### Curriculum Vitae

#### Abedalrhman Alkhateeb

**Contact:**

Work:

 Software Engineering Department, Princess Sumaya University for Technology

P.O.Box 1438 Al-Jubaiha – Amman, 11941 Jordan

Phone: +96265359949 x 5365

E-mail: a.lkhateeb@paut.edu.jo

 Home:

15-Ad-Diwan Street, Tela’a Al-Ali, Amman, Jordan

Phone: +962 79 871 9412

**Citizenships:** Canada/Jordan

**Languages:** English, Arabic

**Date of birth:** March 19, 1982

**Last updated:** 31/05/2022

##### Education

|  |  |
| --- | --- |
|  07/2018 | **Ph.D. in Computer Science**, University of Windsor, Canada. |
|  01/2011 | **Master’s in Computer Science**, University of Windsor, Canada. |
|  06/2004 | **Bachelor in Computer Science**, University of Jordan, Jordan.  |

**Employment Experience**

Academic:

09/2021 –present **Assistant Professor**, Software Engineering Department, Princess Sumaya University for Technology, Jordan.

04/2021 –02/2022 **Assistant Professor – Limited Term (2 years)**, School of Computer Science, University of Windsor, Canada

11/2019 –**present** **Adjunct Assistant Professor**, School of Computer Science, University of Windsor, Canada

05/2019 – 04/2021 **PostDoc Fellow,** Mitacs Accelerate PDF with ITOS Oncology and University of Windsor, Canada

08/2018 – 04/2018 **PostDoc Fellow,** School of Computer Science, University of Windsor, Canada

|  |  |
| --- | --- |
| 01/2017 – present | **Sessional Instructor**, School of Computer Science, University of Windsor, Canada |
| 05/2016 – 12/2016 | **Tutor**, School of Computer Science, University of Windsor, Canada |
| 01/2014 – 04/2016 | **Graduate Assistant**, School of Computer Science, University of Windsor, Canada |
| 01/2014 – present | **Research Assistant**, School of Computer Science, University of Windsor, Canada |
| 01/2008 – 01/2009 | **Graduate Assistant**, School of Computer Science, University of Windsor, Canada |

Industry:

|  |  |
| --- | --- |
| 02/2011 – 11/2013 | **Analyst Programmer**,UAE University,Al-Ain, UAE. |
| 01/2009- 09/2009 | **Business Systems Developer - coop**, Blackberry Ltd, Waterloo, Canada. |
| 07/2005-12/2007 | **System Analysis and reporting**,Emaratech Fzllc, Dubai, UAE |
|  |  |

## Academic Responsibilities

|  |  |
| --- | --- |
| **Instructor****uWin:** |  |
|  | **Undergraduate Courses:**Web data management (Winter 2018)Problem Solving on the Internet (Fall 2017)Advanced Website Design (Winter 2017, Fall 2018, Winter 2019, Fall 2019, Winter 2020, Summer 2020, Winter 2021)WWW System Information Devl. (Summer 2017, Summer 2018, Summer 2019, Summer 2020)Principles of Programing Languages (Fall 2020)Special Topics in Software Engineering (Winter 2021)System Programing (Winter 2021)Computer Architecture and Design (Summer 2021)Project Management: Techniques and Tools (Mentoring under grad student Winter 2021) **Graduate Courses:** Internet Apps and Distributed Sys – Master of Applied Computing (Intercession 2019) Advanced Computing Concepts – Master of Applied Computing (Fall 2019, Winter 2020, Summer 2021, Fall 2021) |
| **Instructor****PSUT:** | **Undergraduate Courses:**Mobile Development and Applications (Fall 2021, Winter 2022, Summer 2022, Fall 20222)Object Oriented Programing Lab (Fall 2021). Server Side Programing (Fall 2021, Winter 2022, Fall 2022)Structured Programming (Winter 2022)Data Structure and Introduction to Algorithm (Summer 2022)**Graduate Courses:** Biostatistics (Fall 2022) |

### Grad Students/Postdoc Supervision

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name | Years | Degree | Institution | Title of Project |
| Noor Kamouneh (Co-advisor) | 2019-2021Graduated | MastersComputer Science | University of Windsor | A Deep Learning Model to Identify a Genomic Signature Driving Sporadic Colorectal Cancer in Young Adults |
| Li Zhou(Co-advisor) | 2020-2022 Graduated | MastersComputer Science | University of Windsor | Clustering of SAR-Cov-2 Sequences from Multiple Outbreaks  |
| Ziad Omar(Co-advisor) | 2020-2021Graduated | MASc Industrial Engineering | University of Windsor | Deep Learning Methods Applications in Medical Bioinformatics. |
| Bashier ElKarami(Co- advisor) | 2020-present | PhD Industrial Engineering | University of Windsor | Machine learning-based prediction of upgrading of adverse pathology on magnetic resonance imaging targeted biopsy of the prostate in patient. |
| Dr. Ashraf Abou Tabl(Co-Investigator) | 2020-2021 | PostDoc Fellow | University of Windsor – ITOS Oncology (Mitacs Fellowship) | COVID19 viral genome sequence analysis to track viral transmission, to understand evolution of viral genome, to develop novel diagnostic tools as well as to identify novel therapeutic targets. |
| Hania AlOmari(Advisor) | 2021-presente | Masters ofHealth Information System  | Princess Sumaya University for Technology | Developing an Enterprise Architecture for Healthcare Providers: TheNational Center for Diabetes, Endocrinology and Genetics in Jordan. |

### Undergraduate Project Supervision

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name | Years | Degree | Institution | Title of Project |
| Haris Ahmad | 2016-2017 | B (Hons)Computer Science | University of Windsor | A System for Integrating Machine Learning and Protein Isoforms. |
| Tommaso Iacobelli | 2016-2018 | B (Hons) Computer Science | University of Windsor | NSERC USRA: Implementation of Algorithms for Finding Protein Isoforms in Transcriptomics Data.Board of Governors Medal Recipient. |
| Julia Zheng&Johan Fernandez | 2017-2019 | B (Hons) Computer Science | University of Windsor | Discovering Biological Public Datasets APIs  |
| Randy Diagle&Dela Akpatsa | 2018 | B (Hons) Computer Science | University of Windsor | Developing Parts of the Faculty of Science Website |
| Matthew Farias(Co-Investigator) | 2020 - | Internship | University of Windsor – ITOS Oncology (Mitacs Fellowship) | COVID19 viral genome sequence analysis to track viral transmission, to understand evolution of viral genome, to develop novel diagnostic tools as well as to identify novel therapeutic targets. |

## Achievements, Awards, and Grants

1. **(PI)** **Faculty of Graduate Studies and Sciences at The Princess Sumaya University for Technology Seed fund grant**, Artificial Intelligence Models for Heterogeneous Health Data Fusion 5,400 JD (~10,000 CAD$) for 1 year.
2. **(PI) Startup with IBM through Ontario Centers of Excellence Grant** 12,000 CAD$ (1,000$ of IBM cloud usage per month – for 1 year).
3. **(The postdoc/ writing the application) Mitacs Accelerate PDF Grant** 180,000 CAD$ for 3 years (60k per year).
4. **(Co-Investigator/ writing the application) Mitacs Accelerate PDF Grant** 175,000 CAD$ for 2 years (2 interns).
5. *Runner-up for Best Paper Award – Travel Award*. Paper presented at CIBCB 2015. S. Singireddy, A. Alkhateeb, I. Rezaeian, D. Cavallo-Medved, L. Porter, L. Rueda, “Identifying Differentially Expressed Transcripts Associated with Prostate Cancer Progression using RNA-Seq and Machine Learning Techniques”, Niagara Falls, Canada, 2015.
6. *Ontario Graduate Scholarship (OGS)* winner, 2017/2018, Ontario, Canada.
7. The University of Windsor, Faculty of Science, ***Going Above & Beyond in Research award 2017 winner****,* value 1000 CAD$.
8. The University of Windsor, Faculty of Science, ***Going Above & Beyond in Research award 2020 (Post-Doc level) winner****,* value 1000 CAD$.
9. Top up the department for many terms as the highest ranked undergrad Instructor/Professor, School of Computer Science, University of Windsor.

## Invited Talks

1. Machine Learning in Cancer Diagnosis and Personalized Medicine, Western Michigan University, Kalamazoo, MI, US. 2020, https://wmich.edu/cs/colloquia.
2. Radio talk, CJAM Radio Station, https://twitter.com/PeerReviewedUoW/status/1055228493028564997.
3. Machine Learning Approaches for Cancer Analysis, Dr. Michael Taylor lab, SickKids Hospital, Toronto, ON, Canada, 2018.
4. Machine Learning Approaches forData Analysis, IEEE Young Professionals, Windsor Section, http://windsor.ieee.ca/2018/06/12/technical-talk-19/, Windsor, ON, Canada, 2017.
5. Time-Series Analysis and Applications in Cancer Research, Computer Science Colloquium, School of Computer Science, University of Windsor, Windsor, ON, Canada, 2017.
6. Machine Learning Approaches for Next Generation Sequencing Data Analysis, Computer Science Colloquium, School of Computer Science, University of Windsor, Windsor, ON, Canada, 2016.

## Publications

## Journal Publications

1. A. Abou Tabl, **A. Alkhateeb**, P. Quang, L. Rueda, W. Elmaraghy, A. Ngom.” A novel approach for identifying relevant genes for breast cancer survivability on specific therapies” Evolutionary Bioinformatics, 2018, *Evolutionary Bioinformatics*, 14, doi: 10.1177/1176934318790266.
2. **A. Alkhateeb**, L. Rueda. “Zseq: an approach for preprocessing next generation sequencing data”, *Journal of Computational Biology*, 2017, 24(8):746-755, doi: 10.1089/cmb.2017.0021.
3. **A. Alkhateeb**, L. Rueda, I. Rezaeian, S. Reddy, D. Cavallo-Medved, L. Porter. “Transcriptomics signature from next-generation sequencing data reveals new transcriptomic biomarkers related to prostate cancer”, 2019, Cancer Informatics, 18, 1176935119835522.
4. A. Abou Tabl, **A. Alkhateeb**, L. Rueda, W. Elmaraghy, A. Ngom. “A machine learning approach for identifying gene biomarkers guiding the treatment of breast cancer”,2019, Frontiers in Genetics, 10, 256.
5. O. Hamzeh, **A. Alkhateeb**, J.Z. Zheng, S. Kandalam, C. Leung, G. Atikukke, D. Cavallo-Medved, N. Palanisamy, L. Rueda, Hierarchical Machine Learning Model to Discover Gleason Grade-Specific Biomarkers in Prostate Cancer. *Diagnostics* 2019, *9*, 219.
6. S. Jubair, **A. Alkhateeb**, A Abou Tabl, L. Rueda, A. Ngom, “Identifying subtype specific network-biomarkers of breast cancer survivability”,2020, *Network Modeling Analysis in Health Informatics and Bioinformatics,* doi*:*10.1007/s13721-020-00249-4.
7. O. Hamzeh**, A. Alkhateeb,** L. Rueda. “Predicting Tumor Locations in Prostate Cancer Tissue Using Gene Expression”, 2019, *BMC Bioinformatics Supplement*. 2020, [doi.org/10.1186/s12859-020-3345-9](https://doi.org/10.1186/s12859-020-3345-9).
8. A. Abou Tabl, **A. Alkhateeb**, W. Elmaraghy. Deep Learning Method based on Big Data for Defects Detection in Manufacturing Systems Industry 4.0. International Journal of Industry and Sustainable Development, 2(1), 1-14, 2021.
9. **A. Alkhateeb** “HC-UAP: Outliers Detection method based-on Hierarchical Clustering for Universally Aligned Time-series RNA-Seq Profiles”. *Decision Science letters*, 2022, Sumitted.
10. K. Stokes, M. Nunes, C. Trombley, D. E. F. L. Florês, G. Wu, C. Curran, Z. Taleb, **A. Alkhateeb**, S. Banskota, C. Harris, O. Love, W. I. Khan, L. Rueda, J. B. The circadian clock gene, Bmal1, suppresses tumour initiation and regulates intestinal stem cell signaling, 2021, Hogenesch; Phillip Karpowicz, *Cellular and Molecular Gastroenterology and Hepatology,* Elsevier, 12(5), 1847-1872.
11. B. ElKarami, D. Sidhom, M. Deebajah, S. MS, J. Peabody, M. Menon, **A. Alkhateeb**, S. Alanee. Machine learning-based prediction on targeted biopsy in patients eligible for active surveillance., Urologic Oncology: Seminars and Original Investigations, 2022, (Vol. 40, No. 5, pp. 191-e15). Elsevier.
12. L. Zhou, M. Rueda, **A. Alkhateeb**. Classification of Breast Cancer Nottingham Prognostic Index using High-dimensional Embedding and Residual Neural Network, *Cancers*, 2022, 14 (4), 934.
13. B. ElKarami, **A. Alkhateeb**, H. Qattous, L. Alshomali, and B. Shahrrava. “Multi-omics Data Integration Model Based on UMAP Embedding and Convolutional Neural Network”. *Cancer Informatics*, 2022, doi.org/10.1177/11769351221124205.

## Book Chapters

1. **A. Alkhateeb**, A Abou Tabl, L. Rueda, Deep Learning in Multi-Omics Data Integration in Cancer Diagnostic, *Deep Learning for Biomedical Data Analysis*, Springer, 2021, ISBN:978-3-030-71676-9.

## Abstracts published in Journals

1. **A. Alkhateeb** et al., Comprehensive targeted gene profiling to determine the genomic signature likely to drive progression of high-grade nonmuscle invasive bladder cancer to muscle invasive bladder cancer, 2020, *Journal of Clinical Oncology,* 38 (6\_suppl), 568-568.
2. G. Atikukke, **A. Alkhateeb** et al. Comprehensive targeted genomic profiling and comparative genomic analysis to identify molecular mechanisms driving cancer progression in young-onset sporadic colorectal cancer", 2020, *Annals of Oncology*. (Supplement\_3), S209-S210.
3. S. Alanee, D. Sidhom, **A.** **Alkhateeb**, B. ElKarami. " Mp62-04 Machine Learning-based Prediction Of Upgrading To Adverse Pathology In Patients Who Are Candidates For Active Surveillance." The Journal of Urology 206.Supplement 3 (2021): e1093-e1093.

## Refereed Conference Publications and Presentations

1. L. Zhou, M. Rueda, **A. Alkhateeb.** “Identifying Biomarkers of Nottingham Prognosis Index in Breast Cancer Survivability”. In Proceedings of the 12th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (pp. 1-9), 2021, Virtual.
2. G. Atikukke, **A. Alkhateeb** et al., A novel bioinformatic approach to analyze large-scale, next-generation
3. sequencing-based targeted gene profiling data for personalizing treatment, WCRG 5th Biennial International Cancer Research Conference – Virtual Edition, 2020, Windsor, ON, Canada.
4. G. Atikukke, **A. Alkhateeb** et al. Comprehensive targeted genomic profiling and comparative genomic analysis to identify molecular mechanisms driving cancer progression in young-onset sporadic colorectal cancer", 2020, World Congress on Gastrointestinal Cancer, Barcelona, Spain (Online).
5. **A. Alkhateeb**, L. Zhou, A. Abou Tabl, L. Rueda. “Deep Learning Approach for Breast Cancer InClust 5 Prediction based on Multiomics Data Integration”. In Proceedings of the 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (2020, September) (pp. 1-6).
6. **A. Alkhateeb**,  G. Atikukke, L. Porter, B. Fifield, D. Cavallo-Medved, J. Facca, Y. El-Gohary, T. Zhang, O. Hamzeh, J. Mathews, A Ghafoor, T Deklaj, R Goel, R Sorenson, B. Al-Farra, H. Khalaff, L. Rueda and S. Kanjeekal, Comprehensive targeted gene profiling to determine the genomic signature likely to drive progression of high-grade non-muscle invasive bladder cancer to muscle invasive bladder cancer, Genitourinary Cancers Symposium, 2020, San Francisco, CA.
7. **A. Alkhateeb**, N. Fatima, G. Atikukke, S. Misra, L. Rueda. “A Deep Learning Model to Identify a Genomic Signature Driving Sporadic Colorectal Cancer in Young Adults”. In Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (pp. 645-645). ACM.
8. O. Hamzeh, **A. Alkhateeb**, L. Rueda. “Predicting Tumor Locations in Prostate Cancer Tissue Using Gene Expression”. 6th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2018), Granada, Spain, 2018. (pp. 343-351). Springer, Cham.
9. A. Abou Tabl, **A. Alkhateeb**, L. Rueda, W. Elmaraghy, A. Ngom. “Identification of the Treatment Survivability Gene Biomarkers of Breast Cancer Patients via a Tree-Based Approach”. 6th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2018), Granada, Spain, 2018. (pp. 166-176). Springer, Cham.
10. O. Hamzeh, **A. Alkhateeb**, L. Rueda. “Prediction of Tumor Location in Prostate Cancer Tissue Using Gene Expression”. Extended Abstract, IEEE Biomedical and Health Science Conference, Las Vegas, NE, USA, 2018.
11. A. Abou Tabl, **A. Alkhateeb**, W. ElMaraghy, L. Rueda, A. Ngom. “Identifying Gene Biomarkers for Breast Cancer Survival Using a Tree-Based Approach”. Extended Abstract, IEEE Biomedical and Health Science Conference, Las Vegas, NE, USA, 2018.
12. A. Abou Tabl, **A. Alkhateeb**, W. ElMaraghy, A. Ngom. “Machine Learning Model for Identifying Gene Biomarkers for Breast Cancer Treatment Survival”, In Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM 2017), Boston, MA.
13. N. Mangalakumar, **A. Alkhateeb**, H. Quang, L. Rueda, A. Ngom. “Outlier Genes as Biomarkers of Breast Cancer Survivability in Time-Series Data”, *ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB 2017), 201*7, Boston, MA, USA, pp. 594-594.
14. N. Mangalakumar, **A. Alkhateeb**, H. Quang, L. Rueda, A. Ngom. “Identifying Gene Biomarkers of Breast Cancer Survivability from Time-Series Data”, Intelligent Systems for Molecular Biology and the 16th European Conference on Computational Biology (ISMB/ECCB 2017), Prague, Czech Republic, 2017. Poster presentation, peer-reviewed.
15. H. Ahmed, O. Hamzeh, **A. Alkhateeb**, L. Rueda. “An Open Source Machine Learning Tool for Identifying Biomarkers in Next Generation Sequencing”, The Great Lakes Bioinformatics Conference (GLBIO 2017), 2017, Chicago, IL, USA. Poster presentation.
16. O. Hamzeh, **A. Alkhateeb**, I. Rezaeian, A. Karkar, L. Rueda. “Finding Transcripts Associated with Prostate Cancer Gleason Stages Using Next Generation Sequencing and Machine Learning Techniques”. The 5th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2017), Granada, Spain, 2017, pp. 337-348.
17. R. Etemadi, **A. Alkhateeb**, I. Rezaeian, L. Rueda, “Identification of Discriminative Genes for Predicting Breast Cancer Subtypes”, Workshop on Health Informatics and Data Science (HI-DS 2016) - IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2016), Shenzhen, China, 2016, pp: 1184-1188.
18. M. Alsheri, **A. Alkhateeb**, I. Rezaeian, L. Rueda. “Discovery of Protein Isoforms for Different Stages of Prostate Cancer”, The Fourth International Society for Computational Biology Latin America Bioinformatics Conference (ISCB-LA 2016), Buenos Aires, Argentina. Oral presentation.
19. M. Alshehri, I. Rezaeian, **A. Alkhateeb**, L. Rueda. “A Machine Learning Model for Discovery of Protein Isoforms as Biomarkers”, *ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACMBCB 2016)*, Seattle, WA, USA, 2016, pp. 474-475.
20. M. Alshehri, **A. Alkhateeb**, I. Rezaeian, L. Rueda, “Potential Protein Isoforms Reveal Additional Information on Biomarkers Obtained from RNA-Seq Data”, Intelligent Systems for Molecular Biology (ISMB 2016), Orlando, Florida, USA, 2016. Poster presentation, peer-reviewed.
21. B. Elkarami, **A. Alkhateeb**, L. Rueda, “Cost-Sensitive Classification on Class-balanced Ensembles for Imbalanced Non-coding RNA Data”, The IEEE Engineering in Medicine and Biology Society (EMBS) International Student Conference (ISC) 2016, Ottawa, Canada, pp. 1-4.
22. M. Kordestani, **A. Alkhateeb**, I. Rezaeian, L. Rueda, M. Saif. “A new clustering method using wavelet-based probability density functions for identifying patterns in time-series data”, The IEEE Engineering in Medicine and Biology Society (EMBS) International Student Conference (ISC) 2016, Ottawa, Canada, pp. 1-4.
23. **A. Alkhateeb**, I. Rezaeian, L. Rueda, “Hierarchal Clustering based on Non-negative Matrix Factorization for Time Series transcriptomes profiles”, The GLBIO/CCBC Great Lakes Bioinformatics and the Canadian Computational Biology Conference, 2016, Toronto, Canada. Poster presentation.
24. **A. Alkhateeb**, I. Rezaeian, L. Rueda, “Nonnegative Matrix Factorization Clustering for Time Series Cancer Progression Data”, 20*th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2016)*, Santa Monica, CA, USA, 2016. Poster and Oral presentation, peer-reviewed.
25. M. Alsheri, **A. Alkhateeb**, I. Rezaeian, L. Rueda, “A standalone tool for finding ORFs and reconstructing potential protein isoforms from RNA-Seq data”, Next Generation Sequencing 2016 (NGS 2016), Barcelona, Spain, 2016, Poster presentation – peer reviewed.
26. **A. Alkhateeb**, I. Rezaeian, L. Rueda, “ZSeq 2.0: A fully automatic preprocessing method for next generation sequencing data”, IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2015), Washington, DC, USA, 2015, pp. 1762-1764.
27. **A. Alkhateeb**, S. Reddy, I. Rezaeian, L. Rueda, “Zseq: an approach for filtering low complex and biased sequences in next generation sequencing data”, *Advanced in Bioinformatics and Artificial Intelligence: Bridging the Gap (IJCAI-BAI 2015)*, Buenos Aires, Argentina, 2015, pp. 2-9.
28. S. Singireddy, **A. Alkhateeb**, I. Rezaeian, D. Cavallo-Medved, L. Porter, L. Rueda, “Identifying Differentially Expressed Transcripts Associated with Prostate Cancer Progression using RNA-Seq and Machine Learning Techniques”, *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2015)*, Niagara Falls, Canada, 2015, pp. 1-5, DOI: 10.1109/CIBCB.2015.7300302.
29. **A. Alkhateeb**, S. Reddy, I. Rezaeian, U. Katiyar, D. Maskoni, J. Kelly, D. Cavallo-Medved, L. Porter, L. Rueda, “Analysis of Novel mRNA Transcripts in Prostate Cancer”, *19th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2015)*, Warsaw, Poland, 2015, pp. 67. Poster presentation (peer-reviewed).

## Professional Activities

* Guest editor for special collection titled by “Machine Learning Models for Multi-omics Data Integration”, Evolutionary Bioinformatics Journal, 2019, https://journals.sagepub.com/page/evb/collections/special-collections/machine-learning-models-data-integration.
* Conference Chair – Organizing Committee:
	+ 2nd IEEE International Workshop on High-Performance Computing and Analytics for Big Omics Data (HPC-BOD), In conjunction with IEEE BIBM 2019. November 18-21, 2019, San Diego, CA, USA
	+ Workshop for Multi-Omics Data Integration (MODI-2019), The 10 ACM on Bioinformatics, Computational Biology, and Health Informatics – ACM BCB, 2019, Niagara Falls, NY, US.
	+ The 2nd Workshop for Multi-Omics Data Integration (MODI-2020), The 11 ACM on Bioinformatics, Computational Biology, and Health Informatics – ACM BCB, Virtual - Online.
	+ Workshop on Transcriptome Analysis in Cancer Diagnosis and Treatment, The IEEE Engineering in Medicine and Biology Society (EMBS) International Student Conference (ISC) 2016, Ottawa, Canada.
* Computer Science Colloquium Student Organizer 2017, School of Computer Science, University of Windsor, Canada
* Professional Memberships:
	+ *Member of the Institute of Electrical and Electronic Engineers (IEEE), 2015-present.*
	+ *Member of Association for Computing Machinery (ACM), 2018 – 2020.*
	+ *Member of Canadian Cancer Society, ROIT group, Sept 2016 – Aug 2018.*
	+ *Member of Windsor Cancer Research group, Windsor, Canada, 2017-present.*
	+ *Member of American Society of Clinical Oncology (ASCO) 2020-2021.*
* Reviewer
	+ *Scientific Reports – Nature.*
	+ *Journal of Biomedical and Health Informatics (JBHI)- IEEE.*
	+ *Cancer Informatics – SAGE.*
	+ *Network Modeling Analysis in Health Informatics and Bioinformatics – Springer.*
	+ *Gene – Elsevier.*
	+ *Computational Biology and Chemistry – Elsevier.*
	+ *Journal of King Saud University - Computer and Information Sciences – Elsevier.*
	+ *Computers in Biology and Medicine – Elsevier.*
	+ *Cancers – MDPI.*
	+ *Applied Computing and Informatics – Elsevier.*
	+ *Evolutionary Bioinformatics – SAGE.*
	+ *Journal of Infection and Public Health – Elsevier.*
	+ *Toxics – MDPI.*
	+ *Neurocomputing – Elsevier.*