Qualifications

1995	Ph.D.	Computer Science, Université de Montréal, Canada
		(Supervisors: Guy Lapalme and Robert Cedergren)
1993	M.Sc.	Computer Science, Université de Montréal, Canada
		(Supervisors: Guy Lapalme and Robert Cedergren)
1989	B.Sc.	Computer Science, Université de Montréal, Canada

Professional Experience

2020–23	Director	Program Evaluation, Office of Vice-Provost, Academic Affairs
2016–	Full Professor	School of Electrical Engineering and Computer Science, uOttawa
2013–2018	Vice-Dean	Undergraduate Studies, Faculty of Engineering, uOttawa
2012	Interim Vice-Dean	Undergraduate Studies, Faculty of Engineering, uOttawa
2008–2009	Invited Professor	Biochemistry Department, Université de Montréal
2007–	Associate Professor	School of Electrical Engineering and Computer Science, uOttawa
2000–2007	Assistant Professor	School of Electrical Engineering and Computer Science, uOttawa
1997-2000	Postdoctoral Fellow	Imperial Cancer Research Fund, London, UK (M.J.E. Sternberg)
1995-1997	Postdoctoral Fellow	Chemistry, University of Florida, Gainesville, USA (S.A. Benner)

Awards

2021	Best Oral Presentation for Session 4 at ICBBT 2021
1996-98	FCAR Postdoctoral Research Fellowship
1995	Université de Montréal Ph.D. Student Award
1993-95	Medical Research Council Ph.D. Student Award
1992	NSF Young Investigator Travel Award
1991-95	Université de Montréal Student Award
1991-92	NSERC M.Sc. Student Award
1991	FCAR Master's Research Scholarship (declined)
1990	Molecular Graphics Society Travelling Award

Funding

2014–2022	Principal Investigator, NSERC Discovery
	Development of bioinformatics tools to understand mechanisms of non-coding small RNA interactions
	$120,000
2014	(One of 5) Co-applicants, NSERC Research Tools and Instruments
	Experimental Platform for Big Data and Text Mining
	$59,146
2011–2014	Principal Investigator, NSERC Discovery
	Development of bioinformatics tools for RNomics research
	$42,000
2009–2010	Principal Investigator, NSERC Research Tools and Instruments
	Computer equipment for RNomics research
	$14,900
2007–09	Co-investigator, CIHR Strategic Training Initiative in Health Research
	Bioinformatics training for biomedical research (Gertraud Burger, PI)
	$621,000
2007–2011	Principal Investigator, NSERC Discovery
	Combinatorial Algorithms for Pattern Discovery in RNA Sequences
	$70,000
2006–2007	Principal Investigator, Interfaculty Collaborative Research Initiatives
	Bioinformatics detection and experimental validation of new secondary structure motifs involved in viroid-host interactions (with M. Pelchat)
	$23,500

2002–2006	Principal Investigator, NSERC Discovery
	Bioinformatics Tools to Assist Functional Genomics
	$56,000
2002–2007	Project Leader, CFI/OIT New opportunities
	Computing Infrastructure for Bioinformatics, Coding and Cryptography, and Algorithm Design
	$399,642
2002–2003	Principal Investigator, Communication & Information Technology Ontario
	Learning Grammatical Representations of Regulatory Elements
	$40,000
2003	Co-applicant, CHEO Seed Fund
	$30,000
2000	Startup
	$50,000

Publications

Papers submitted to refereed journals

[1] Aseel Awdeh, Marcel Turcotte, and Theodore J. Perkins. Cell type specific DNA signatures of transcription factor binding. *bioRxiv*, Preprint posted on July 18, 2022.

Papers in refereed journals

[1] K. Sutanto and M. Turcotte. Assessing global-local secondary structure fingerprints to classify RNA sequences with deep learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(05):2736–2747, sep 2023.

[2] Aseel Awdeh, Marcel Turcotte, and Theodore J. Perkins. WACS: improving ChIP-seq peak calling by optimally weighting controls. *BMC Bioinformatics*, 22(1):69, 2021.

[3] Alexander Gawronski and Marcel Turcotte. RiboFSM: Frequent subgraph mining for the discovery of RNA structures and interactions. *BMC Bioinformatics*, 15 Suppl 13:S2, November 2014.

[4] Ghada Badr, Isra Al-Turaiki, Marcel Turcotte, and Hassan Mathkour. IncMD: Incremental trie-based structural motif discovery algorithm. *Journal of Bioinformatics and Computational Biology*, 12(05):1450027, October 2014. PMID: 25362841.

[5] Georgette Kiethega, Yifei Yan, Marcel Turcotte, and Gertraud Burger. RNA-level unscrambling of fragmented genes in Diplonema mitochondria. *RNA biology*, 10(2):301–313, January 2013.

[6] Georgette N Kiethega, Marcel Turcotte, and Gertraud Burger. Evolutionarily Conserved cox1 Trans-Splicing Without cis-Motifs. *Molecular biology and evolution*, 28(9):2425–2428, September 2011.

[7] Mikhail Jiline, Stan Matwin, and Marcel Turcotte. Annotation Concept Synthesis and Enrichment Analysis: a Logic-Based Approach to the Interpretation of High-Throughput Experiments. *Bioinformatics*, 27(17):2391–2398, July 2011.

[8] A. Bellamy-Royds and M. Turcotte. Can clustal-style progressive pairwise alignment of multiple sequences be applied to RNA secondary structure prediction? *BMC Bioinformatics*, 8:190, 2007.

[9] V. X. Jin and M. Turcotte. Detecting localized interspersed motifs in genomic sequences: Application to the mouse genome. *IEEE Transactions on Instrumentation and Measurement*, 56(5):1770–1775, October 2007.

[10] S. D. Baird, S. M. Lewis, M. Turcotte, and M. Holcik. A search for structurally similar cellular internal ribosome entry sites. *Nucl. Acids Res.*, 35(14):4664–4677, 2007.

[11] S. D. Baird, M. Turcotte, R. G. Korneluk, and M. Holcik. Searching for IRES. *RNA Journal*, 12(10):1755–1785, 2006.

[12] M. Anwar, T. Nguyen, and M. Turcotte. Identification of consensus RNA secondary structures using suffix arrays. *BMC Bioinformatics*, 7:244, 2006.

[13] B. Masoumi and M. Turcotte. Simultaneous alignment and structure prediction of three RNA sequences. *International Journal of Bioinformatics Research and Applications*, 1(2):230–245, 2005.

[14] M. Turcotte, S.H. Muggleton, and M.J.E. Sternberg. Generating protein three-dimensional fold signatures using inductive logic programming. *Computers & Chemistry*, 26(1):57–64, December 2001.

[15] M. Turcotte, S.H. Muggleton, and M.J.E. Sternberg. Automated discovery of structural signatures of protein fold and function. *J. Mol. Biol.*, 306(3):591–605, 2001.

[16] M. Turcotte, S.H. Muggleton, and M.J.E. Sternberg. The effect of relational background knowledge on learning of protein three-dimensional fold signatures. *Machine Learning*, 43:81 – 95, 2001.

[17] M. Turcotte, S.H. Muggleton, and M.J.E. Sternberg. Use of inductive logic programming to learn principles of protein structure. *Electronic Transactions on Artificial Intelligence, ETAI*, 5(39), 2000.

[18] S. A. Benner, G. Cannarozzi, D. Gerloff, M. Turcotte, and G. Chelvanayagam. *Bona Fide* prediction of protein secondary structure using transparent analyses of multiple sequence alignments. *Chemical Review*, 97(8):2725 – 2843, 1997.

[19] D.L. Gerloff, F.E. Cohen, C. Korostensky, M. Turcotte, G.H. Gonnet, and S.A. Benner. A predicted concensus for the N-terminal fragment of the heat shock protein HSP90 family. *Proteins: Struct. Funct. Genet.*, 27:450–458, 1996.

[20] M. Turcotte, G. Lapalme, and F. Major. Exploring the conformations of nucleic acids. *J. Funct. Prog.*, 5(3):443–460, 1995.

[21] M. Feeley, M. Turcotte, and G. Lapalme. Using Multilisp for solving constraint satisfaction problems: an application to nucleic acid 3D structure determination. *LISP AND SYMBOLIC COMPUTATION*, 7(2/3):232–247, 1994.

[22] F. Major, M. Turcotte, , D. Gautheret, G. Lapalme, E. Fillion, and R. Cedergren. The combination of symbolic and numerical computation for three-dimensional modeling of RNA. *Science*, 253:1255–1260, September 1991.

Papers in refereed conferences submitted

Papers in referred conference proceedings

[1] Kevin Sutanto and Marcel Turcotte. Extracting and evaluating features from RNA virus sequences to predict host species susceptibility using deep learning. In *13th International Conference on Bioinformatics and Biomedical Technology (ICBBT 2021)*, Northwestern Polytechnical University, Xi'an, China, May 21-23 2021.

[2] Kevin Sutanto and Marcel Turcotte. Assessing the use of secondary structure fingerprints and deep learning to classify RNA sequences. In *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, Seoul, South Korea, December 16-19 2020.

[3] Manuel Belmadani and Marcel Turcotte. MotifGP: Using multi-objective evolutionary computing for mining network expressions in DNA sequences. In *IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2016)*, Chiang Mai, Thailand, October, 5-7, 2016 2016.

[4] Isra Al-Turaiki, Ghada Badr, Marcel Turcotte, and Hassan Mathkour. Incremental structural motif discovery. In *International Symposium on Bioinformatics Research and Applications (ISBRA)*, 2013.

[5] Alexander Gawronski and Marcel Turcotte. Novel framework for the discovery of RNA elements and its application to *Euglenozoa*. In *International Symposium on Bioinformatics Research and Applications (ISBRA)*, 2013.

[6] Oksana Korol and Marcel Turcotte. Learning relationships between over-represented motifs in a set of DNA sequences. In *CIBCB 2012 : IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, San Diego, USA, May 9–12 2012.

[7] Sandrine Moreira, Marcel Turcotte, and Gertraud Burger. NGS: Neglected genome sequencing assembly and annotation challenges in a highly divergent protozoan genome. In *JOBIM 2011 : Journées Ouvertes en Biologie, Informatique et Mathématiques*, Paris, France, June 28 – July 1 2011.

[8] Ghada Badr and Marcel Turcotte. Component-based matching for multiple interacting rna sequences. In Jianer Chen, Jianxin Wang, and Alexander Zelikovsky, editors, *Bioinformatics Research and Applications*, volume 6674 of *LNCS*, pages 73–86. Springer Berlin / Heidelberg, 2011.

[9] Mikhail Jiline, Stan Matwin, and Marcel Turcotte. Annotation concept synthesis and enrichment analysis: a logic-based approach to interpretation of high-throughput experiments. In A. Farzindar and V. Keselj, editors, *Canadian Conference on Artificial Intelligence 2010*, Lecture Notes in Artificial Intelligence 6085, pages 304–308, Ottawa, May 31–June 2 2010.

[10] Étienne Ogoubi, David Pouliot, M. Turcotte, and Abdelhakim Hafid. Parallel multiprocessor approaches to the RNA folding problem. In *Parallel Processing and Applied Mathematics*, pages 1230–1239, 2008.

[11] Étienne Ogoubi, Abdelhakim Hafid, and M. Turcotte. An Isometric on on-Chip Multiprocessor Architecture. In *Electronics, Circuits and Systems, 2007. ICECS 2007. 14th IEEE International Conference on*, pages 991–994, December 11–14, 2007 2007.

[12] M. Anwar and M. Turcotte. An approach to selecting putative RNA motifs using MDL principle. In *BIO-COMP'06 — The 2006 International Conference on Bioinformatics & Computational Biology*, pages 560–565, Las Vegas, Nevada, USA, June 26–29 2006.

[13] M. Anwar and M. Turcotte. Evaluation of RNA secondary structure motifs using regression analysis. In *IEEE CCECE 2006 — Canadian Conference on Electrical and Computer Engineering*, pages 1716–1721, Ottawa, Canada, May 7–10 2006.

[14] T. Nguyen and M. Turcotte. Exploring the space of RNA secondary structure motifs using suffix arrays. In S. Blair *et al.*, editor, *6th International Symposium on Computational Biology and Genome Informatics (CBGI 2005)*, pages 1291–1298, Salt Lake City, Utah, USA, July 21-26 2005.

[15] B. Masoumi and M. Turcotte. Simultaneous alignment and structure prediction of RNAs: Are three input sequences better than two? In V.S. Sunderam, G.D. van Albada, P.M.A. Sloot, and J. Dongarra, editors, *2005 International Conference on Computational Science (ICCS 2005)*, Lecture Notes in Computer Science 3515, pages 936–943, Atlanta, USA, May 22-25 2005.

[16] V. Jin and M. Turcotte. Detecting localized interspersed motifs in genomic sequences. In *IMTC/05 IEEE Instrumentation and Measurement Technology Conference*, pages 267–270, Ottawa, Canada, May 17-19 2005.

[17] M. Turcotte, S.H. Muggleton, and M.J.E. Sternberg. Application of inductive logic programming to discover rules governing the three-dimensional topology of protein structure. In C. D. Page, editor, *Proc. of the 8th International Workshop on Inductive Logic Programming (ILP-98)*, Lecture Notes in Artificial Intelligence 1446, pages 53–64, Berlin, 1998. Springer-Verlag.

Abstracts and/or papers read

[1] Bhagya C Thimmappa, Lila Naouelle Salhi, Lise Forget, Matt Sarrasin, Peniel Bustamante Villalobos, Marcel Turcotte, B. Franz Lang, and Gertraud Burger. Cranberry plant growth promotion by a fungal endosymbiont. In *16th European Conference on Fungal Genetics*, Innsbruck, Austria, March, 5–8 2023. Poster.

[2] Bhagya C Thimmappa, Lila Naouelle Salhi, Lise Forget, Matt Sarrasin, Peniel Bustamante Villalobos, Marcel Turcotte, B. Franz Lang, and Gertraud Burger. Endophytic fungi as biocontrol agents of cranberry plant pathogens. In *16th European Conference on Fungal Genetics*, Innsbruck, Austria, March, 5–8 2023. Talk and Poster.

[3] Bhagya C Thimmappa, Lila Naouelle Salhi, Lise Forget, Matt Sarrasin, Peniel Bustamante Villalobos, Marcel Turcotte, B. Franz Lang, and Gertraud Burger. Plant pathogen resistance and growth promotion: the role of fungal endosymbionts (secrete life inside plants: the role of fungal endosymbionts). In *XIII International Fungal Biology Conference (IFBC) & IV International Symposium on Fungal Stress (ISFUS)*, São José dos Campos, SP, Brazil, September 25 – 29 2022. Journal of Fungi Gold Award.

[4] Aseel Awdeh, Marcel Turcotte, and Theodore J. Perkins. Cell type specific DNA signatures of transcription factor binding. In *Intelligent Systems for Molecular Biology (ISMB) 2022*, July 10–14 2022.

[5] Aseel Awdeh, Marcel Turcotte, and Theodore J. Perkins. Cell type specific binding preferences of transcription factors. In *Great Lakes Bioinformatics Conference, GLBIO 2021*, May 10–13 2021.

[6] Aseel Awdeh, Marcel Turcotte, and Theodore J. Perkins. WACS: Improving peak calling by optimally weighting controls. In *Great Lakes Bioinformatics Conference, GLBIO 2019*, May 19–22 2019.

[7] Andrew Sowinski, Marcel Turcotte, Gilbert Arbez, and David Taylor. One-minute quizzes to identify potential students atc risk in engineering courses. In *Proceedings of the Canadian Engineering Education Association (CEEA)*, University of Toronto, June 4–7 2017.

[8] Mikhail Jiline, Stan Matwin, and Marcel Turcotte. Annotation concept synthesis and enrichment analysis: A logic-based approach to the interpretation of high-throughput biological experiments. In *2012 Learning Workshop*, Snowbird, Utah, April 3-6 2012. Computational and Biological Learning Society and the NIPS.

[9] S. Moreira, S. Breton, M. Valach, M. Aoulad Aissa, M Turcotte, and G Burger. Identification of an elusive trans-splicing machinery. In *Annual meeting of the Society for Molecular Biology & Evolution (SMBE 2012)*, Dublin, Ireland, June 23-26 2012. Poster.

[10] Sandrine Moreira, Marcel Turcotte, and Gertraud Burger. In silico identification of the elusive trans-splicing machinery of a highly divergent protozoan. In *2011 MonBUG Bioinformatics Symposium*, Montréal, September 23 2011.

[11] Sandrine Moreira, Marcel Turcotte, and Gertraud Burger. Diversité géomique : le curieux mode d'expression des gènes d'un eucaryote unicellulaire. In *Association francophone pour le savoir (ACFAS)*, Sherbrooke, Canada, May 9–13 2011.

[12] Georgette Kiethega, Marcel Turcotte, and Gertraud Burger. Nouveau mécanisme de trans-splicing dans la mitochondrie des diplonḿides. In *Association francophone pour le savoir (ACFAS)*, Sherbrooke, Canada, May 9–13 2011.

[13] Oksana Korol and Marcel Turcotte. Mining for relationships between biological markers in high-throughput sequence data. In *2011 MonBUG Bioinformatics Symposium*, Montréal, September 23 2011.

[14] Gertraud Burger, Georgette Kiethega, and Marcel Turcotte. Unconventional trans-splicing and RNA-editing in mitochondria of an Euglenozoan. In *ICPMB 2011. International Conference for Plant Mitochondrial Biology*, Hohenroda, Germany, May 14–19 2011.

[15] Oksana Korol and Marcel Turcotte. Module Inducer — a tool to automatically extract knowledge from biological sequences. In *RECOMB2011, 15th Annual International Conference of Research in Computational Molecular Biology*, Vancouver, March 28–31 2011.

[16] Yifei Yan, Seyed Amir Malekpour, Marcel Turcotte, Georgette Kiethega, and Gertraud Burger. RNA editing and trans-splicing directed by gRNAs? In *2011 Gordon Research Conference on RNA Editing*, January 9–14 2011. Poster.

[17] Sandrine Moreira, Marcel Turcotte, and Gertraud Burger. Analysis of potential nuclear RNA editing sites in a highly divergent protozoa. In *2010 Robert Cedergren Bioinformatics Colloquium*, 2010.

[18] Seyed Amir Malekpour, Marcel Turcotte, and Gertraud Burger. gRNA mediated trans-splicing of gene modules in *diplonema papillatum*. In *2010 Robert Cedergren Bioinformatics Colloquium*, 2010.

[19] Georgette Kiethega, Marcel Turcotte, and Gertraud Burger. *cox1* gene fragmentation and rna editing in diplonemid mitochondria. In *18th meeting of International Society for Evolutionary Protistrogy (ISEP XVIII)*, Kanazawa, Japan, July 2–7 2010 2010.

[20] S. Kannan, M. Turcotte, and M. Burger. Automated (RNA) motifs discovery in the mitochondrial genome of *diplonema papillatum*. Oral presentation, Robert Cedergren Bioinformatics Colloquium 2008, Montréal, Canada, 2008.

[21] M. Jiline, K. Baetz, M. Turcotte, and S. Matwin. Knowledge enriched mining of systematic genome screens using inductive logic programming. In *Progress in Systems Biology 2006*, Ottawa, November 9 and 10 2006. Oral presentation.

[22] S. Baird, M. Turcotte, R. Korneluk, and M. Holcik. Discovery of novel internal ribosome entry site motifs from searches with the XIAP IRES structure. 2006 Cold Spring Harbor Laboratory Meeting on Translational Control, Poster, September 6 – 10 2006.

[23] S. Baird, M. Turcotte, R. Korneluk, and Holcik M. Searching for IRES structurally similar to the XIAP IRES. In RNA 2005, the Tenth Annual Meeting of the RNA Society, Banff, Canada. Poster #566, May 24-29 2005.

[24] S. Baird, M. Turcotte, R. Korneluk, and Holcik M. Searching for IRES. CIHR National Student Research Poster Competition, Winnipeg, Canada, Poster Session, June 7-8 2005.

[25] B. Masoumi and M. Turcotte. A dynamic programming algorithm for [the] simultaneous alignment and structure prediction of 3 RNA sequences. BioNorth 2004 — 11th Annual Ottawa Life Sciences International Conference & Exhibition, Poster #114, Nov 29-Dec 1st 2004.

[26] S. Baird, M. Turcotte, R. Korneluk, and Holcik M. Structural determination of internal ribosome entry sites with currently available software. In RNA 2004, the Ninth Annual Meeting of the RNA Society, Madison, Wisconsin, Poster Session, June 1-6 2004.

[27] S. Baird, M. Turcotte, R. Korneluk, and M. Holcik. Searching for IRES. In The Canadian Genetic Diseases Network Annual Scientific Meeting, Kimberly, Ontario, Poster Session, May 27-30 2004.

[28] M. Turcotte. Détermination de structures secondaires conservées dans les ARNs: Application à l'étude des transcrits du gène c-myc des mammifères. 72e congrès de l'ACFAS, Montréal, Canada, May 10-14 2004. Oral Presentation.

[29] S. Baird, S. Balabanian, R. G. Korneluk, M. Turcotte, and M. Holcik. Unique sequence characteristics of internal ribosome entry sites useful for database search. BioNorth 2002 — 9th Annual Ottawa Life Sciences International Conference & Exhibition, Poster session, November 4–6 2002.

[30] M. Turcotte. Automatic discovery of structural motifs. First Canadian Working Conference on Computational Biology (CCCB'00), November 12 2000. Oral Presentation.

[31] M. Turcotte, S.H. Muggleton, and M.J.E. Sternberg. Generating protein three-dimensional folds signatures using inductive logic programming. In *2000 Convention of the Society for the Study of Artificial Intelligence and the Simulation of Behaviour*, Birmingham, UK, April 17-20 2000. Oral Presentation.

[32] M. Turcotte, S.H. Muggleton, and M.J.E. Sternberg. Learning protein structure principles. In *The 17th Machine Intelligence Workshop*, Suffolk, UK, July 19-21 2000. Oral Presentation.

[33] M. J. E. Sternberg, P. A. Bates, L. A. Kelley, R. M. MacCallum, A. Müller, S. Muggleton, and M. Turcotte. Exploiting protein structure in the post-genome era. In *Intelligent Systems for Molecular Biology 1999*, 1999. Oral Presentation.

[34] M. Turcotte, S.H. Muggleton, and M.J.E. Sternberg. Learning rules which relate local structure to specific protein taxonomic classes. In *The 16th Machine Intelligent Workshop*, King's Manor, York, December 1–3 1998.

[35] M. Turcotte, S.H. Muggleton, and M.J.E. Sternberg. A Prolog database unifying taxonomic and structural information. In *Intelligent Systems for Molecular Biology (ISMB 1998) Book of Abstracts, Poster Session*, Montréal, Canada, June 28–July 1 1998.

[36] M. Turcotte and M. Feeley. A parallel functional program for searching a discrete space of nucleic acid 3d structures. In *Dagstuhl-Seminar*, Germany, 1994. Oral Presentation.

[37] F. Major, M. Turcotte, and G. Lapalme. Constraint satisfaction in functional programming. In *Principles and Practice of Constraint Programming*, pages 174–177, Newport, Rhode Island, April 28–30 1993.

[38] M. Turcotte, G. Lapalme, and R. Cedergren. A measure of association for coordinated substitutions in proteins. In *Book of Abstracts*, Patterns of Biological Organizations, Rensselaerville, NY, October 1992. 1992 Albany Conference. Poster Session.

[39] D. Gautheret, M. Turcotte, R. Cedergren, F. Major, and G. Lapalme. Modeling and prediction of RNA 3-D structures by combining symbolic and numerical approaches. *J. Biomol. Struct. Dynam.*, 8(6):a061, June 1991.

[40] R. Cedergren, F. Major, D. Gautheret, E. Fillion, L. Jolicoeur, M. Turcotte, and R. Cedergren. A 3-D model of the hammerhead domain derived from experimental and topological constraints. International Conference on Catalytic RNA as Anti-HIV agent: Design and Delivery to Cells, San Diego, California, October 1990. Oral Presentation.

[41] M. Turcotte, F. Major, G. Lapalme, D. Gautheret, E. Fillion, and R. Cedergren. Using functional and logic programming in molecular graphics applications. 9th annual meeting of the Molecular Graphics Society, helded Uppsala, Sweeden, Poster Session, July 1990.

[42] M. Turcotte, G. Lapalme, R. Cedergren, and F. Major. A user-interface for the folding and unfolding system (FUS). 1st C.I.A.R. Evolution Group Meeing for Graduate Students, Université de Montréal, Montréal, Canada, Oral Presentation, 1989.

Contributions to publications via supervisions

[1] Aseel R. Awdeh. *Wide scale analysis of transcription factor biases and specificity.* Computer science, University of Ottawa, November 2022.

[2] Kevin Sutanto. RNA sequence classification using secondary structure fingerprints, sequence-based features, and deep learning. Master of computer science, University of Ottawa, School of Electrical Engineering and Computer Science, 2021.

[3] Amirhossein Hajianpour. A simple and fast homology-based gene prediction in mitochondrial genomes. Computer science, University of Ottawa, School of Electrical Engineering and Computer Science, December 2021.

[4] Sandrine Moreira. *Décodage de l'expression de gènes cryptiques.* Bio-informatique, Université de Montréal, Département de Biochimie et Médecine moléculaire, March 2017.

[5] Manuel Belmadani. MotifGP: DNA motif discovery using multiobjective evolution. Master of computer science, University of Ottawa, School of Electrical Engineering and Computer Science, 2016.

[6] Aseel Awdeh. The potential power of dynamics in epistasis analysis. Master of computer science, University of Ottawa, School of Electrical Engineering and Computer Science, 2015.

[7] Alexander Gawronski. RiboFSM: Frequent subgraph mining for the discovery of RNA structures and interactions. Master's thesis, School of Electrical Engineering and Computer Science, University of Ottawa, 2013.

[8] Oksana Korol. ModuleInducer: automating the extraction of knowledge from biological sequences. Master's thesis, University of Ottawa, School of Electrical Engineering and Computer Science, Defended on September 20, 2011 2011.

[9] Mikhail Jiline. *Annotation Concept Synthesis and Enrichment Analysis: a Logic-Based Approach to the Interpretation of High-Throughput Biological Experiments.* PhD thesis, Ottawa-Carleton Institute for Computer Science, University of Ottawa, 2011.

[10] Etienne Elie. *Approche efficace pour la conception des architectures multiprocesseurs sur puce électronique.* Informatique, Université de Montréal, Département d'informatique et de recherche opérationnelle, December 2011.

[11] Predrag Mizdrak. Novel iterative approach to joint sequence alignment and tree inference under maximum likelihood: a critical assessment. Master's thesis, Ottawa-Carleton Institute for Computer Science, University of Ottawa, 2008.

[12] Stephen Baird. *Searching for IRES.* PhD thesis, Human and Molecular Genetics Program, Biochemistry, Microbiology and Immunology Department, Faculty of Medicine, University of Ottawa, 2006.

[13] Mohammad Anwar. Implementation and evaluation of scoring schemes for the automated discovery of nucleic acid structures. Master's thesis, Ottawa-Carleton Institute for Computer Science, 2006.

[14] Mohak Shah. *Sample Compression, Margins and Generalization: Extensions to the Set Covering Machine.* PhD thesis, Ottawa-Carleton Institute for Computer Science, University of Ottawa, 2006.

[15] Beeta Masoumi. A dynamic programming algorithm for the simultaneous alignment and structure prediction of three RNA sequences. Master's thesis, School of Information Technology and Engineering, Faculty of Engineering, University of Ottawa, 2005.

[16] Truong Nguyen. Efficient determination of concensus secondary structures in RNA. Master of applied science in engineering, School of Information Technology and Engineering, Faculty of Engineering, University of Ottawa, 2004.

[17] Victor Jin. A computational approach to the analysis of localized interspersed motifs in complete genomic sequences. Master's thesis, Ottawa-Carleton Institute for Computer Science, 2003.

Other contributions

[1] E. Ogoubi, Hafid A., and Turcotte M. An isometric on chip multiprocessor architecture. Technical Report 1287, Université de Montréal, June 2006.

Supervision

Years	Name	Degree	Topic	Status
2019–	Bhagya C Thimmappa	Ph.D.[†‡]	Plant-microbe interactions	In progress
2019–21	Kevin Sutanto	M.C.S.	RNA Structure Fingerprints	Completed
2018–21	Amirhossein Hajianpour	M.C.S.	Gene annotation of short exons	Completed
2016–20	Imane Chdaoui	M.C.S.	Non-coding RNA precursors	Incomplete
2015–22	Aseel Awdeh	Ph.D[†]	Co-supervision with T. Perkins	Completed
2014–19	Alkaldi Wejdan	Ph.D.	To be determined	Incomplete
2013–15	Aseel Awdeh	M.Sc.[†]	Co-supervision with T. Perkins	Completed
2012–15	Manuel Belmadani	M.Sc.	MotifGP	Completed
2011–13	Alexander Gawronski	M.C.S.	RiboFSM – Frequent Subgraph Mining	Completed
2010–16	Sandrine Moreira Rousseau	Ph.D.[†‡]	RNA processing genes	Completed
2009–11	Oksana Korol	M.Sc.	Promotors architecture	Completed
2009–11	Ghada Badr	PDF	Multiple String Pattern Matching	Completed
2008–08	Predrag Mizdrak	M.Sc.[†]	Alignment and tree inference under ML	Completed
2008	Sivakumar Kannan	PDF[†‡]	Guide RNAs	Completed
2006–08	Abolfazl Keshtkar	Ph.D.	Detection of noncoding RNAs	Incomplete
2006–11	Misha Jiline	Ph.D.[†]	Relational learning and systems biology	Completed
2006–11	Etienne Ogoubi	Ph.D.[†‡]	Architecture and RNA Algos	Completed
2006–08	Abdelmounaim Dahbi	M.Sc.	RNA Motifs Discovery	Incomplete
2006–07	Amir Hossein Razavi	Ph.D.	RNA Secondary Structure	Incomplete
2004–06	Mohammad Anwar	M.Sc.	RNA Motifs Discovery	Completed
2003–05	Beeta Masoumi	M.Sc.	RNA Secondary Structure	Completed
2002–04	Truong Nguyen	M.Sc.	RNA Motifs Discovery	Completed
2001–06	Mohak Shah	Ph.D.[†]	Set Covering Machines	Completed
2001–06	Stephen Baird	Ph.D.[†]	IRES Motifs	Completed
2001–03	Victor Jin	M.Sc.	DNA Motifs Discovery	Completed

† Co-supervision
‡ Université de Montréal

Services

University Service

2020–23	Senate Committee on the Evaluation of Undergraduate Programs (SCEUP), Chair
2020–23	Senate Graduate Program Evaluation Committee (GPEC), Chair
2020–23	Council on Undergraduate Studies, ex officio
2020–23	Council on Graduate Studies, ex officio
2018–23	Senate Committee on Teaching and Teaching Evaluation (SCTTE)
2018–19	Working Group on Academic Integrity
2018	*Groupe de travail sur la francophonie*
2012–18	Council on Undergraduate Studies, ex officio
2010–11	Associate Director of the Ottawa-Carleton Joint Collaborative Program in Bioinformatics
2010–11	Faculty of Graduate and Postdoctoral Studies Theses Sub-Committee
2006–08	Co-op Co-ordinating Committee
2004	Member of the steering committee for the creation of the Institute for Systems Biology and Centre in Bioinformatics at the University of Ottawa

Faculty Service

2022–23	Faculty Council
2018–19	Academic Integrity Inquiry Committee
2012–18	Faculty Curriculum Committee, Chair
2012–18	Faculty Council, ex officio

School Service

2018–19	Computer Science Curriculum Committee
2011–12	EECS Appointments Committee
2009–11	Computer Science and Software Engineering Promotion Ambassador
2006–08	Co-Op Coordinator for the Computer Science program
2002–03	School Computing Facilities Committee
2001–02	NSERC/OGS Computer Science Scholarship Committee
2001–02	School Space Committee

Service to the Community

2023	External expert for the evaluation of the graduate programs in Computer Science and Software Engineering at *Université de Sherbrooke*
2022	External expert for the creation of a Computer Science doctorate degree at *Université du Québec à Chicoutimi*
2014	External expert for the evaluation of the undergraduate Computer Science program at *Université Laval*
2010	External expert for the evaluation of the Bioinformatics programs at *Université de Montréal*
2007–08	Work on Canadian Health Institutes Strategic Training Initiative in Health Research Grant Application *(Joint initiative U. Montréal, U. Ottawa and Carleton, Co-applicant and Coordinator for Ottawa)*
2004	Reviewer for a bioinformatics book project for Oxford University Press
2002–03	Canadian Bioinformatics Workshops (local coordination)
2002	Member of the Human Research Ethics Board, University of Ottawa Heart Institute
1995–97	Consultant for EraGene
	Reviewer for journals: Nucleic Acids Research, Journal of Molecular Biology, Bioinformatics, BMC Bioinformatics, Computer Methods and Programs in Biomedicine, Machine Learning, Current Medicinal Chemistry, BioSystems, J. Molecular Graphics and Modelling
	Reviewer for granting agencies: NSERC, *Fonds de Recherche du Québec Nature et Technologies (FRQNT)*, *Fonds de Recherche du Québec en Santé, double chaire IA et santé [FRQS]*, Michael Smith Foundation for Health Research (British Columbia), Peer Reviewer (PR) for the National Priorities Research Program (NPRP), Qatar National Research Fund (QNRF)

Scientific Committees

2022	14th International Conference on Bioinformatics and Biomedical Technology (ICBBT)
	May 27-29, 2022, Northwestern Polytechnical University, Xi'an, China (PCM)
2021	13th International Conference on Bioinformatics and Biomedical Technology (ICBBT)
	May 21-23, 2021, Northwestern Polytechnical University, Xi'an, China (PCM)
2019	10th Annual Conference of the Canadian Engineering Education Association (CEEA)
	CEEA 2019, June 8-12, 2019 - Ottawa, Canada (Scientific Program Co-chair)
2018	Ninth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies
	BIOTECHNO 2018, May 20, 2018 to May 24, 2018 - Nice, France (PCM)
2017	Ninth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies
	BIOTECHNO 2017, May 21 - 25, 2017 - Barcelona, Spain (PCM)
2016	Eighth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies
	BIOTECHNO 2016, June 26 - 30, 2016 - Lisbon, Portugal (PCM)
2015	Seventh International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies
	BIOTECHNO 2015, May 24 - 29, 2015 - Rome, Italy (PCM)
2014	External expert for the evaluation of the undergraduate computer science program at Université Laval
2014	Sixth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies
	BIOTECHNO 2014, April 20 - 24, 2014 - Chamonix, France (PCM)
2013–	International Association for Pattern Recognition (IAPR)
	Member of the Technical Committee 20 (TC20)

Scientific Committees (continued)

2013	Honoring 50 years of Models and Algorithms for Genome Evolution (MAGE) from David Sankoff
	August 23–26, 2013, Bromont, Québec, Canada (PCM)
2013	9th International Symposium on Bioinformatics Research and Applications (ISBRA2013)
	May 20–22, 2013 in Charlotte, North Carolina, USA (PCM)
2013	Eight IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2013)
	June 17–19 2013, Nice, France (PCM)
2013	Tenth International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics
	(CIBB 2013) June 20–22 2013, Nice, France (PCM)
2012	23rd Genome Informatics Workshop (GIW), Dec 12-14, Tainan, Taiwan, (PCM)
2012	8th International Symposium on Bioinformatics Research and Applications (ISBRA2012) (PCM)
2011–	Editorial review board member for Frontiers in Systems Biology
2010	Member of the Scientific Program Committee for the Robert-Cedergren Colloquium 2010
2010	Member of the Local Organizing Committee for the 2010 RECOMB satellite workshop on
	comparative genomics, University Ottawa, October 9–11
2009	Member of the Biomedical Engineering Technical Program Committee (TPC) of the
	IEEE Toronto International Conference Science and Technology for Humanity (TIC-STH '09)
2009	Member of the Organizing Committee for the Robert-Cedergren Colloquium 2009
2008–09	Member of the program committee for the 2009 Canadian Artificial Intelligence Conference (AI09)
2008	Member of the Scientific Program Committee for the Robert-Cedergren Colloquium 2008
2007–08	Member of the program committee for the 2008 Canadian Artificial Intelligence Conference (AI08)
2007-08	Member of the Biomedical Engineering Technical Program Committee (TPC) of the
	IEEE Canadian Conference on Electrical and Computer Engineering 2008 (CCECE'08)
	to be held May 4-7, 2008 in Niagara Falls, Ontario, Canada
2007	Member of the technical program committee of the Bioinformatics Track for the Conference
	BIONETICS 2007, Budapest, Hungry, 10–12 December 2007 (an event sponsored by IEEE and ACM)
2006-007	Member of the program committee for the 2007 Canadian Artificial Intelligence Conference (AI07)
2006	Judge for the Robert-Cedergren Bioinformatics Colloquium, Montréal, November 14–15, 2006
2005–06	Member of the program committee for the 2006 Canadian Artificial Intelligence Conference (AI06)
2005	Judge for the Robert-Cedergren Bioinformatics Colloquium, Montréal, November 2–4, 2005
2005–08	Member of *Comité des bourses d'excellence biT (bio-informatique) du programme stratégique de bourses de formation des Instituts de recherches en santé du Canada*
2004	Scientific Committee for JOBIM (*Journées Ouvertes de Biologie, Informatique et Mathématiques*)
	Montréal, June 28-30, 2004

Invited Talks

- Learning relationships between over-represented motifs in a set of DNA sequences. The First Bioinformatics Scientific Meeting in KSU (BioSM-KSU). Invited Speaker. King Saud University (KSU), May 4, 2014.

- Consensus RNA secondary structures determination. Université du Québec en Outaouais. February 24, 2010.

- Automated (RNA) motifs discovery in the mitochondrial genome of *Diplonema papillatum*, University of Ottawa, Faculty of Medicine, RNAClub. May 6, 2009.

- Predicting the consensus RNA secondary structure for $k > 2$ sequences, University of Memphis, February 27, 2009.

- Applying Relational Learning to Structural Molecular Biology Problems, IEEE Computational Intelligence Society (CIS) — Ottawa Chapter, 2008/07/03.

- Bioinformatics 101. Interview at CHUO, the radio station on the campus of the University of Ottawa, 2007/10/19.

- Simultaneous Progressive Pairwise Alignment of Multiple Sequences and RNA Secondary Structure Prediction. University of Ottawa, Faculty of Medicine, RNAClub. January 3, 2007.

- Prédiction de la structure secondaire commune à k ARNs, pour $k > 2$. Université de Montréal, Colloque du DIRO. November 16, 2006.

- Consensus RNA secondary structures determination. University of Ottawa, Faculty of Medicine, RNAClub. February 1, 2006.

- Consensus RNA secondary structures determination. University of Ottawa, Mathematics and Statistics Probability and Statistics Seminars. November 11, 2005.

- Two computational approaches to RNA secondary structure motifs discovery. Ottawa — Carleton Combinatorics and Optimization Seminar. Friday, March 4, 2005.

- Computational RNAomics. 2005 University of Ottawa Research Showcase, Advanced Technologies for Better Health Tuesday, February 22, 2005.

- Deux approches informatiques à la découverte de motifs de structure secondaire d'ARNs. Conférences Robert-Cedergren, Université de Montréal, February 21, 2005.

- Exploring the space of RNA secondary structure motifs. TAMALE Seminars, University of Ottawa, September 16, 2004.

- Pattern Discovery in Genomics Data. TAMALE Seminar, University of Ottawa. January 24, 2003.

- How mathematics & computer science saved the Human Genome project. Annual Meeting of the Ontario Association for Mathematics Education, Ottawa, February 22, 2002.

- Bioinformatics: an example of interdisciplinary research. 5th Annual Interdisciplinary Conference, organized by the Graduate Students of the University of Ottawa, February 15-17, 2002.

- Mining Knowledge of Protein Topology — Application of Inductive Logic Programming to Discover Structural Principles. Department of Biology. September 21, 2000.

- Mining Knowledge of Protein Topology — Application of Inductive Logic Programming to Discover Structural Principles. BBSRC. Cambridge. February 29, 2000.

- Application of Inductive Logic Programming to Discover Rules Explaining Protein Three-Dimensional Structure. BBSRC. October 21, 1999.

- Application of Inductive Logic Programming to Structural Molecular Biology Problems. University of Toronto, University of Ottawa, Biotechnology Research Institute (Montreal), University of Montreal, Université de Sherbrooke, University of Florida, 1999.

- University of Beijing, Beijing, China, Ocbtober 1997.

- Millennium Pharmaceuticals, Boston, USA, 1996.

- Smithkline Beecham, Philadelphia, USA, 1996.

Further Academic Activities

- I am actively involved with all the efforts of the Faculty of Engineering to create new bioinformatics programs at the undergraduate and graduate levels. I have developed a bioinformatics course, CSI 4126 Algorithms in bioinformatics. I have also developed a service course, CSI 2303 Computing Concepts for Genomics, for the Department of Biology.

- Instructor for the new course "Introduction to Programming" for the Canadian Bioinformatics Workshops (CBW), Montreal, July 15–27, 2002, instructor and local host for the "Bioinformatics" course from CBW, Ottawa, May 26 – June 7, 2003.

Professional societies

International Society for Computational Biology (ISCB)

Personal Development

- Santé et sécurité - rôles et responsabilités (17 juin 2023)

- Internationalisation of the Curriculum in Higher Education, with Professor Emerita Betty Leask, from La Trobe University, Australia (May 12, 2021 to June 16, 2021, 5 sessions)

- *Autodéfense numérique* (July 12, 2019)

- BI-1200 *Veille stratégique (cours avancé) : Créer des rapports* (November 3, 2016)

- BI-1100 *Veille stratégique (cours de base) : Utiliser le tableau de bord et les rapports types* (October 26, 2016)

- PS-2100 *Session de mise à niveau pour employés (transactions effectuées par les étudiants et les professeurs)* (October 26, 2016)

- PS-1100 Access to uoCampus Data and Information (October 25, 2016)

- Students in Distress and Intervention Strategies (September 20, 2016)

- *Initiation au modèle de conseillance scolaire* (March 16, 2016)

- International Students: Teaching Toward the Success of All Students (January 15, 2016)

- *Gestion du temps pour leaders universitaires* (December 15, 2015)

- Understanding the Budgeting Process at uOttawa (September 29, 2015)

- *L'harcèlement et l'agression à caractère sexuel faite aux filles et aux femmes* (September 16, 2015)

- *Comment contribuer au développement et au maintien d'un climat de confiance lors d'un changement au travail* (September 11, 2015)

- *Sensibilisation des superviseurs à la santé et à la sécurité* (May 18, 2015)

- *Sensibilisation des travailleurs à la santé et à la sécurité* (May 18, 2015)

- *Travaillons ensemble: Le Code des droits de la personne de l'Ontario et la LAPHO* (May 17, 2015)

- *Respect en milieu de travail* (May 16, 2015)

- *Prévention de la violence* (May 15, 2015)

- Accessibility Standards for Customer Service (November 30, 2012)

- Workplace Hazardous Materials Information System (WHMIS) - for office workers (October 19, 2012)

- Leadership Development Workshop (December 8–9, 2011)

- Workshop "L'art du théatre et l'enseignement" (Octobre 12, 2010)

- *Loi sur l'accessibilité pour les personnes handicapées de l'Ontario* (April 28, 2009)

- Roles and Responsibilities Training (Ontario Health and Safety Act) (November 29, 2006, April 27, 2012)

- Teamwork and Strategic Collaborations (April 18–19, 2005)