

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– Director Cyclical Program Reviews, Office of Vice-Provost, Academic Affairs
- 2016– Full Professor School of Electrical Engineering and Computer Science, University of Ottawa
- 2013–2018 Vice-Dean Undergraduate Studies, Faculty of Engineering, University of Ottawa
- 2012 Interim Vice-Dean Undergraduate Studies, Faculty of Engineering, University of Ottawa
- 2008–2009 Invited Professor Biochemistry Department, Université de Montréal
- 2007– Associate Professor School of Electrical Engineering and Computer Science, University of Ottawa
- 2000–2007 Assistant Professor School of Electrical Engineering and Computer Science, University of Ottawa
- 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 <i>Bioinformatics Tools to Assist Functional Genomics</i> \$56,000
2002–2007	Project Leader, CFI/OIT New opportunities <i>Computing Infrastructure for Bioinformatics, Coding and Cryptography, and Algorithm Design</i> \$399,642
2002–2003	Principal Investigator, Communication & Information Technology Ontario <i>Learning Grammatical Representations of Regulatory Elements</i> \$40,000
2003	Co-applicant, CHEO Seed Fund \$30,000
2000	Startup \$50,000

Publications

Papers submitted to refereed journals

- [1] **Kevin Sutanto** and **Marcel Turcotte**. Assessing global-local secondary structure fingerprints to classify RNA sequences with deep learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics Special Issue*, Submitted on 2021-02-28; Major Revision Requested on 2021-05-12.

Papers in refereed journals

- [1] **Aseel Awdeh**, **Marcel Turcotte**, and **Theodore J. Perkins**. WACS: improving ChIP-seq peak calling by optimally weighting controls. *BMC Bioinformatics*, 22(1):69, 2021.
- [2] **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.
- [3] **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.
- [4] **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.
- [5] **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.
- [6] **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.
- [7] **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.
- [8] **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.
- [9] **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.
- [10] **S. D. Baird**, **M. Turcotte**, **R. G. Korneluk**, and **M. Holcik**. Searching for IRES. *RNA Journal*, 12(10):1755–1785, 2006.
- [11] **M. Anwar**, **T. Nguyen**, and **M. Turcotte**. Identification of consensus RNA secondary structures using suffix arrays. *BMC Bioinformatics*, 7:244, 2006.

- [12] **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.
- [13] 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.
- [14] 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.
- [15] 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.
- [16] 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.
- [17] 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.
- [18] 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.
- [19] M. Turcotte, G. Lapalme, and F. Major. Exploring the conformations of nucleic acids. *J. Funct. Prog.*, 5(3):443–460, 1995.
- [20] 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.
- [21] 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 *Lecture Notes in Computer Science*, pages 73–86. Springer Berlin / Heidelberg, 2011. 10.1007/978-3-642-21260-4_11.
- [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] **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.
- [2] **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.
- [3] Andrew Sowinski, Marcel Turcotte, Gilbert Arbez, and David Taylor. One-minute quizzes to identify potential students at risk in engineering courses. In *Proceedings of the Canadian Engineering Education Association (CEEA)*, University of Toronto, June 4–7 2017.
- [4] **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.

- [5] **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.
- [6] **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.
- [7] **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.
- [8] Georgette Kiethega, Marcel Turcotte, and Gertraud Burger. Nouveau mécanisme de trans-splicing dans la mitochondrie des diplomnides. In *Association francophone pour le savoir (ACFAS)*, Sherbrooke, Canada, May 9–13 2011.
- [9] **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.
- [10] 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.
- [11] **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.
- [12] 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.
- [13] **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.
- [14] **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.
- [15] Georgette Kiethega, Marcel Turcotte, and Gertraud Burger. *cox1* gene fragmentation and rna editing in diplomemid mitochondria. In *18th meeting of International Society for Evolutionary Protistology (ISEP XVIII)*, Kanazawa, Japan, July 2–7 2010 2010.
- [16] **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.
- [17] **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.
- [18] **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.
- [19] **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.
- [20] **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.
- [21] **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.

- [22] **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.
- [23] **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.
- [24] 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.
- [25] **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.
- [26] M. Turcotte. Automatic discovery of structural motifs. First Canadian Working Conference on Computational Biology (CCCB'00), November 12 2000. Oral Presentation.
- [27] 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.
- [28] 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.
- [29] 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.
- [30] 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.
- [31] 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.
- [32] 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.
- [33] 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.
- [34] 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.
- [35] 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.
- [36] 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.
- [37] 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, Sweden, Poster Session, July 1990.
- [38] 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 Meeting for Graduate Students, Université de Montréal, Montréal, Canada, Oral Presentation, 1989.

Contributions to publications via supervisions

- [1] **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.
- [2] **Manuel Belmadani**. MotifGP: DNA motif discovery using multiobjective evolution. Master of computer science, University of Ottawa, School of Electrical Engineering and Computer Science, 2016.
- [3] **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.
- [4] **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.
- [5] **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.
- [6] **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.
- [7] **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.
- [8] **Stephen Baird**. *Searching for IRES*. PhD thesis, Human and Molecular Genetics Program, Biochemistry, Microbiology and Immunology Department, Faculty of Medicine, University of Ottawa, 2006.
- [9] **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.
- [10] **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.
- [11] **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.
- [12] **Truong Nguyen**. Efficient determination of consensus secondary structures in RNA. Master of applied science in engineering, School of Information Technology and Engineering, Faculty of Engineering, University of Ottawa, 2004.
- [13] **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.

Papers in preparation for referred journals

- [1] Aminur Rab Ratul, Marcel Turcotte, M. Hamed Mozaffari, and WonSook Lee. Prediction of 8-state protein secondary structures by 1D-Inception and BD-LSTM. *bioRxiv*, 2019.

Supervision

2019–	Bhagya C Thimmappa	Ph.D. ^{†‡}	Plant-microbe interactions	In progress
2019–21	Kevin Sutanto	M.C.S.	RNA Structure Fingerprints	Completed
2018–	Amirhossein Hajianpour	M.C.S.	Gene annotation of short exons	In progress
2016–	Imane Chdaoui	M.C.S.	Non-coding RNA precursors	In progress
2015–	Aseel Awdeh	Ph.D. [†]	Co-supervision with T. Perkins	Completed
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.	Promoters 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
2006–11	Misha Jiline	Ph.D. [†]	Relational learning and systems biology	Completed
2006–11	Etienne Ogoubi	Ph.D. ^{†‡}	Architecture and RNA Algos	Completed
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

2021	13th International Conference on Bioinformatics and Biomedical Technology (ICBBT) May 21-23, 2021, Northwestern Polytechnical University, Xi'an, China (Program Committee Member - 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)
- 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*
- 2010–11 Program coordinator of Ottawa-Carleton Joint Collaborative Program in Bioinformatics
- 2010–11 Associate Director of Ottawa-Carleton Joint Collaborative Program in Bioinformatics
- 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 Québec Recherche Nature et Technologies* and
Michael Smith Foundation for Health Research (British Columbia)
- Peer Reviewer (PR) for the National Priorities Research Program (NPRP),
Qatar National Research Fund (QNRF)

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.

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

- *Loi sur l'accessibilité pour les personnes handicapées de l'Ontario* (April 28, 2009)
- Workshop "L'art du théâtre et l'enseignement" (Octobre 12, 2010)
- Leadership Development Workshop (December 8–9, 2011)
- Workplace Hazardous Materials Information System (WHMIS) - for office workers (October 19, 2012)
- Accessibility Standards for Customer Service (November 30, 2012)
- *Prévention de la violence* (May 15, 2015)
- *Respect en milieu de travail* (May 16, 2015)
- *Travaillons ensemble: Le Code des droits de la personne de l'Ontario et la LAPHO* (May 17, 2015)
- *Sensibilisation des travailleurs à la santé et à la sécurité* (May 18, 2015)
- *Sensibilisation des superviseurs à la santé et à la sécurité* (May 18, 2015)
- *Comment contribuer au développement et au maintien d'un climat de confiance lors d'un changement au travail* (September 11, 2015)
- *L'harcèlement et l'agression à caractère sexuel faite aux filles et aux femmes* (September 16, 2015)
- Understanding the Budgeting Process at uOttawa (September 29, 2015)
- *Gestion du temps pour leaders universitaires* (December 15, 2015)
- International Students: Teaching Toward the Success of All Students (January 15, 2016)
- *Initiation au modèle de conseillanc scolaire* (March 16, 2016)
- Students in Distress and Intervention Strategies (September 20, 2016)
- PS-1100 Access to uoCampus Data and Information (October 25, 2016)
- PS-2100 *Session de mise à niveau pour employés (transactions effectuées par les étudiants et les professeurs)* (October 26, 2016)
- BI-1100 *Veille stratégique (cours de base) : Utiliser le tableau de bord et les rapports types* (October 26, 2016)
- BI-1200 *Veille stratégique (cours avancé) : Créer des rapports* (November 3, 2016)
- *Autodéfense numérique* (July 12, 2019)