007), CSREA Press, 362–369 (2007).

[27] *Gupta, A., Maňuch, J., Stacho, L., Zhao, X., Algorithm for haplotype inferring via galled-tree networks with simple galls (extended abstract), Proc. of *International Symposium on Bioinformatics Research and Applications* (ISBRA, Atlanta, Georgia, USA, 2007), LNBI **4463**, 121–132 (2007).

[28] *Gaur, D. R., Maňuch, J., Fitting protein chains to cubic lattice is NP-complete, Proc. of *Asia Pacific Bioinformatics Conference* (APBC, Hong Kong, 2007), Advances in Bioinformatics and Computational Biology **5**, 153–164 (2007).

[29] Kavanagh, J., Mitchell, D., Ternovska, E., Maňuch, J., Zhao, X., Gupta, A., Constructing Camin-Sokal phylogenies via answer set programming, Proc. of *Logic for Programming, Artificial Intelligence, and Reasoning* (LPAR, Phnom Penh, Cambodia, 2006), LNCS **4246**, 452–466 (2006).

[30] *Gaur, D. R., Krishnamurti, R., Maňuch, J., Improved approximation algorithm for scheduling tasks with a choice of start times, Proc. of *Algorithms and Complexity in Durham* (ACiD, Durham, UK 2006), Texts in Algorithmics **7**, 85–94 (2006).

[31] *Maňuch, J., Zhao, X., Stacho, L., Gupta, A., Characterization of the existence of galled-tree networks (extended abstract), Proc. of *Asia Pacific Bioinformatics Conference* (APBC, Taipei, Taiwan, 2006), Imperial College Press, 297–306 (2006).

[32] Brown, T., Maňuch, J., A simple proof of Lerch's formula, Proc. of *Fibonacci Numbers and Their Applications* (Braunschweig, Germany, 2004), Applications of Fibonacci Numbers **10**, Kluwer Academic Publishers (to appear).

[33] *Gupta, A., Maňuch, J., Stacho, L., Inverse protein folding in 2D HP model (extended abstract), Proc. of *Computational Systems Bioinformatics* (CSB, Stanford, California, USA, 2004), IEEE Computer Society, 311–318 (2004).

[34] *Gupta, A., Maňuch, J., Stacho, L., Zhu, C., Small phylogeny problem: Character evolution trees, Proc. of *Combinatorial Pattern Matching* (CPM, Istanbul, Turkey, 2004), LNCS **3109**, 230–243 (2004).

[35] *Gupta, A., Maňuch, J., Stacho, L., Fault tolerant forwarding and optical indexes: A design theory approach, Proc. of *Colloquium on Structural Information and Communication Complexity* (SIROCCO, Smolenice Castle, Slovak Republic, 2004), LNCS **3104**, 197–208 (2004).

[36] *Ďuriš, P., Maňuch, J., On the computational complexity of infinite words, Proc. of *Math. Foundations of Comp. Sci.* (MFCS, Mariánske Lázne, Czech Republic, 2001), LNCS **2136**, 328–337 (2001).

[37] *Maňuch, J., Characterization of a word by its subwords, in: Rozenberg, Grzegorz (ed.) et al., Proc. of *Developments in language theory: Foundations, applications, and perspectives* (DLT, Aachen, Germany, 1999), World Scientific, 210–219 (2000).

[38] Maňuch, J., Stacho, L., Fault-tolerant wavelength allocations in all-optical hypercubes, Proc. of *Colloquium on Structural Information and Communication Complexity* (SIROCCO, Lacanau-Ocean, France, 1999), Carleton Scientific, 219–222 (1999).

[39] *Maňuch, J., Multiparty communication complexity: Very hard functions, Proc. of *Math. Foundations of Comp. Sci.* (MFCS, Szklarszka Poreba, Poland, 1999), LNCS **1672**, 160–169 (1999).

[40] *Karhumäki, J., Maňuch, J., Plandowski, W., On defect effect of bi-infinite words, Proc. of *Math. Foundations of Comp. Sci.* (MFCS, Brno, Czech Republic, 1998), LNCS **1450**, 674–682 (1998).

Short abstracts (refereed)

[41] Maňuch, J., Stacho, L., Stoll, C., Two lower bounds for self-assemblies at temperature 1 (poster abstract), Proc. of *Annual ACM Symposium on Applied Computing (Bioinformatics Track)* (ACM SAC BIO, Honolulu, USA, 2009), 808–809 (2009).

[42] Heuvel, J., Gupta, A., Maňuch, J., Stacho, L., Zhao, X., On the complexity of ordered colorings (short abstract), Proc. of *Algorithms and Complexity in Durham* (ACiD, Durham, UK, 2006), Texts in Algorithmics **7**, 156 (2006).

[43] Mead, C.R., Maňuch, J., Huang, X., Bhattacharyya, B., Stacho, L., Gupta, A., Investigating lattice structure for inverse protein folding (poster abstract), Proc. of *FEBS Congress & IUBM Conference: The Protein World* (Budapest, Hungary, 2005), *FEBS Journal* **272** (s1), 4739_1_380 (2005).

Without proceedings (not refereed)

[44] Chauve, C., Maňuch, J., Rajaraman, A., Zanetti, J.P.P., Algorithms and complexity results for genome mapping problems (poster abstract), *Annual International Conference on Research in Computational Molecular Biology* (RECOMB, Pittsburgh, Pennsylvania, USA, 2014).

[45] Dobrev, S., Eftekhari, M., MacQuarrie, F., Maňuch, J., Morales Ponce, O., Narayanan, L., Opatrny, J., Stacho, L., Connectivity with directional antennas in the symmetric communication model, *Mexican Conference on Discrete Mathematics and Computational Geometry* (Oaxaca, Mexico, 2013).

[46] *Maňuch, J., Some algorithmic and combinatorial problems in the RNA and DNA world, *Dagstuhl Seminar 11081: Combinatorial and Algorithmic Aspects of Sequence Processing* (Dagstuhl, Germany, 2011).

[47] *Khodabakhshi, A.H., Maňuch, J., Rafiey, A., Stacho, L., Gupta, A., Protein designs in HP models, *Foundations of Nanoscience: Self-Assembled Architectures and Devices* (Snowbird, Utah, USA, 2008).

[48] Thomas D., Maňuch, J., Gaur, D., Experiments on fitting protein chains to lattices (poster), *Asia Pacific Bioinformatics Conference* (Taipei, Taiwan, 2007).

[49] *Maňuch, J., Gaur, D. R., Huang, X., Benkoczi, R., Fitting protein chains to lattices, *SIAM Conference on Discrete Mathematics* (Victoria, B.C., Canada, 2006).

[50] Gupta, A., Maňuch, J., Stacho, L., Zhao, X., On intractability of haplotype inferring via galled-tree networks, *Workshop on Networks in Computational Biology* (Ankara, Turkey, 2006).

[51] *Maňuch, J., Mead, C.R., Huang, X., Bhattacharyya, B., Stacho, L., Gupta, A., On design of stable proteins in 3D HP Model (poster), *Metalloprotein and Protein Design Conference* (Chicago, Illinois, USA, 2005).

[52] *Cassaigne, J., Karhumäki, J., Maňuch, J., Conjugation of languages, *WORDS* (Palermo, Italy, 2001).

[53] *Karhumäki, J., Maňuch, J., Multiple factorizations of words and defect effect, *WORDS* (Rouen, France, 1999).

[54] Verdier, A., Maňuch, J., Computation on fixed points in a circular machine, *Particle Accelerator Conference* (Vancouver, B.C., Canada, 1997).

Publications in preparation

- Dobrev, S., Eftekhari, M., MacQuarrie, F., Maňuch, J., Morales Ponce, O., Narayanan, L., Opatrny, J., Stacho, L., *Connectivity with directional antennas in the symmetric communication model*, manuscript.
- Maňuch, J., Rafiey, A., *Finding minimum Tucker submatrices*, manuscript.
- Condon, A., Kirkpatrick, B., Maňuch, J., *Design of nucleic acid strands with long low-barrier folding pathways*, in preparation.

Research interests

- *Computational Biology and Bioinformatics:* Molecular Self-assembly, RNA Secondary Structures and Strand Displacement Systems, Chemical Reaction Networks, Genome Rearrangement Models, Kinase Cell Signaling Pathways, Phylogenetic Networks and Haplotyping, Forward and Inverse Protein Folding, String Matching
- *Networks:* Wireless Networks (connectivity, directional antennas, plane monitoring), Graph Traversal, Fault-tolerant Routings
- *Complexity Theory:* NP-completeness, Approximation Algorithms, FPT Algorithms
- *Discrete Mathematics and Graph Theory:* Coloring Problems, Graph Decomposition, Graph Drawing

PhD Dissertation

Title:	Defect theorems and infinite words
Supervisor:	Juhani Karhumäki, Turku University, Finland
Examiner:	Christian Choffrut, University Denis Diderot – Paris VII, LIAFA, France
Reviewers:	Wojciech Rytter, Liverpool University, UK Lila Kari, University of Western Ontario, Canada
Short abstract:	The thesis attacks different problems of Combinatorics on Words. Several defect-type theorems are developed for bi-infinite words. The problem of conjugacy of languages is considered and solved in two-element case. In the last chapter two open problems in the theory of computational complexity of infinite words are studied.

Master's thesis

Title:	Nondeterministic communication complexity on the multiparty model
Supervisor:	Pavol Ďuriš, Comenius University, Slovakia
Reviewer:	Dana Pardubská, Comenius University, Slovakia
Short abstract:	Functions with the worst possible nondeterministic communication complexity are constructed. It is also proved that almost all functions have complexity at least $M-n-2$, where M is the maximum complexity and n is the number of parties.

Other research activities

- MITACS Accelerate Lead Associate Research Review Committee (ARRC) member (2009 – present).
- Program Committee member for CPM 2012.
- Research collaboration with Kinexus Bioinformatics Corporation (September, 2005 – February 2006; and January, 2008 – present). Co-investigator on the NSERC Collaborative Research and Development (CRD) Grant "Mapping the Human Kineome and Phosphoproteome" (PI: Dr. Ladislav Stacho, duration: September 2009 – August 2011).
- Committee work: Member of examining committee for MSc student Vivija You (Math., SFU, 2009) supervised by Dr. Cedric Chauve.
- Co-organizer of the BIRS workshop "The Biology-Combinatorics Interface: Addressing New Challenges in Computational Biology" (July, 2008).
- Organizer of the MITACS Bioinformatics Series seminar 2007/2008 (`http://www.pims.math.ca/~manuch/MBS/`).
- Co-organizer of the BIRS workshop "Inverse Protein Folding" (September, 2006).
- Reviewer for conferences: MFCS, SIROCCO, DLT, ADHOC-NOW, CNSR, WG, CPM, STACS, WALCOM; and journals: Discrete Applied Mathematics, Theoretical Computer Science, Graphs and Combinatorics, Information Sciences, Opuscula Mathematica, Discrete Mathematics, J. Math. Biology, Nucleic Acids Research, Information Processing Letters, Mathematica Slovaca, J. Graph Theory, Natural Computing, Distributed Computing.

References

Anne Condon

Address:	Professor, Department of Computer Science University of British Columbia 201–2366 Main Mall Vancouver, BC V6T 1Z4, Canada
Email:	`condon@cs.ubc.ca`
Phone:	(604) 822-8175

Arvind Gupta

Address: Professor, Department of Computer Science
University of British Columbia
201-2366 Main Mall
Vancouver, BC V6T 1Z4, Canada
Email: arvind.gupta@ubc.ca
Phone: (604) 822-3061

Pavol Hell

Address: Professor, School of Computing Science
Simon Fraser University
8888 University Drive
Burnaby, BC V5A 1S6, Canada
Email: pavol@cs.sfu.ca
Phone: (778) 782-3391

Juhani Karhumäki

Address: Professor, Department of Mathematics
University of Turku
FIN-20014 Turku, Finland
Email: karhumak@utu.fi
Phone: +358 2 333 5613

Evangelos Kranakis

Address: Professor, School of Computer Science
Carleton University
1125 Col. By Dr.
Ottawa, ON, K1S 5B6, Canada
Email: kranakis@scs.carleton.ca
Phone: (613) 520-2600 x 8090, (613) 520-4333 (SCS Main office)

Moshe Rosenfeld

Address: Professor, Computing & Software Systems
Institute of Technology, University of Washington
1900 Commerce Street, Box 358426
Tacoma, Washington 98402-3100
Email: moishe@u.washington.edu
Phone: (253) 692-4520