

Curriculum Vitae

Luis Gabriel Rueda

Contact:

Work:

School of Computer Science, University of Windsor
401 Sunset Ave., Windsor, ON, N9B 3P4, Canada
Phone: +1 519 253-3000 x 3002 – Fax: +1 519 973-7093
E-mail: lrueda@uwindsor.ca - Web: luisrueda.cs.uwindsor.ca

Education

- 04/2002 **Ph.D. in Computer Science**, Carleton University, Canada.
- 12/1998 **Master's in Computer Science**, Carleton University, Canada.
- 03/1993 **Bachelor in Computer Science**, National University of San Juan, Argentina.

Employment Experience

Academic:

- 07/2013 – present **Professor**, School of Computer Science, University of Windsor, Canada
- 07/2008 – 06/2013 **Associate Professor**, School of Computer Science, University of Windsor, Canada
- 01/2006 – 06/2008 **Associate Professor**, Department of Computer Science, University of Concepcion, Chile.
- 07/2002 – 12/2005 **Assistant Professor**, School of Computer Science, University of Windsor, Canada
- 09/2001 – 12/2001 **Sessional Instructor**, School of Computer Science, Carleton University, Ottawa, Canada
- 09/1998 – 04/2002 **Teaching Assistant**, School of Computer Science, Carleton University, Canada
- 03/1998 – 04/2002 **Research Assistant**, School of Computer Science, Carleton University, Canada
- 01/1996 – 12/1997 **Instructor**, Computer Science Department, National University of San Juan, Argentina
- 04/1993 – 12/1995 **Teaching Assistant**, Computer Science Department, National University of San Juan, Argentina
- 03/1996 – 12/1997 **Research Assistant**, Computer Science Institute, National University of San Juan, Argentina

Industry:

- 08/2001 – 08/2002 **Consultant**, Quarterstone Communications Inc. (QCI), Ottawa, Canada
- 05/1988 - 06/1992 **Software Developer**, The Bank of San Juan, San Juan, Argentina

Academic Responsibilities

Instructor:

Graduate courses:

Advanced Computing Concepts (Fall 2014, Fall 2015, Fall 2016, Fall 2017, Winter 2017, Fall 2018, Winter 2019, Fall 2019, Winter 2020, Fall 2020)
Bioinformatics (2006, 2007, Fall 2010, Fall 2012)
Machine Learning-Pattern Recognition (2003, 2006, 2007, Winter 2008, Fall 2008, Fall 2009, Fall 2011, Fall 2013, Fall 2014, Fall 2015, Fall 2016, Fall 2017, Fall 2018, Fall 2019, Fall 2020, Winter 2021)
DNA Microarray Data Analysis (2005, 2007)

Undergraduate courses:

Operating Systems Fundamentals (Winter 2016)
Machine Learning (Fall 2013, Fall 2014, Fall 2016, Fall 2017, Fall 2018, Fall 2019, Fall 2020)
Design and Analysis of Computer Algorithms (2004, 2005, 2006, 2007)
Theory of Computation (Fall 2012)
Data Structures and Algorithms (Fall/Winter 2003, 2004, Winter 2009, Winter 2010, Winter 2011, Winter 2012, Winter 2013, Winter 2014, Winter 2017, Winter 2018, Winter 2019, Winter 2020)
Computer Languages, Grammars, and Translators (Winter 2009, Winter 2016)
Introduction to Object Oriented Programming in Java (2001)
Artificial Intelligence (1996, 1997, Winter 2014)
Information Theory (1996, 1997)
Programming I (1996-Fall/Winter, 1997)

Teaching Assistant:

Theory of Computing (1999, 2000, 2002)
Statistical and Syntactic Pattern Recognition (2001)
Introduction to Object Oriented Programming (2000)
Design and Implementation of Computer Applications (2000)
Discrete Mathematics I (1998, 1999)
Temporal Reasoning and Constraint Logic Programming (1996)
Knowledge Engineering (1995, 1996)
Programming I (1994, 1995)
Expert Systems (1993, 1994)
Information Theory (1993, 1994, 1995, 1996)

Administrative Responsibilities

2019-2022 Member of the NSERC Evaluation Group – Computer Science, Natural Sciences and Engineering Research Council of Canada.
2020-2021 Member of the Promotion, Tenure and Renewal Committee, School of Computer Science, University of Windsor.
2020-2021 Member of the PhD Admissions and Progress Committee, School of Computer Science, University of Windsor
2020-2021 Member of the Master's Admissions and Progress Committee, School of Computer Science, University of Windsor
2019-2020 Member of the Graduate Council, Faculty of Graduate Studies, University of Windsor.
2019-2020 Graduate Chair, School of Computer Science, University of Windsor.
2012-2020 Member of the Committee for the Master of Applied Computing, School of Computer Science, University of Windsor.

- 2015-2021 Member of the Student Recruitment and Retention Committee, School of Computer Science, University of Windsor.
- 2018-2019 Member of the Awards Committee, School of Computer Science, University of Windsor.
- 2018-2019 Member of the PhD Program Committee, School of Computer Science, University of Windsor.
- 2017-2019 Member of the Promotion, Tenure and Renewal Committee, School of Computer Science, University of Windsor.
- 2015-2018 Computer Science Colloquium Coordinator, School of Computer Science, University of Windsor.
- 2015-2018 Member of the Graduate Executive Committee, School of Computer Science, University of Windsor.
- 2016-2017 Member of the Appointments Committee. School of Computer Science, University of Windsor.
- 2015-2016 Member of the Dean of Science Search Committee, University of Windsor.
- 2015-2016 Member of the Promotion, Tenure and Renewal Committee, School of Computer Science, University of Windsor.
- 2013-2014 Member of the Promotion, Tenure and Renewal Committee, School of Computer Science, University of Windsor.
- 2013-2014 Member of the Doctoral Committee, School of Computer Science, University of Windsor.
- 2012-2013 Member of the Appointments Committee and Graduate Committee. School of Computer Science, University of Windsor.
- 2011-2012 Member of the Promotion, Tenure and Renewal Committee, School of Computer Science, University of Windsor.
- 2010-2012 Member of the University Strategic Research Plan Committee, University of Windsor.
- 2009-2011 Member of the Graduate Council, University of Windsor.
- 2009-2011 Graduate Chair, School of Computer Science, University of Windsor.
- 2008-2009 Member of Committees: Undergraduate Curriculum, Industrial Liaison, Student Recruitment and Retention. School of Computer Science, University of Windsor.
- 2007-2008 Member of the Grant Selection Committee, Engineering Group II, National Council for Scientific and Technical Research of Chile (CONICYT).
- 2006-2007 PhD in Computer Science Program Creation Committee and Program Chair, Department of Computer Science, University of Concepcion.
- 2005 Member of the Appointments Committee, School of Computer Science, University of Windsor.
- 2004-2005 Member of the Promotion, Tenure and Renewal Committee, School of Computer Science, University of Windsor.
- 2003-2005 Member of the Graduate Curriculum Committee, School of Computer Science, University of Windsor.
- 2003-2004 Member of the Appointments Committee, School of Computer Science, University of Windsor.
- 2002-2004 Member of the Web Site Design Committee, School of Computer Science, University of Windsor.
- 2002-2003 Member of the Undergraduate Curriculum Committee, School of Computer Science, University of Windsor.
- 1995/1996 Member of the Undergraduate Curriculum Committee, National University of San Juan, Argentina. Undergraduate Curriculum Committee.

Supervision of Postdoctoral Fellows

Name	Years	Topic
------	-------	-------

Ashraf Abu Tabl	08-2020 to 07-2022	COVID-19 Genome Sequence Analysis Tools to Identify Novel Therapeutic Targets
Abed Alkhateeb	06-2019 to 05-2022	Machine learning-based data analysis for cancer targeted gene panels
Abed Alkhateeb	08-2018 to 05-2019	Deep Machine Learning Approaches for Analyzing Genomics Data
Mina Maleki	09-2014 to 12-2016	Prediction and analysis of protein-protein interactions
Iman Rezaeian	09-2014 to 01-2017	Identification of biomarkers in breast cancer and prostate cancer

Graduate Student Supervision

Name	Years	Degree	Thesis Topic
Mehfuz Rahman	05/2020-	M.Sc.	
Karan Kashyap	05/2020-	M.Sc.	
Li Zhou	2020-	M.Sc.	Classification via Distributed Stochastic Network Embedding and Convolutional Neural Networks
Yash Trivedi	2020-	M.Sc.	Single-cell RNA-seq Data Analysis
Sheena Hora	2020-	M.Sc.	Graph Convolutional Neural Networks
Akram Vasighizaker	2020-	Ph.D.	Representation Learning Approaches for Single-cell RNA-seq Data Analysis
Abdala Nour	2019-2020	Ph.D.	Convolutional Neural Networks for Biomedical Image Classification
Saiteja Danda	2019-	M.Sc.	Identification of Cell-types in scRNA-seq data via Enhanced Local Embedding and Clustering
Rui Xu (co-supervision)	2018-	M.Sc.	Artificial Intelligence Phishing Campaign Engine
Nour Kammona	2019-2021	M.Sc.	A Deep Learning Approach for Multi-Omics Data Integration to Diagnose Early-Onset Colorectal Cancer
Nachiket Bhide	2019-2021	M.Sc.	Efficient Clustering via Spectral Dimensionality Reduction and Optimal One-dimensional Thresholding
Musab Naik	2018-2020	M.Sc.	Finding Binding Sites via a Linear-time Multi-level Thresholding Algorithm
Alexandru Filip	2018-2020	M.Sc.	A Deep Learning Approach to Discriminative Motif Discovery
Ashraf Neisari	2018-2020	M. Sc.	Spam Review Detection Using Self-Organizing Maps and Convolutional Neural Networks
Nazia Fatima	2018-2019	M.Sc.	iSOM-GSN: An Integrative Approach for Transforming Multi-omic Data into Gene Similarity Networks via Self-organizing Maps

Susha Suresh (co-supervision)	2017- 2019	M.Sc.	Attributed Graph Classification via Deep Graph Convolutional Networks
Osama Hamzeh	2016- 2020	Ph.D.	Machine Learning Approaches for Identifying Cancer Biomarkers Using Next Generation Sequencing
Pham Quang Huy (co-supervision)	2015- 2020	Ph.D.	Machine Learning Approaches for Breast Cancer Survivability Prediction
Abedalrhman Alkhateeb	2014- 2018	Ph.D.	Algorithms for Transcriptomics Biomarkers in Prostate Cancer Data
Wenxiao Xu (co-supervision)	2016- 2017	M. Sc.	Drug-target Interaction Network Prediction using Short Linear Motifs
Sheikh Jubair (co-supervision)	2016- 2017	M. Sc.	Identifying the Network Biomarkers of Breast Cancer Survivability
Naveen Mangalakumar	2016- 2017	M. Sc.	An Adaptive Clustering Algorithm for Gene Expression Time-series Data
Emamuzo Ogemuno	2016- 2018	M. Sc.	A Machine Learning Method for User Authentication Using Keystroke Dynamics
Sowndarya Krishnamoorthy	2016- 2018	M. Sc.	Identification of User Behavioral Biometrics for Authentication using Keystroke Dynamics and Machine Learning
Forough Firoozbakht	2015-	Ph.D.	Network Biomarker Discovery in Breast Cancer Subtypes
Yixun Li (co-supervision)	2014- 2016	M.Sc.	Prediction of High-throughput Protein-Protein Interactions and Calmodulin Binding Using Short Linear Motifs
Behzad Rezaei (co-supervision)	2014- 2016	M.Sc.	Finding Short-linear Motifs Large Protein Datasets
Mrinalini Pandit	2014- 2016	M.Sc.	A Machine Learning Model for Prediction of Calmodulin-binding Proteins
Manal Alshehri	2014- 2016	M.Sc.	A Machine Learning Model for Discovery of Protein Isoforms as Biomarkers
Siva Reddy	2013- 2015	M.Sc.	A Machine Learning Scheme for Finding Transcripts in RNA-Seq Data for Progression of Prostate Cancer
Forough Firoozbakht	2014- 2014	M.Sc.	Identification of Biomarkers in Breast Cancer Subtypes
Ahmad Tavakoli	2011- 2013	M.Sc.	A System for Prostate Cancer Diagnosis Using Splice Junctions in RNA-Seq Data
Manish Pandit	2011- 2012	M.Sc.	Prediction and Analysis of Protein-protein Interaction Types Using Short Linear Motifs
Navid Shakibapour	2010- 2012	M.Sc.	Identifying MicroRNA Precursors Using Linear Dimensionality Reduction with Explicit Mapping
Gokul Vasudev	2010- 2012	M.Sc.	A Model to Predict and Analyze Protein-protein Interaction Types Using Electrostatic Energies
Mina Maleki	2010- 2014	Ph.D.	Prediction of Obligate Protein-protein Interactions

Muhammad Aziz	2010-2011	M.Sc.	Prediction of Obligate and Non-obligate Protein-Protein Interactions
Iman Rezaeian	2010-2014	Ph.D.	Machine Learning Approaches for Transcriptomics Data Analysis
Yifeng Li	2009-2013	Ph.D.	Sparse Machine Learning Models in Bioinformatics
Sridip Banerjee	2009-2011	M. Sc.	Prediction of Crystal Packing and Biological Protein-protein Interactions with Linear Dimensionality Reduction-SVD
Priyanka Trivedi (co-supervision)	2009-2010	M. Sc.	Delta Bloom Filter Compression Using Stochastic Learning-based Weak Estimation
Numanul Subhani	2008-2009	M. Sc.	Clustering Microarray Time-series Data via Multiple Alignment
Juan Rojas	2007-2008	MCS	Pattern Recognition Techniques for DNA Microarray Image Segmentation
Dario Rojas	2007-2008	MCS	Segmentation of Confocal Laser Biofilm Images
Tatiana Gutierrez	2006-2008	MCS	Finding Relevant Features in Protein-Protein Interaction
Leon French (co-supervision)	2003-2005	M. Sc.	Fast and Accurate Protein Family Classification
Wei Yang	2003-2005	M.Sc.	Finding the Optimal Number of Clusters in DNA Microarray Data
Archana Balagondar (co-supervision)	2003-2005	M.Sc.	Compression of Triangular and Quadrilateral Meshes
Yuanquan Zhang	2003-2005	M.Sc.	Visualization of Fuzzy-clustered Data
Vidya Vidyadharan	2003-2004	M.Sc.	Automatic Gridding of DNA Microarray Images
Li Qin	2002-2004	M.Sc.	New Machine Learning Techniques for DNA Microarray Image Segmentation

Graduate Committee Membership

Name	Year	Degree	Thesis title
Ehsan Hallaji	2021	Ph.D.	
Xue Qin	2021	MASc.	Security Enhancement for Mobile Computing
Kelvin Vuu	2021	M.Sc.	Designing Primers for a Universal Gene Chip to Quantify RNA Expression
Rumana Islam	2021	Ph.D.	Biomedical Signal Processing
Ala Alam Falaki	2021	Ph.D.	Deep Learning Models for Text Summarization
Sudipta Modak	2020	MASc.	QRS Complex and Ectopic beats Detection Analysis based on Multilevel Thresholding and Peak-to-Peak Distance Statistics
Martin Bakht	2019	Ph.D.	Molecular imaging targets in prostate cancers with neuroendocrine gene signature

Seth Munholland	2019	Ph.D.	Genome Organization and Introgression Mechanics in Common Bean <i>Phaseolus vulgaris</i>
Mohammed Ismail	2019	Ph.D.	Optimal Three-dimensional Transient Heat Transfer in Crossflow Minichannel Heat Exchange Apparatus
Yihan Zhu	2019	M.Sc.	Almost Periodic Functions on Topological Groups
Raturaj Raval	2019	M.Sc.	An Improved Approach of Intention Discovery with Machine Learning for POMDP-based Dialogue Management
Maher Husein	2019	M.Sc.	Using Concordantly Expressed Genes to Repurpose Drugs for the Ten Subtypes of Breast Cancer
Roopesh Dhara	2019	M.Sc.	Computational Drug Repurposing for Breast Cancer Subtypes
Antonio Sze-To	2018	Ph.D.	Discovering Patterns from Sequences with Applications on Protein-Protein and Protein-DNA Interactions
Ehsan Hallaji	2018	MASc	Semi-supervised Learning for Diagnosis Faults in Electromechanical Systems
Shiladitya Chakrabarti	2018	MASc	Design of Diagnostic and Prognostic Schemes Under Incomplete Scenarios
Mojtaba Kordestani	2018	Ph.D.	Fault Diagnosis and Prognosis of Safety Critical Systems
Keith Stringer	2017	Ph.D.	The Role and Impact of Spy1 in Cancer Formation
AbdulWahab Kabani	2017	Ph.D.	Improving Deep Learning Image Recognition Performance Using Region of Interest Localization Networks
Paramvir Nagpal	2017	MASc	Indoor Navigation
Maryam Farajzadeh-Zanjani	2017	MASc	Data-driven Techniques for Diagnosing Bearing Defects in Induction Motors
Ruiqing Dong	2016	MASc	Efficient Multiplication Architectures for Truncated Polynomial Ring
Shane Peelar	2016	M.Sc.	Accommodating Prepositional Phrases in Highly Modular Natural Language Queries
Xitian Cui	2016	M.Sc.	Identifying Suspended Accounts in Twitter
Ejeh Chukwuma	2016	M.Sc.	Aspect-based Opinion Mining of Product Reviews in Microblogs Using Most Relevant Clusters of Terms
Morteza Mashayekhi	2015	Ph.D.	Individual-based Modeling and Data Analysis of Ecological Systems using Machine Learning Techniques
Bharadwaja Allapalli	2014	M.Sc.	Instance based learning approach to predict drug target interactions
Raiyan Kamal	2014	M.Sc.	Ant Colony Optimization for Hierarchical Wireless Sensor Networks
Manpreet Kaler	2014	M.Sc.	An Interactive Approach of Software Visualization for Software Customization

Sara Bandehbaham	2013	M.Sc.	Investigating the Effects of Food Chain on Sympatric Speciation Using ECOSIM
Raiyan Kamal	2013	M.Sc.	Algorithms for Wireless Sensor Networks with Mobile Data Collectors
Arushi Arora	2013	M.Sc.	Multiple Alignment of Protein Interaction Networks by Three-Index Assignment Algorithm
Mohammad Shamsur Rahman	2013	M.Sc.	FAC-PIN: An Efficient and Fast Agglomerative Clustering Algorithm for Protein Interaction Networks to Predict Protein Complexes and functional Modules
Hao Wang	2013	M.Sc.	Comparative Study of Sampling Methods for Online Social Networks
Kevin Durda	2013	Ph.D.	Embodied Properties of Semantic Knowledge Acquired From Natural Language
Claudia DiNatale	2012	M.Sc.	<i>Arabidopsis thaliana</i> : A Model Organism for the Modification and Expansion of The Protein Ontology
Vida Sadri	2012	M.Sc.	A Petri Net Based Approach of Software Visualization for Software Customization
Anton Chertov	2012	M.Sc.	Extension of Graph Clustering Algorithms Based on SCAN Method in Order to Target Weighted Graphs
Yuqing Guo	2012	MAS	Adaptive Channel Estimation for Turbo Decoding
Priyatora Das	2012	M.Sc.	Dynamic Sub-Goaling A*
Karl Leboeuf	2012	Ph.D.	ASIC and GPU Acceleration of Elliptic Curve Scalar Point Multiplication
Md. Shafiul Alam	2012	Ph.D.	Some computational problems in the interface of biology and geometry
Rahmatullah Hafiz	2011	Ph.D.	Executable Attribute Grammars for Modular and Efficient Natural Language Processing
Amirali Jafarian	2011	M.Sc.	Gene Subset Selection Approaches Based On Linear Separability
Kashif Saeed	2011	M.Sc.	Mining very long sequences with PLWAP-Long Algorithms
Miguel Carrasco	2010	Ph.D.	A System for Automatic Visual Inspection in Non-calibrated Multiple Views
Fernando Canales	2007	MCS	Growing Neural Network Algorithms for Clustering Analysis
Daniel Langdon	2006	MCS	Automatic Extraction of Visual Landmarks with Multiple Segmentations
Haojun Sun	2005	Ph.D.	Determining the Number of Clusters and Distinguishing Overlap Clusters in Data Analysis
Yasser Alginahi	2004	Ph.D.	Computer Analysis of Composite Documents with Non-uniform Background
Srabanti Dey	2004	M.Sc.	An Efficient Routing Strategy for WDM Networks

Xiaoguang Wang	2004	M.Sc.	Efficient Signature System using Optimized Elliptic Curve Cryptosystem over GF(2 ⁿ)
Xi Zhang	2004	M.Sc.	Protein Family Classification Using Multiple-class Neural Networks
Yu Liu	2003	M.Sc.	A Categorical Data Clustering Approach with Expectation Maximization and k-Nearest Neighbor
Hong Tao Zhang	2002	M.Sc.	On Finding Maximum Empty Rectangle of Arbitrary Orientation: Theory and Implementation

Graduate Students-Internship Supervision

Name	Years	Degree	Institution	Title of Project
Jankiben Patel	2019-2019	Master of Applied Computing	University of Windsor	A Python API for Generation of Random Histograms
Nirmal Purohit	2019-2019	Master of Applied Computing	University of Windsor	Deep Learning Tools for Genomics Data Analysis
Diljeet Alag Sukhbir Singh	2018-2019	Master of Applied Computing	University of Windsor	Software Tools for Retrieving Literature from PubMed Central
Prabhpauhul Singh Ankit Angra	2018-2019	Master of Applied Computing	University of Windsor	A Pharmacogenomics Database for Precision Medicine
Srinath Kandalam	2018	Master of Medical Biotechnology	University of Windsor	Clinical and Biological Validation of Biomarkers of Prostate Cancer
Shane Peelar	2016-2017	M.Sc. Computer Science	University of Windsor	An Intelligent System that Supports Additive Manufacturing and Machining
Xiaoliang Tang Zhihao Yan Yiwei Liu	2016	Master of Applied Computing	University of Windsor	Software tools for Integration of Transcriptomics and Interactomics Data
Rachit Bhatia	2015	Master of Applied Computing	University of Windsor	Data Mining Tool Developer: Retrieval of Protein Interactions
Debanjan Banik	2015	Master of Applied Computing	University of Windsor	Data Mining Tool Developer: Integration of Protein Interactions and Gene Expression

Undergraduate Project Supervision

Name	Years	Degree	Institution	Title of Project
Ahmad Nassar	2021-2021	B (Hons) Computer Science	U. of Windsor	Clustering via Kernel Principal Component Analysis
Krishna Brahmbhatt	2021-2021	B (Hons) Computer Science	U. of Windsor	Single-cell RNA-seq Data Analysis
Gabriela Peralta Milla	2020-2020	B (Hons) Computer Science	U. of Windsor	Clustering and Biological Validation

				of Single-cell RNA-seq Data
Vlad Rus	2020-2020	B (Hons) Computer Science	U. of Windsor	Self-organizing Maps for Single-cell RNA-seq Data Analysis
Jose Guillen Santos	2019-2020	B (Hons) Computer Science	U. of Windsor	Software Prototype for Performing Phishing Cyberattacks
David Collins	2019-2020	B (Hons) Computer Science	U. of Windsor	A Deep Learning Model to Predict Rheumatoid Arthritis Patients
Habib Mohamed	2019-2020	B (Hons) Computer Science	U. of Windsor	Data Engineering and Pre-processing for Cancer Gene Panels
Selin Ozoglu	2019-2020	B (Gen) Computer Science	U. of Windsor	Biological Assessment of Disease-Gene Association Biomarkers
Crystal Leung	2018-2019	Doctor of Medicine	Schulich School of Medicine and Dentistry – Western University	Clinical Study of Transcriptomic Biomarkers in Prostate Tumour Location
Tianmin Zhang	2018-2019	Doctor of Medicine	Schulich School of Medicine and Dentistry – Western University	Clinical Study of Biomarkers in Muscle-invasive Bladder Cancer
Johan Fernandes	2018-2018	B (Hons) Computer Science	University of Windsor	Tools for Genomics and Transcriptomics Data Integration
Julia Zheng	2017-2018	B (General) Computer Science	University of Windsor	Biological Assessment of Genomic Biomarkers in Prostate Cancer
Sara Al-Hayale	2017-2018	B (Hons) Computer Science	University of Windsor	Machine Learning Approaches for Finding Biomarkers in Bladder Cancer
Maher Husein (co-supervision)	2016-2017	B (Hons) Computer Science	University of Windsor	Tools for Analysis of Transcriptomics Biomarkers in Breast Cancer Subtypes
David Valleau (co-supervision)	2016-2017	B (Hons) Computer Science	University of Windsor	A Web Server for Indexing Publications in Breast Cancer

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
Michele D'Agnillo	2015-2018	B (Hons) Biological Sciences	University of Windsor	Biological Validation of Transcriptomics Biomarkers in Breast Cancer Subtypes
Aram Karkar	2016-2017	Doctor of Medicine	Schulich School of Medicine and Dentistry – Western University	Biological Analysis of Transcriptomics Biomarkers for Prostate Cancer Progression
Stephen Askew	2016	B (Hons) Applied Computing	University of Windsor	Web and Text Mining Tools for Bioinformatics Data Integration
Jeremy High Stephen Nusko William Roeder	2014-2015	B (Hons) Computer Science	University of Windsor	Implementation of the Heteroscedastic Linear Classifier
William Roeder	2014	B (Hons) Computer Science	University of Windsor	NSERC USRA: Algorithms for Matching RNA Transcripts and Protein Isoforms in RNA-Seq Data
Anthony Deschamps	2014	B (Hons) Computer Science	University of Windsor	CIHR USRA: Design and Implementation of Algorithms for Finding Short Motifs in Protein-protein Interactions Associated with Prostate Cancer
Mani Mahal	2013-2014	B (Hons) Applied Computing	University of Windsor	Developing a Web Application and Interface for a Database of Salivary Protein Interactions
Adedamola Adekola	2012-2013	B (Hons) Applied Computing	University of Windsor	A Web server for Prediction of Protein Interactions using SLIMs

Jebin Varghese Madhur Munjal	2012-2013	B (Hons) Applied Computing	University of Windsor	A Prototype for a Database on Oral Cavity Protein Interactions
Michael Hall	2011-2012	B (Hons) Computer Science	University of Windsor	Retrieval and Classification of Structural Domains in Protein-protein Interactions
Matthew Renaud	2012-2012	B (Hons) Computer Science	University of Windsor	Short Linear Motif Discovery in Protein Complex Interfaces
Sunit Bhalotia	2010-2011	B (Hons) Computer Science	University of Windsor	A Fast Algorithm to Compute Interface Properties in Protein Complexes
Ahsan Raza Wale Agboola Kennis Gumbs Rasika Bandraniyke	2010-2011	B (Hons) Computer Science	University of Windsor	A Web-based System for Prediction of Protein-protein Interactions
Justin Barolak	2009-2010	B (Hons) Computer Science	University of Windsor	Implementation of the Quadratic-time Optimal Multi-level Thresholding
Muhannad Asfour Samsur Rahman	2009-2010	B (Hons) Applied Computing	University of Windsor	Feature Extraction for Protein-Protein Interaction Prediction
Ripudamanla Il Ramlall	2008-2009	B (Hons) Computer Science	University of Windsor	An Implementation of a Linear-time Multilevel Thresholding Algorithm in C++
Ricardo Mendoza	2007-2008	Engineering in Computer Science	University of Concepcion, Chile	Feature Selection using Chernoff Distance in the Transformed Space
Carolina Gárate	2007-2008	Engineering in Computer Science	University of Concepcion, Chile	An Efficient Linear Dimensionality Reduction Algorithm
Claudio Henríquez	2007	Engineering in Computer Science	University of Concepcion, Chile	Multi-class Classification of Linear Dimensionality Reduction Techniques
Cesar Monsalve	2007	Engineering in Computer Science	University of Concepcion, Chile	A Hierarchical Refinement Algorithm for Gridding Microarray Images

Omar Uyarte (co-supervision)	2006	B (Hons) Biochemistry	University of Concepcion, Chile	Genotyping Eucalyptus Globulus by Using Random Amplified Polymorphism DNA
Rodrigo Burgos	2006	Engineering in Computer Science	University of Bio Bio, Chile	Pattern Recognition of Images Generated by Epifluorescence Microscopy
Anh Tran Gopinarth Nesarajah Zelalem Gerbie	2004	B (Hons) Computer Science	University of Windsor	Developing a Software Package for Microarray Image Analysis
Ataul Bari Ahmed Ullah Semsettin Ilyas Guorui Li	2003- 2004	B (Hons) Computer Science	University of Windsor	A Prototype to Estimate the Classification Error of Linear Classifiers
Sherri Wheeler Ian Middleton Justin Griffin	2002- 2003	B (Hons) Computer Science	University of Windsor	A Graphical-User- Interface File Compression/Decompr ession Utility
Ryan Craig Leon French Gordon Edwards Robert Maxwell	2002- 2003	B (Hons) Computer Science	University of Windsor	An Intelligent System that Recognizes Benign/Malignant Tumors and Other Objects

Research Grants

1. NSERC Idea2Innovation Grant. Source: NSERC. Project title: “Market Assessment of an intelligent framework for social engineering cyber security training”. Years: 2021. \$20,000. Principal Investigator: L. Rueda. Co-investigator: S. Saad Ahmad
2. *Mitacs Accelerate Grant*. Source: Mitacs. Project: 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. Years: Aug-2020 – Jul-2022. \$165,000 (55,000/year). Principal Investigator: L. Rueda. Industry partner: ITOS Oncology Inc.
3. *Mitacs Research Training Internship Grant*. Source: Mitacs. Projects: “Machine Learning Methods and Tools for RNA-Seq Data Analysis”. Sep-2020 – Dec-2020. \$6,000. Principal Investigator: L. Rueda. Intern: Saiteja Danda
4. *Mitacs Research Training Internship Grant*. Source: Mitacs. Projects: “Assessment of Existing Phishing Campaign Frameworks and Social Engineering Training Programs”. Sep-2020 – Dec-2020. \$ 6,000. Principal Investigators: S. Saad-Ahmed/L. Rueda. Intern: Rui Xu
5. *NSERC RTI Grant*. Source: Natural Sciences and Engineering Research Council of Canada. Project: Multi-user in vivo animal imaging system. Years Apr-2020 – Mar-2022 (\$180,965). Principal Investigator: M. Rahim. Co-Investigators: L. Porter, T. Emadi, M. Crawford, L. Rueda, H. Zhang, D. Xiao.
6. *Mitacs Accelerate Grant*. Source: Mitacs. Project: Machine learning-based data analysis for cancer targeted gene panels. Years: Jul-2019 – Jun-2022. \$ 180,000 (60,000/year). Principal Investigator: L. Rueda. Industry partner: ITOS Oncology Inc.

7. *NSERC Discovery Grant*. Source: Natural Sciences and Engineering Research Council of Canada. Project: Integrative Machine Learning Models for Identification and Validation of Biological Biomarkers. Years: 2019 – 2024. Amount: \$170,000 (34,000/year). Principal Investigator: L. Rueda.
8. *SWORP - Schulich-UWindsor Opportunities for Research Excellence Program*. Source: Schulich School of Medicine and Dentistry, Western University. Years: 2018 – 2019. Amount: \$5,000. Principal Investigator: L. Rueda.
9. *Seeds4Hope Grant*. Source: Windsor & Essex County Cancer Centre Foundation. Project: Genomic profiling to identify age and stage specific drivers of sporadic colorectal cancers. Years: 2018-2020. Amount: \$89,244. Principal Investigator: S. Misra. Co-investigators: L. Porter, D. Cavallo-Medved, L. Rueda (15%), T. Elfiki, A. Ravid, G. Atikukke.
10. *TalentEdge Internship Program*. Source Ontario Centres of Excellence. Project: An Intelligent System that Supports Additive Manufacturing and Machining. Years: 2017-2019. Amount: \$97,750. Principal Investigator: L. Rueda. Intern: Shane Peelar. Industrial Partner: CAMufacturing Solutions Inc.
11. *Seeds4Hope Grant*. Source: Windsor & Essex County Cancer Centre Foundation. Project: Identifying a genetic signature that predicts progression of non-invasive urothelial carcinoma to invasive cancer. Years: 2016-2018. Amount: \$77,236. Principal Investigator: S. Kanjeekal. Co-investigators: D. Cavallo-Medved, L. Porter, L. Rueda (16.83%).
12. *NSERC Engage Grant*. Source: Natural Sciences and Engineering Research Council of Canada. Project: An intelligent system that supports additive manufacturing and machining. Year: 2016. Amount: \$55,000. Principal Investigator: L. Rueda. Industrial Partner: CAMufacturing Solutions Inc.
13. *SWORP - Schulich-UWindsor Opportunities for Research Excellence Program*. Source: Schulich School of Medicine and Dentistry, Western University. Years: 2016 – 2017. Amount: \$5,000. Principal Investigator: L. Rueda.
14. *NSERC Discovery Grant*. Source: Natural Sciences and Engineering Research Council of Canada. Project: Integrative machine learning methods for prediction of protein-protein interactions and analysis of the dynamics of interactomes. Years: 2014 – 2019. Amount: \$130,000 (26,000/year). Principal Investigator: L. Rueda.
15. *Research Infrastructure Grants in Science*. Source: Faculty of Science, University of Windsor. Project Title: Integrative Machine Learning Approaches for Transcriptomic and Interactomic Data Analysis in Breast and Prostate Cancer. Year: 2014. Amount: \$4,500. Principal Investigator: L. Rueda
16. *Seeds4Hope Grant*. Source: Windsor & Essex County Cancer Centre Foundation. Project: Transcriptomic analysis of prostate cancer using RNA-seq data. Years: 2013-2015. Amount: \$77,500. Principal Investigator: L. Rueda. Co-investigator: D. Cavallo-Medved.
17. *NSERC Collaborative Grant*. Bioinformatics Analysis of Protein Interactions in Oral Fluids. Source NSERC, University of Western Ontario. \$6,500. Years: 2010-2011. Principal Investigator: W. Siqueira, Co-Investigator: L. Rueda.
18. *Internal VP Research Grant*. Source: University of Windsor, Office of Research Services. Project: A Research Lab for Pattern Recognition and Bioinformatics. Years: 2010-2011. Amount: \$25,000. Principal Investigator: L. Rueda. Co-Investigator: A. Ngom.
19. *Seeds4Hope Grant*. Source: Windsor & Essex County Cancer Centre Foundation. Project: Role of Stress Factor Signaling in Breast Cancer Initiation and Progression. Years: 2010-2011. Amount: \$70,000 (35,000/year). Principal Investigator: L. Porter. Co-investigators: A. Ngom, L. Rueda, R. Gras.
20. *NSERC Discovery Grant*. Source: Natural Sciences and Engineering Research Council of Canada. Project: Efficient Linear Dimensionality Reduction and Optimal Multi-dimensional Clustering. Years: 2009 – 2013. Amount: \$120,000 (24,000/year). Principal Investigator: L. Rueda.
21. *Start-up Grant*. Machine Learning Methods for Bioinformatics. Source: University of Windsor. Years: 2008-present. Amount: \$17,500. Principal Investigator: L. Rueda.
22. *International Collaboration Travel Fund*. Source: National Council for Scientific and Technical Research of Chile (CONICYT). Year 2007. Amount: \$3,500 (CLP 1,780,000). Principal Investigator: L. Rueda. Co-investigator: B. John Oommen.

23. *Bicentennial Program on Science and Technology*. Source: National Council for Scientific and Technical Research of Chile (CONICYT) and World Bank. Year: 2006-2008. Amount: \$192,000 (CLP 96,000,000). Principal Investigator: L. Rueda. Co-investigators: A. Rodriguez and J. Atkinson.
24. *FONDECYT Operating Grant*. Source: National Council for Scientific and Technical Research of Chile (CONICYT). Project: Robust Analysis of DNA Microarray Time-series Data. Years: 2006-2008. Amount: \$58,500 (CLP 29,279,000). Principal Investigator: L. Rueda.
25. *New Opportunity Fund*. Source: Canadian Foundation for Innovation, Ontario Innovation Trust, and Dell Canada Inc. Project: A research facility for pattern recognition and data compression. Years: 2003 – 2005. Amount: \$94,457. Principal Investigator: L. Rueda.
26. *NSERC Discovery Grant*. Source: Natural Sciences and Engineering Research Council of Canada. Project: Novel Linear Classification Techniques and Efficient Adaptive Encoding Schemes. Years: 2003 – 2007. Amount: \$64,000 (16,000/year). Principal Investigator: L. Rueda.
27. *Start-up Grant*. Source: University of Windsor. Years: 2002-2005. Amount: \$35,000. Principal Investigator: L. Rueda.

Achievement Awards

1. *Mitacs Accelerate Award*. Office of Research and Innovation Services, University of Windsor, 2021.
2. *Mitacs Accelerate Award*. Office of Research and Innovation Services, University of Windsor, 2020.
3. *Ontario Centres of Excellence – TalentEdge Award*. University of Windsor, 2018.
4. *Collaborative & Interdisciplinary Research Award*. Faculty of Science, University of Windsor, 2016.
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. *Certificate of Appreciation*. In recognition for contributions toward the development of the Master’s of Applied Computing Program. Faculty of Science, University of Windsor, 2015.
7. *Faculty Performance Award*. In recognition of outstanding overall performance in research, teaching and service. Faculty of Science, University of Windsor, 2010.
8. Elevated to the grade of *Senior Member* in the Institute of Electrical and Electronics Engineers (IEEE), 2009.
9. *Dean’s Special Recognition Award*. In recognition of excellence in research, scholarship and creative activity. Faculty of Science, University of Windsor, 2009.
10. *Best Paper Award*. Paper presented at CIBCB 2008, Sun Valley, Idaho, USA, with L. Wang, A. Ngom and R. Gras, titled “Evolution Strategy with Greedy Probe Selection Heuristics for the Non-Unique Oligonucleotide Probe Selection Problem”.
11. *University of Windsor Research Achievement Award*, University of Windsor, Canada, 2003.
12. *New Opportunities Fund Award*, Canadian Foundation for Innovation, 2003.
13. *NSERC Postgraduate Scholarship (PGS-B)*. Natural Sciences and Engineering Research Council of Canada, 2001 – 2002.
14. *Ontario Graduate Scholarship (OGS)* winner, 2001/2002, Ontario, Canada.
15. *Postgraduate Scholarship*. Bureau of International Cooperation, Ministry of Education and Culture, Argentina, 1998 – 1999.
16. *Honor Diploma*, (Highest overall average in the Faculty of Mathematics, Physics and Natural Sciences), National University of San Juan, Argentina, 1993.
17. *National Flag Award*, Faculty of Science, National University of San Juan, Argentina, 1992.

Invited Talks

1. iSOM-GSN: An Integrative Approach for Transforming Multi-omic Data into Gene Similarity Networks via Self-organizing Maps. 11th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2020). Highlights Track.

2. Machine Learning Algorithms to Identify Cancer Biomarkers. Ontario Institute for Cancer Research (OICR) & Fight Against Cancer Innovation Trust (FACIT), Windsor, Ontario, Canada, 2019. Invited Speaker.
3. Machine Learning in Finding Biomarkers from Multiple Datasets and Clinical Variables. The Precision Medicine World Conference (PMWC 2018), Ann Arbor, MI. 2018. Invited Speaker.
4. How Machine Learning Helps Find Relevant Transcriptomic Biomarkers in Prostate Cancer, 6th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2018), Granada, Spain, 2018. Keynote Speaker.
5. How Machine Learning Helps Find Relevant Biomarkers in Cancer, *IEEE Youngprofessionals Workshop*, IEEE Windsor Section, Windsor, ON, Canada, 2017. Keynote Speaker.
6. How Machine Learning Helps Finding Meaningful Biomarkers in Cancer Progression, Computer Science Colloquium, School of Computer Science, University of Windsor, Windsor, ON, Canada, 2016.
7. Collaborative Approach to Prostate Cancer Research in Windsor-Essex, Windsor-Essex Prostate Cancer Support Group, Windsor, ON, Canada, 2015.
8. The Role of Sequence and Structural Domains in Mediating Protein-protein Interactions. *5th IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012)*, Philadelphia, USA, 2012. Invited Talk.
9. The Role of Sequence and Structural Domains in Prediction of Protein-protein Interaction Types, Schulich School of Medicine and Dentistry, Western University, Ontario, Canada, 2012. Invited talk.
10. Applications of Multilevel Thresholding Algorithms to Transcriptomics Data, *16th Iberoamerican Congress on Pattern Recognition (CIARP 2011)*, Pucon, Chile, 2011. Keynote talk.
11. Automatic Algorithms for Analysis of cDNA Microarray and Chip-seq Data, *Microarray World Congress (MWC 2011)*, San Francisco, USA, 2011. Invited talk.
12. Profile Alignment Methods for Clustering Gene Expression Time-Series Data, Centre for Addiction and Mental Health, University of Toronto, Toronto, Canada, 2010. Invited talk.
13. DNA Microarray Image Processing, the *IEEE Pacific-Rim Symposium on Image and Video Technology (PSIVT 2007)*, 2007. Invited tutorial.
14. DNA Microarrays, Department of Computer Science, Catholic University of Chile, 2005.
15. DNA Microarrays, Department of Computer Science, University of Concepcion, 2005.
16. Optimal Pairwise Linear Classifiers, School of Computer Science, University of Windsor, 2002.
17. Optimal Pairwise Linear Classifiers, Department of Computer Science, University of Manitoba, 2002.
18. Optimal Pairwise Linear Classifiers, Department of Computer Science, University of Regina, 2002.
19. Optimal Pairwise Linear Classifiers, Department of Mathematics and Computer Science, University of Lethbridge, 2002.
20. Optimal Pairwise Linear Classifiers, School of Information Technology and Engineering, University of Ottawa, 2002.
21. Optimal Pairwise Linear Classifiers, Department of Computer Science, University of Western Ontario, 2001.
22. Optimal Pairwise Linear Classifiers, Department of Computing and Software, McMaster University, 2001.

Publications

Books

1. **L. Rueda**. *Microarray Image and Data Analysis: Theory and Practice*. CRC Press. 2014.

Conference Proceedings

1. D. Mery and **L. Rueda**. Advances in Image and Video Technology, Proceedings of the *IEEE Pacific-Rim Symposium on Image and Video Technology (PSIVT 2007)*. Lecture Notes in Computer Science (LNCS), Vol. 4872, Springer, 2007.

2. **L. Rueda**, D. Mery and J. Kittler. Progress in Pattern Recognition, Image Analysis and Applications, Proceedings of the 12th Iberoamerican Congress on Pattern Recognition (CIARP 2007), Lecture Notes in Computer Science (LNCS), Vol. 4756, Springer, 2007.

Book Chapters

1. A. Alkhateeb, A. Abou Tabl, **L. Rueda**, “Deep Learning in Multi-Omics Data Integration in Cancer Diagnostics”, *Deep Learning for Biomedical Data Analysis*, Springer, 2021. Published.
2. M. Maleki, M. Hall, **L. Rueda**, “Structural Domains in Prediction of Biological Protein-Protein Interactions”, *Pattern Recognition in Computational Molecular Biology: Techniques and Approaches*, Wiley, 2015, pp. 291-314.
3. **L. Rueda**, A. Ali, “Introduction to Microarrays”, *Microarray Image and Data Analysis: Theory and Practice*, CRC Press, 2014, pp. 1-39.
4. I. Rezaeian, **L. Rueda**, “Automatic Methods for DNA Microarray Image Gridding”, *Microarray Image and Data Analysis: Theory and Practice*, CRC Press, 2014, pp. 77-108.
5. D. Rojas, **L. Rueda**, H. Urrutia, A. Ngom, G. Cárcamo, “Automatic Segmentation Methods and Applications to Biofilm Image Analysis”, *Data Mining in Biomedical Signaling, Imaging and Systems*, CRC Press, 2011, pp. 319-350.
6. N. Subhani, **L. Rueda**, A. Ngom, “On Clustering Gene Expression Time-series Signals”, *Data Mining in Biomedical Signaling, Imaging and Systems*, CRC Press, 2011, pp. 227-262.
7. B. John Oommen, **L. Rueda**, “Stochastic Learning-based Weak Estimation of Multinomials and Its Applications to Pattern Recognition and Data Compression”, *Knowledge-Based Intelligent System Advancements: Systemic and Cybernetic Approaches*, IGI Global Publishers, ISBN 978-1-61692-811-7, 2010, pp. 1-29.
8. **L. Rueda**, A. Bari, “Clustering Time-series Gene Expression Data”, *Oligonucleotide Array Sequence Analysis*, Nova Science Publishers, ISBN 978-1-60456-542-3, 2008, pp. 121-159.

Journal Publications

1. A. Alkhateeb, G. Atikukke, **L. Rueda**. “Machine learning methods for prostate cancer diagnosis”, *Journal of Cancer Biology*, 1(3): 70-75, 2020.
2. S. Jubair, A. Alkhateeb, A Abou Tabl, **L. Rueda**, A. Ngom, “A novel approach to identify subtype specific network biomarkers of breast cancer survivability”, *Network Modeling Analysis in Health Informatics and Bioinformatics*, 9:43, 2020. DOI : 10.1007/s13721-020-00249-4.
3. N. Fatima, **L. Rueda**. “iSOM-GSN: An Integrative Approach for Transforming Multi-omic Data into Gene Similarity Networks via Self-organizing Maps”, *Bioinformatics*, Volume 36, Issue 15, 2020, Pages 4248–4254.
4. A. Alkhateeb, G. Atikukke, L. Porter, B.A. Fifield, D. Cavallo-Medved, J. Facca, Y. El-Gohary, T. Zhang, O. Hamzeh, **L. Rueda**, S. Kanjeekal. “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”, *Journal of Clinical Oncology*, 2020, 38(6_suppl):568-568. DOI: 10.1200/JCO.2020.38.6_suppl.568.
5. O. Hamzeh, A. Alkhateeb, J. Zheng, S. Kandalam, **L. Rueda**. “Prediction of tumor location in prostate cancer tissue using a machine learning system on gene expression data”. *BMC Bioinformatics*, 2020, **21**,78, 2020. DOI: 10.1186/s12859-020-3345-9
6. O. Hamzeh, A. Alkhateeb, J. Zheng, S. Kandalam, C. Leung, G. Atikukke, D. Cavallo-Medved, N. Palanisamy, **L. Rueda**. “A Hierarchical Machine Learning Model to Discover Gleason Grade-Specific Biomarkers in Prostate Cancer”, *Diagnostics*, 2019, 9(4):219.
7. A. Abou Tabl, A. Alkhateeb, W. El-Maraghy **L. Rueda**, A. Ngom. “A machine learning approach for identifying gene biomarkers guiding the treatment of breast cancer.” *Frontiers in Genetics*, 2019, 10:256.

8. A. Alkhateeb, I. Rezaeian, S. Reddy, D. Cavallo-Medved, L. Porter, **L. Rueda**. “Transcriptomics signature from next-generation sequencing data reveals new transcriptomic biomarkers related to prostate cancer”, 2019, *Cancer Informatics*, 18, 1176935119835522.
9. A. Abou Tabl, A. Alkhateeb, **L. Rueda**, W. El-Maraghy, A. Ngom. “A novel approach for identifying relevant genes for breast cancer survivability on specific therapies”, *Evolutionary Bioinformatics*, 2018, 14:1176934318790266. doi: 10.1177/1176934318790266.
10. S. Peelar, J. Urbanic, B. Hedrick, **L. Rueda**. “Real-Time Visualization of Bead Based Additive Manufacturing Toolpaths Using Implicit Boundary Representations”, *Computer-Aided Design and Applications*, 2018, pp. 322-326.
11. Y. Li, M. Maleki, N. Carruthers, P. Stemmer, A. Ngom, **L. Rueda**. “The predictive performance of short-linear motif features in the prediction of Calmodulin-binding proteins”, *BMC Bioinformatics*, 2018, 19 (Suppl 14) :410.
12. F. Firoozbakht, I. Rezaeian, M. D’Agnillo, L. Porter, **L. Rueda**, A. Ngom. “An integrative approach for identifying network biomarkers of breast cancer subtypes using genomics, interactomics and transcriptomics data”, *Journal of Computational Biology*, 2017, 24(8):756-766, doi: 10.1089/cmb.2017.0010.
13. 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.
14. E.J. Mucaki, K. Baranova, H.P. Quang, I. Rezaeian, D. Angelov, A. Ngom, **L. Rueda**, P.K. Rogan. “Predicting Outcomes of Hormone and Chemotherapy in the Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) Study by Machine Learning”. *F1000Research*, 2017, 5:2124. (doi: 10.12688/f1000research.9417.2)
15. M. Alshehri, I. Rezaeian, A. Alkhateeb, **L. Rueda**. “Potential protein isoforms reveal additional information on biomarkers obtained from RNA-Seq data” [v1; not peer reviewed]. *F1000Research* 2016, 5(ISC Comm J):1820 (poster) (doi: 10.7490/f1000research.1112702.1).
16. I. Rezaeian, A. Tavakoli, D. Cavallo-Medved, L. Porter, **L. Rueda**. “A model used to detect differential splice junctions as biomarkers in prostate cancer from RNA-seq data”, *Journal of Biomedical Informatics*, 2016, 60:422-30. doi: 10.1016/j.jbi.2016.03.010.
17. Y. Li, B. J. Oommen, A. Ngom, **L. Rueda**. “Pattern Classification Using a New Border Identification Paradigm: The Nearest Border Technique”, *Neurocomputing*, Vol. 157, 2015, pp. 105–117.
18. I. Rezaeian, **L. Rueda**. “CMT: A Constrained Multi-level Thresholding Approach for ChIP-Seq Data Analysis”, *PLoS ONE*, 2014, 9(4): e93873. doi:10.1371/journal.pone.0093873.
19. M. Maleki, M. Hall, **L. Rueda**. “The Role of Structural Domains in Prediction of Protein-protein Interaction Types”. *Network Modeling Analysis in Health Informatics and Bioinformatics*, 2013, 2(4):267-275. DOI 10.1007/s13721-013-0043-9.
20. M. Maleki, G. Vasudev, **L. Rueda**. “The role of electrostatic energies in prediction of obligate protein-protein interactions”. *Proteome Science*, 2013, 11(Suppl 1):S11.
21. N. Shakiba, **L. Rueda**. “MicroRNA Identification Using Linear Dimensionality Reduction with Explicit Feature Mapping”. *BMC Proceedings (Supplements)*, 2013, 7(Suppl 7):S8.
22. Md. Aziz, M. Maleki, **L. Rueda**, M. Raza, S. Banerjee, “Prediction of Biological Protein-protein Interactions using Atom-type and Amino Acid Properties”, *Proteomics*, 2011, 11(19):3802–3810, DOI: 10.1002/pmic.201100186.
23. **L. Rueda**, I. Rezaeian, “A Fully Automatic Gridding Method for cDNA Microarray Images”, *BMC Bioinformatics*, 2011, 12:113.
24. D. Rojas, **L. Rueda**, A. Ngom, H. Urrutia, G. Carcamo, “Image Segmentation of Biofilm Structures Using Optimal Multi-Level Thresholding”, *International Journal of Data Mining and Bioinformatics*, 2011, 5(3):266-286.
25. A. Ngom, **L. Rueda**, L. Wang, R. Gras, “Selection Based Heuristics for the Non-Unique Oligonucleotide Probe Selection Problem in Microarray Design”, *Pattern Recognition Letters*, 2010, 31(14): 2113-2125.
26. N. Subhani, **L. Rueda**, A. Ngom, C. Burden, “Multiple Gene Expression Profile Alignment for Microarray Time-series Data Clustering”, *Bioinformatics*, 2010, 26(18):2281-2288.

27. **L. Rueda**, B. J. Oommen, C. Henriquez, “Multi-class Pairwise Linear Dimensionality Reduction Using Heteroscedastic Schemes”, *Pattern Recognition*, 43(2010) 2456–2465.
28. P. Jopia, N. Ruiz-Tagle, M. Villagrán, K. Sossa, S. Pantoja, **L. Rueda**, H. Urrutia, “Biofilm Growth Kinetics of a Monomethylamine Producing Alphaproteobacteria Strain Isolated from an Anaerobic Reactor”, *Anaerobe*, 16(2010) 19-26.
29. L. Wang, A. Ngom, **L. Rueda**, R. Gras, “An Evolutionary Approach to the Non-unique Oligonucleotide Probe Selection Problem”, *Springer Trans. on Computational Systems Biology*, Springer, LNBI 5410, 2008, pp. 143-162.
30. **L. Rueda**, A. Bari, A. Ngom, “Clustering Time-series Gene Expression Data with Unequal Time Intervals”, *Springer Trans. on Computational Systems Biology*, Springer, LNBI 5410, 2008, pp. 100-123.
31. **L. Rueda** and M. Herrera, “A Theoretical Comparison of Two-class Fisher’s and Heteroscedastic Linear Dimensionality Reduction Schemes”, *Pattern Recognition Letters*, Vol. 29, Issue 16, 2008, pp. 2092-2098.
32. **L. Rueda** and B. John Oommen, “An Efficient Compression Scheme for Data Communication which Uses a New Family of Self-Organizing Binary Search Trees”, *International Journal of Communication Systems*, Vol. 21, Issue 10, 2008, pp. 1091-1120.
33. **L. Rueda** and M. Herrera, “Linear Dimensionality Reduction by Maximizing the Chernoff Distance in the Transformed Space”, *Pattern Recognition*, Vol. 41, Issue 10, 2008, pp. 3138-3152.
34. W. Yang, **L. Rueda** and A. Ngom, “On Finding the Best Parameters of Fuzzy k -Means for Clustering Microarray Data”, *Multiple-Valued Logic and Soft-Computing Journal*, Vol. 13, Issue 1/2, 2007, pp. 145-178.
35. B. Schell, M. Vargas-Martin, P. Hung, and **L. Rueda**, “Cyber Child Pornography: A Review Paper of the Social and Legal Issues and Remedies—and A Proposed Technological Solution”, *Aggression and Violent Behavior*, 2007, Vol. 12, Issue 1, pp. 45-63.
36. A. Shupo, M. Vargas-Martin, **L. Rueda**, A. Bulkan, Y. Chen and P. Hung, “Toward Efficient Detection of Child Pornography in the Network Infrastructure”, *International Journal on Computer Science and Information Systems*, Vol. 1, No. 2, 2006, pp. 15-31.
37. **L. Rueda** and B. J. Oommen, “Stochastic Automata-based Estimators for Adaptively Compressing Files with Non-Stationary Distributions”. *IEEE Transactions on Systems, Man and Cybernetics*. Vol. 36, Issue 5, 2006, pp. 1196-1200.
38. **L. Rueda** and Y. Zhang, “Geometric Visualization of Clusters Obtained from Fuzzy Clustering Algorithms”. *Pattern Recognition*, Vol. 39, 2006, pp. 1415-1429.
39. **L. Rueda** and B. J. Oommen, “A Fast and Efficient Nearly-Optimal Adaptive Fano Coding Scheme”, *Information Sciences*, Vol. 276, 2006, pp. 1656–1683.
40. B. J. Oommen and **L. Rueda**, “Stochastic Learning-based Weak Estimation of Multinomial Random Variables and Its Applications to Pattern Recognition in Non-stationary Environments”, *Pattern Recognition*, Vol. 39, Issue 3, 2006, pp. 328-341.
41. **L. Rueda** and V. Vidyadharan, “A Hill-climbing Approach for Automatic Gridding of cDNA Microarray Images”. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, Vol. 3, No. 1, 2006, pp. 72-83.
42. L. Qin, **L. Rueda**, A. Ali and A. Ngom, “Spot Detection and Image Segmentation in DNA Microarray Data”. *Applied Bioinformatics*, 2005, 4(1):1-12.
43. **L. Rueda**, “A One-dimensional Analysis for the Probability of Error of Linear Classifiers for Normally Distributed Classes”. *Pattern Recognition*, Vol. 38, Issue 8, 2005, pp. 1197-1207.
44. B. J. Oommen and **L. Rueda**, “A Formal Analysis of Why Heuristic Functions Work”. *Artificial Intelligence*, Vol. 164, 2005, pp. 1-22.
45. **L. Rueda**, “An Efficient Approach to Compute the Threshold in Multi-dimensional Linear Classifiers”. *Pattern Recognition*, Vol. 37, Issue 4, 2004, pp. 811-826.
46. **L. Rueda** and B. J. Oommen, “A Nearly-Optimal Fano-based Coding Algorithm”. *Information Processing & Management*, Vol. 40, Issue 2, 2004, pp. 257-268.
47. **L. Rueda**, “Selecting the Best Hyperplane in the Framework of Optimal Pairwise Linear Classifiers”. *Pattern Recognition Letters*, Vol. 25, Issue 1, 2004, pp. 49-62.

48. **L. Rueda** and B. J. Oommen, "On Optimal Pairwise Linear Classifiers for Normal Distributions: The d -Dimensional Case". *Pattern Recognition*, Vol. 36, Issue 1, 2003, pp. 13-23.
49. B. J. Oommen and **L. Rueda**, "The Efficiency of Modern-Day Histogram-Like Techniques for Query Optimization". *The Computer Journal*, Vol. 45, No. 5, 2002, pp. 494-510.
50. Dimensional Case". *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 24, No. 2, 2002, pp. 274-280.

Refereed Conference Publications and Presentations

1. A. Vasighizaker, S. Danda, **L. Rueda**. "Cell Type Identification via Convolutional Neural Networks and Self-Organizing Maps on Single-Cell RNA Sequencing Data". ICCIBCB 2021: International Conference on Computational Intelligence in Bioinformatics and Computational Biology. Madrid, Spain, 2021. In Press.
2. S. Danda, A. Vasighizaker, **L. Rueda**. "Unsupervised Identification of SARS-CoV-2 Target Cell Groups via Nonlinear Dimensionality Reduction on Single-cell RNA-Seq Data," 2020 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Seoul, Korea (South), 2020, pp. 2737-2744, doi: 10.1109/BIBM49941.2020.9313378.
3. A. Alkhateeb, L. Zhou, A. Abou Tabl, **L. Rueda**. "Deep Learning Approach for Breast Cancer InClust 5 Prediction based on Multiomics Data Integration". Machine Learning Models for Multi-omics Data Integration Workshop (MODI), in conjunction with the 10th ACM Conference on Bioinformatics, Computational Biology (ACM BCB), Virtual, 2020, pp. 1-6.
4. **L. Rueda**, N. Fatima. "iSOM-GSN: An Integrative Approach for Transforming Multi-omic Data into Gene Similarity Networks via Self-organizing Maps". 11th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2020). Highlight Presentation, Atlanta, USA, 2020, Article No. 38. pp. 1.
5. G. Atikukke, A. Alkhateeb, L. Porter, B. Fifield, D. Cavallo-Medved, J. Facca, T. Elfiki, A. Elkeilani, **L. Rueda**, S. Misra. "P-370 Comprehensive targeted genomic profiling and comparative genomic analysis to identify molecular mechanisms driving cancer progression in young-onset sporadic colorectal cancer", ESMO 22nd World Congress on Gastrointestinal Cancer, 2020, Vol. 31, Suppl. 3, S209-S210.
6. M. Shah, A. Nour, A. Ngom, **L. Rueda**. "Cancer Detection Based on Image Classification by Using Convolution Neural Network", 8th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2020), Granada, Spain, 2020, pp. 275-286.
7. H. Pham, A. Ngom, **L. Rueda**, "A Data Integration Approach for Detecting Biomarkers of Breast Cancer Survivability". 8th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2020), Granada, Spain, 2020, pp. 49-60.
8. N. Fatima, J. Fernandes, **L. Rueda**, "Self-organizing Maps Combined with Convolutional Neural Networks Reveal Predictive Gene Similarity Networks on Multi-omics", 24th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2020), Padua, Italy, 2020. Poster presentation, peer-reviewed.
9. S. Ozoglu, O. Hamzeh, **L. Rueda**, "An Integrative Knowledge-based Method to Identify Cancer Biomarkers Based on Gene-Disease Relations", 24th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2020), Padua, Italy, 2020. Poster presentation, peer-reviewed.
10. 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. Eklaj, R. Goel, R. Sorenson, B. Al-Farra, H. Khalaff, **L. Rueda**, S. Kanjeekal. 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 ASCO Genitourinary Cancers Symposium. San Francisco, CA, USA. 2020. Poster presentation. Peer-reviewed.
11. O. Hamzeh, **L. Rueda**. "A gene-disease-based machine learning approach to identify prostate cancer biomarkers", Machine Learning Models for Multi-omics Data Integration Workshop (MODI), in

- conjunction with the 10th ACM Conference on Bioinformatics, Computational Biology (ACM BCB), Niagara Falls, NY, USA, 2019, pages 633-638.
12. A. Alkhateeb, N. Fatima, **L. Rueda**, G. Atikukke, S. Misra. "A Deep Learning Model to Identify a Genomic Signature Driving Sporadic Colorectal Cancer in Young Adults", Machine Learning Models for Multi-omics Data Integration Workshop (MODI), in conjunction with the 10th ACM Conference on Bioinformatics, Computational Biology (ACM BCB), Niagara Falls, NY, USA, 2019, pages 645-645.
 13. O. Hamzeh, **L. Rueda**. "A multi-modal knowledge-based hybrid feature selection model for identification of cancer biomarkers". 27th Conference on Intelligent Systems for Molecular Biology - 18th European Conference on Computational Biology (ISMB/ECCB 2019), Basel, Switzerland, 2019. Poster presentation, peer-reviewed.
 14. S. Peelar, J. Urbanic, **L. Rueda**, B. Hedrick. "Real-Time Visualization of Bead Based Additive Manufacturing Toolpaths Using Implicit Boundary Representations". 15th Annual International CAD Conference (CAD 2018), Paris, France, 2018, pp. 322-326.
 15. O. Hamzeh, T. Zhang, B. Fifield, Y. El-Gohary, R. Goel, T. Deklaj, R. Sorenson, T. Eldson, J. Mathews, A. Ghafoor, G. Atikukke, D. Cavallo-Medved, L. Porter, **L. Rueda**, S. Kanjeeal. "Muscle invasion in bladder cancer is associated with copy number alterations of TP53, DDR2 and MLL2", 26th Conference on Intelligent Systems for Molecular Biology (ISMB 2018), Chicago, IL, USA, 2018. Poster presentation, peer-reviewed.
 16. S. Jubair, **L. Rueda**, A. Ngom. "Identifying subtype specific network-biomarkers of breast cancer survivability", IEEE World Congress on Computational Intelligence/International Joint Conference on Neural Networks (WCCI 2018)/IJCNN 2018), Rio de Janeiro, Brazil, 2018. Pages 1-9.
 17. S. Krishnamoorthy, **L. Rueda**, S. Saad, H. Elmiligi. "Identification of User Behavioral Biometrics for Authentication using Keystroke Dynamics and Machine Learning", 2nd International Conference on Biometric Engineering and Applications (ICBEA 2018), Amsterdam, The Netherlands, 2018, Pages 50-57.
 18. O. Hamzeh, A. Alkhateeb, **L. Rueda**, "Using Gene Expression to Predict Tumor Location in Prostate Cancer Tissue", 22nd Annual International Conference on Research in Computational Molecular Biology (RECOMB 2018), Paris, France, 2018. Poster presentation, peer-reviewed.
 19. 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.
 20. 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.
 21. A. Abou Tabl, A. Alkhateeb, W. El-Maraghy, **L. Rueda**, A. Ngom. "Identifying Gene Biomarkers for Breast Cancer Survival Using a Tree-based Approach". *IEEE Biomedical and Health Informatics (BHI 2018)*, Las Vegas, NV, 2018. Poster presentation.
 22. R. Razavi-Far, E. Hallaji, M. Saif, **L. Rueda**. "A Hybrid Scheme for Fault Diagnosis with Partially Labeled Sets of Observations", 16th IEEE International Conference on Machine Learning and Applications (ICMLA 2017), Cancun, Mexico, 2017, pp. 61-67.
 23. H. Quang, **L. Rueda**, A. Ngom. "Predicting Breast Cancer Outcome under Different Treatments by Feature Selection Approaches", *ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB 2017)*, 2017, Boston, MA, USA, pp. 617-617.
 24. N. Mangalakumar, H. Quang, A. Alkhateeb, **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)*, 2017, Boston, MA, USA, pp. 594-594.
 25. W. Xu, **L. Rueda**, A. Ngom. "Drug-Target Interaction Networks Prediction using Short-Linear Motifs", 25th Conference on Intelligent Systems for Molecular Biology and the 16th European Conference on Computational Biology (ISMB/ECCB 2017), Prague, Czech Republic, 2017. Poster presentation, peer-reviewed.
 26. A. Karkar, O. Hamzeh, A. Alkhateeb, **L. Rueda**, "Finding Biomarkers Associated with Prostate Cancer Gleason Stages using Next Generation Sequencing and Machine Learning Techniques", 25th Conference

- on Intelligent Systems for Molecular Biology and the 16th European Conference on Computational Biology (ISMB/ECCB 2017), Prague, Czech Republic, 2017. Poster presentation, peer-reviewed.
27. N. Mangalakumar, A. Alkhateeb, H. Quang, **L. Rueda**, A. Ngom. "Identifying Gene Biomarkers of Breast Cancer Survivability from Time-Series Data", 25th Conference on Intelligent Systems for Molecular Biology and the 16th European Conference on Computational Biology (ISMB/ECCB 2017), Prague, Czech Republic, 2017. Poster presentation, peer-reviewed.
 28. 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.
 29. S. Chakrabarti, R. Razavi-Far, M. Saif, **L. Rueda**. "Multi-Class Heteroscedastic Linear Dimensionality Reduction Scheme for Diagnosing Process Faults", 30th Canadian IEEE Conference on Electrical and Computer Engineering (CCECE 2017), Windsor, ON, Canada, 2017.
 30. 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". 5th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2017), Granada, Spain, 2017, pp. 337-348.
 31. Y. Li, M. Maleki, N.J. Carruthers, **L. Rueda**, P.M. Stemmer, A. Ngom. "Prediction of Calmodulin Binding Proteins Using Short Linear Motifs". 5th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2017), Granada, Spain, 2017, pp. 107-117.
 32. 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.
 33. H. Quang, A. Ngom, **L. Rueda**, "A new feature selection approach for optimizing prediction models, applied to breast cancer subtype classification", IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2016), Shenzhen, China, 2016, pp. 1535-1541.
 34. H. Quang, I. Rezaeian, E. Mucaki, A. Ngom, **L. Rueda**, P. Rogan. "Predicting Breast Cancer Drug Response via an Apriori-like Gene Selection Approach", The Fourth International Society for Computational Biology Latin America Bioinformatics Conference (ISCB-LA 2016), Buenos Aires, Argentina. Poster presentation.
 35. 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.
 36. H. Pham, A. Ngom, **L. Rueda**, "AFSP – an efficient method for classifier-specific feature selection", IEEE Symposium Series on Computational Intelligence (IEEE SSCI 2016), Athens, Greece, 2016, pp. 1-8.
 37. 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.
 38. F. Firoozbakht, I. Rezaeian, A. Ngom, **L. Rueda**, "An Integrative Approach for Identification of Network Biomarkers in Breast Cancer Subtypes", 12th International Symposium on Bioinformatics Research and Applications (ISBRA 2016), Minsk, Belarus, 2016, pp. 1-4.
 39. M. Alshehri, A. Alkhateeb, I. Rezaeian, **L. Rueda**, "Potential Protein Isoforms Reveal Additional Information on Biomarkers Obtained from RNA-Seq Data", 24th Conference on Intelligent Systems for Molecular Biology (ISMB 2016), Orlando, Florida, USA, 2016. Poster presentation, peer-reviewed.
 40. 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.
 41. 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.

42. M. D'Agnillo, I. Rezaeian, A. Ngom, **L. Rueda**, "Machine Learning Approaches for Breast Cancer Subtypes Reveal Key Genes as Potential Biomarkers", The GLBIO/CCBC Great Lakes Bioinformatics and the Canadian Computational Biology Conference, 2016, Toronto, Canada. Poster presentation.
43. Y. Li, **L. Rueda**, A. Ngom, "Prediction of High-throughput Protein-protein Interactions Using Short Linear Motifs", The GLBIO/CCBC Great Lakes Bioinformatics and the Canadian Computational Biology Conference, 2016, Toronto, Canada. Poster presentation.
44. A. Alkhateeb, I. Rezaeian, **L. Rueda**, "Hierarchical 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.
45. I. Rezaeian, E. Mucaki, K. Baranova, H.P. Quang, D. Angelov, L. Ilie, A. Ngom, **L. Rueda**, P. Rogan, "Predicting patient outcomes of hormone therapy in the METABRIC breast cancer study", The GLBIO/CCBC Great Lakes Bioinformatics and the Canadian Computational Biology Conference, 2016, Toronto, Canada. Poster presentation.
46. M. Pandit, M. Maleki, N. J. Carruthers, P. Stemmer, **L. Rueda**, "Prediction of Calmodulin-binding Proteins Using Canonical Motifs", The GLBIO/CCBC Great Lakes Bioinformatics and the Canadian Computational Biology Conference, 2016, Toronto, Canada. Poster presentation.
47. M. Farajzadeh-Zanjani, R. Razavi-Far, M. Saif, **L. Rueda**, "Efficient feature extraction of vibration signals for diagnosing bearing defects in induction motors", *The Annual International Joint Conference on Neural Networks (IJCNN 2016)*, Vancouver, Canada, 2016, pp. 4504-4511.
48. F. Firoozbakht, I. Rezaeian, A. Ngom, **L. Rueda**, "Breast Cancer Network Biomarker Identification by Incorporating Genomics, Transcriptomics and Proteomics Data", *20th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2016)*, Santa Monica, CA, USA, 2016. Poster and Oral presentation, peer-reviewed.
49. A. Alkhateeb, I. Rezaeian, **L. Rueda**, "Nonnegative Matrix Factorization Clustering for Time Series Cancer Progression Data", *20th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2016)*, Santa Monica, CA, USA, 2016. Poster and Oral presentation, peer-reviewed.
50. 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.
51. 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.
52. 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.
53. F. Firoozbakht, I. Rezaeian, A. Ngom, **L. Rueda**, "Identifying the Network Biomarkers of Breast Cancer Subtypes by Interaction", *Advanced in Bioinformatics and Artificial Intelligence: Bridging the Gap (IJCAI-BAI 2015)*, Buenos Aires, Argentina, 2015, pp. 24-32.
54. M. Maleki, M.H. Dezfulian, **L. Rueda**, "Identification of High Affinity Ubiquitin Variants: an in Silico Mutagenesis-based Approach", *Advanced in Bioinformatics and Artificial Intelligence: Bridging the Gap (IJCAI-BAI 2015)*, Buenos Aires, Argentina, 2015, pp. 56-57. Poster presentation.
55. 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.
56. Y. Li, B. Rezaei, A. Ngom, **L. Rueda**, "Prediction of High-Throughput Protein-Protein Interactions based on Protein Sequence Information", *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2015)*, Niagara Falls, Canada, 2015, pp. 1-6, DOI: 10.1109/CIBCB.2015.7300310.

57. F. Firoozbakht, I. Rezaeian, L. Porter, A. Ngom, **L. Rueda**, “A Novel Approach for Finding Informative Genes in Ten Subtypes of Breast Cancer”, *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2015)*, Niagara Falls, Canada, 2015, pp. 1-6, DOI: 10.1109/CIBCB.2015.7300301.
58. M. Maleki, **L. Rueda**, “Classification via Correlation-based Feature Grouping”, *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2015)*, Niagara Falls, Canada, 2015, pp. 1-6, DOI: 10.1109/CIBCB.2015.7300293.
59. 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).
60. M. Maleki, M. Dezfulian, **L. Rueda**, “Computational modeling of the effect of amino acid substitutions on the formation of Ubiquitin-based complexes”, *19th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2015)*, Warsaw, Poland, 2015, pp. 66. Poster presentation (peer-reviewed).
61. M. Maleki, M. Dezfulian, **L. Rueda**, “A Computational Domain-based Feature Grouping Approach for Prediction of Stability of SCF Ligases”, *3rd International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2015)*, Granada, Spain, 2015. LNCS, Vol. 9043, pp. 630-640.
62. M. Maleki, **L. Rueda**, M. Dezfulian, W. Crosby, “Computational Analysis of the Stability of SCF Ligases Employing Domain Information”, *ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACMBCB 2014)*, Newport Beach, CA, USA, 2014, pp. 625-626.
63. F. Firoozbakht, I. Rezaeian, L. Porter, **L. Rueda**, “A New Compact Set of Biomarkers for Distinguishing among Ten Breast Cancer Subtypes”, *4th IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Miami, USA, 2014.
64. I. Rezaeian, **L. Rueda**, “A New Multi-level Thresholding Algorithm for Finding Peaks in ChIP-Seq Data”, *4th IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Miami, USA, 2014.
65. I. Rezaeian, A. Tavakoli, D. Cavallo-Medved, L. Porter, **L. Rueda**, “Finding Differential Splice Junctions as Biomarkers in Prostate Cancer from Next Generation Sequencing Data”, *18th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2014)*, Pittsburgh, USA, 2014. Poster presentation (peer-reviewed).
66. M. Maleki, M. Dezfulian, B. Crosby, **L. Rueda**, “Computational Analysis of Domain Interactions between Components of the SCF Ligase”, *18th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2014)*, Pittsburgh, USA, 2014. Poster presentation (peer-reviewed).
67. F. Firoozbakht, I. Rezaeian, A. Ngom, L. Porter, **L. Rueda**, “Using a Hierarchical Classification Model for Predicting Ten Breast Cancer Subtypes”, *18th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2014)*, Pittsburgh, USA, 2014. Poster presentation (peer-reviewed).
68. **L. Rueda**, M. Pandit, “A Model Based on Minmotifs for Classification of Stable Protein-protein Complexes”, *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2014)*, Honolulu, Hawaii, USA, 2014, pp. 1-6.
69. Y. Li, B. John Oommen, A. Ngom, **L. Rueda**, “A New Paradigm for Pattern Classification: Nearest Border Techniques”, *26th Australasian Joint Conference on Artificial Intelligence (AI 2013)*, Dunedin, New Zealand, 2013, pp. 441-446.
70. M. Pandit, **L. Rueda**, “Prediction of Biological Protein-protein Interaction Types Using Short, Linear Motifs”, *ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACMBCB 2013)*, Washington, DC, USA, 2013, pp. 699-700.
71. N. Shakiba, **L. Rueda**. “MicroRNA Identification Using Linear Dimensionality Reduction with Explicit Feature Mapping”. *8th Great Lakes Bioinformatics Conference (GLBIO 2013)*. Pittsburgh, USA, 2013.
72. I. Rezaeian, Y. Li, M. Crozier, E. Andrechek, A. Ngom, **L. Rueda**, L. Porter. “Identifying Informative Genes for Prediction of Breast Cancer Subtypes”. *8th IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2013)*, Nice, France, 2013. pp. 138-148.

73. M. Pandit, **L. Rueda**, “Prediction of Obligate Protein-protein Interactions Using Short, Linear Motifs”, *17th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2013)*, Beijing, China, 2013. Poster presentation (peer-reviewed).
74. Y. Li, A. Ngom, **L. Rueda**, “A Framework of Gene Subset Selection Using Multiobjective Evolutionary Algorithm”, *7th IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2012)*, Tokyo, Japan, 2012, pp. 38-48.
75. I. Rezaeian, **L. Rueda**, “A New Algorithm for Finding Enriched Regions in ChIP-Seq Data”, *ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACMBCB 2012)*, Orlando, USA, 2012, pp. 282-288.
76. M. Hall, M. Maleki, **L. Rueda**, “Multi-level Structural Domain-domain Interactions for Prediction of Obligate and Non-obligate Protein-protein Interactions”, *ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACMBCB 2012)*, Orlando, USA, 2012, pp. 518-520.
77. I. Rezaeian, **L. Rueda**, “Finding Enriched Regions and Genomic Features in ChIP-Seq Data”, *5th IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012)*, Philadelphia, USA, 2012, pp. 487-490.
78. G. Vasudev, **L. Rueda**, “A Model to Predict and Analyze Protein-protein Interaction Types Using Electrostatic Energies”, *5th IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012)*, Philadelphia, USA, 2012, pp. 543-547.
79. S. Banerjee, **L. Rueda**, M. Maleki, “Prediction of Crystal Packing and Biological Protein-protein Interactions”, *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2012)*, San Diego, USA, 2012, pp. 16-20.
80. M. Maleki, M. Hall, **L. Rueda**, “Using Structural Domain to Predict Obligate and Non-obligate Protein-protein Interactions”, *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2012)*, San Diego, USA, 2012, pp. 9-15.
81. M. Maleki, M. Aziz, **L. Rueda**, “Analysis of Relevant Physicochemical Properties in Obligate and Non-obligate Protein-protein Interactions”, *4th IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBM 2011)*, Atlanta, USA, 2011. pp. 345-351
82. M. Maleki, **L. Rueda**, “Domain-domain Interactions in Obligate and Non-obligate Protein-protein Interactions”. *4th IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBM 2011)*, Atlanta, USA, 2011. pp. 907-908. Poster presentation.
83. A. Jafarian, A. Ngom, **L. Rueda**, “A Novel Recursive Feature Subset Selection Algorithm”, *11th IEEE International Conference on Bioinformatics and Bioengineering (BIBE 2011)*, Taichung, Taiwan, 2011, pp. 78-83.
84. A. Jafarian, A. Ngom, **L. Rueda**, “New Gene Subset Selection Approaches Based on Linear Separating Genes and Gene-Pairs”, *6th IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2011)*, Delft, The Netherlands, 2011, pp. 50-62.
85. **L. Rueda**, I. Rezaeian, “Applications of Multilevel Thresholding Algorithms to Transcriptomics Data”, *16th Iberoamerican Congress on Pattern Recognition*, Pucón, Chile, 2011, LNCS 7042, PP. 26-37. Plenary talk.
86. **L. Rueda**, I. Rezaeian, “Automatic Algorithms for Analysis of cDNA Microarray and Chip-seq Data”, *Microarray World Congress*, San Francisco, USA, 2011. Invited talk.
87. M. Maleki, Md. Aziz, **L. Rueda**, “Analysis of Obligate and Non-obligate Complexes using Desolvation Energies in Domain-domain Interactions”, *10th International Workshop on Data Mining in Bioinformatics (BIOKDD 2011) in conjunction with ACM SIGKDD 2011*, San Diego, USA, 2011, pp. 21-26.
88. I. Rezaeian, **L. Rueda**, “Biological Assessment of Grid and Spot Detection in cDNA Microarray Images”, *ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB 2011)*, Chicago, USA, 2011, pp. 12-19.
89. M. Maleki, Md. Aziz, **L. Rueda**, M. Raza, S. Banerjee, “Domain-domain Interactions in Transient and Obligate Protein-protein Complexes”, *Systems Biology Symposium*, Ann Arbor, MI, USA, 2011. Poster presentation.

90. I. Rezaeian, **L. Rueda**, "A Parameterless Automatic Spot Detection Method for cDNA Microarray Images", *3rd IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2010)*, Hong Kong, 2010, pp. 388-392.
91. L. Rueda, S. Banerjee, Md. Aziz, M. Raza, "Protein-protein Interaction Prediction using Desolvation Energies and Interface Properties", *3rd IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2010)*, Hong Kong, 2010, pp. 17-22.
92. I. Rezaeian, **L. Rueda**, "Sub-grid and Spot Detection in DNA Microarray Images using Optimal Multi-level Thresholding", *5th IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2010)*, Nijmegen, The Netherlands, 2010, pp. 277-288.
93. **L. Rueda**, C. Garate, S. Banerjee, Md. Mominul Aziz, "Biological Protein-protein Interaction Prediction using Binding Free Energies and Linear Dimensionality Reduction", *5th IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2010)*, Nijmegen, The Netherlands, 2010, pp. 383-394.
94. Y. Li, N. Subhani, A. Ngom, **L. Rueda**, "Alignment-based versus Variation-based Transformation Methods for Clustering Microarray Time-Series Data", *ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB 2010)*, Niagara Falls, USA, 2010, pp. 53-61.
95. N. Subhani, Y. Li, A. Ngom, **L. Rueda**, "Alignment versus Variation Methods for Clustering Microarray Time-Series Data", *2010 IEEE World Congress on Computational Intelligence (WCCI 2010)*, Barcelona, Spain, 2010, pp. 818-825.
96. Y. Li, A. Ngom, **L. Rueda**, "Missing Value Imputation Methods for Gene-Sample-Time Microarray Data Analysis", *2010 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2010)*, Montreal, Canada, 2010, pp. 183-189.
97. N. Subhani, **L. Rueda**, A. Ngom, C. Burden, "New Approaches to Clustering Microarray Time-Series Data Using Multiple Expression Profile Alignment", *2010 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2010)*, Montreal, Canada, 2010, pp. 170-176.
98. N. Subhani, A. Ngom, **L. Rueda**, C. Burden, "Clustering Microarray Time-series Data using Expectation Maximization and Multiple Profile Alignment", *Applications of Machine Learning in Bioinformatics Workshop (held at BIBM 2009)*, Washington, D.C., USA, 2009, pp. 2-7.
99. D. Rojas, **L. Rueda**, A. Ngom, H. Urrutia, G. Carcamo, "Biofilm Image Segmentation Using Optimal Multi-Level Thresholding", *IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2009)*, Washington, D.C., USA, 2009, pp. 185-190.
100. **L. Rueda**, J. Rojas, "A Pattern Classification Approach to DNA Microarray Image Segmentation", *4th IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2009)*, Sheffield, UK, LNCS 5780, 2009, pp. 319-330.
101. D. Rojas, **L. Rueda**, H. Urrutia, A. Ngom, "Efficient Optimal Multi-Level Thresholding for Biofilm Image Segmentation", *4th IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2009)*, Sheffield, UK, LNCS 5780, 2009, pp. 307-318.
102. N. Subhani, A. Ngom, **L. Rueda**, C. Burden, "Microarray Time-Series Data Clustering via Multiple Alignment of Gene Expression Profiles", *4th IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2009)*, Sheffield, UK, LNCS 5780, 2009, pp. 377-390.
103. M. Pinninghoff, R. Contreras, **L. Rueda**, "An Evolutionary Approach for Correcting Random Amplified Polymorphism DNA Images", *3rd International Work Conference on the Interplay between Natural and Artificial Computation (IWINAC 2009)*, Santiago de Compostela, Spain, LNCS 5602, 2009, pp. 469-477.
104. V.A. Gallardo, H. Urrutia, N. Ruiz-Tagle, C. Espinoza, **L. Rueda**, A. Ngom, C. Monsalve, A. Fonseca, J. Gutierrez, S. Rojas and L. Abarzua, High Throughput Sequencing to Assess Benthic Bacteria Biodiversity off Central Chile, Census of Marine Life Synthesis Workshop, (CoML 2009), February 1-5, Long Beach, California, 2009.
105. **L. Rueda**, "An Efficient Algorithm for Optimal Multilevel Thresholding of Irregularly Sampled Histograms", *7th International Workshop on Statistical Pattern Recognition (S+SSPR 2008)*, Orlando, Florida, USA, Springer, LNCS 5432, 2008, pp. 612-621.

106. L. Wang, A. Ngom, **L. Rueda**, “Sequential Forward Selection Approach to the Non-Unique Oligonucleotide Probe Selection Problem”, *Third IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2008)*, Melbourne, Australia, Springer, LNBI 5265, 2008, pp. 262-275.
107. A. Bari, **L. Rueda**, A. Ngom, “Microarray Time-Series Data Classification via Multiple Alignment of Gene Expression Profiles”, *Third IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2008)*, Melbourne, Australia, Supplementary Proceedings, ISBN 978-0-7326-2226-8, 2008, pp. 25-36.
108. X. Li, A. Ngom and **L. Rueda**, “Minimal siRNA Set Cover Heuristic for Gene Family Knockdown”, *Third IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2008)*, Melbourne, Australia, Supplementary Proceedings, ISBN 978-0-7326-2226-8, 2008, pp. 37-48.
109. **L. Rueda**, C. Henriquez, B. J. Oommen, “Chernoff-Based Multi-class Pairwise Linear Dimensionality Reduction”, *13th Iberoamerican Congress on Pattern Recognition (CIARP 2008)*, Havana, Cuba, 2008, LNCS 5197, pp. 301-308.
110. L. Wang, A. Ngom, R. Gras, **L. Rueda**, “Evolution Strategy with Greedy Probe Selection Heuristics for the Non-Unique Oligonucleotide Probe Selection Problem”, *IEEE Symposium on Computational Intelligence in Bioinformatics and Bioengineering (CIBCB 2008)*, Sun Valley, Idaho, USA, 2008, pp. 54-61. Selected as the *Overall Best Paper Award*.
111. V. Gallardo, A. Teske, J. L. Nielsen, H. Urrutia, N. Ruiz-Tagle, C. Espinoza, L. Abarzua, D. Andrades, **L. Rueda**, C. Monsalve, “16S Ribosomal RNA Gene Sequence Analysis of Sediment Macrobacteria from the Central Chile Oxygen Minimum Zone”, *12th Biennial Symposium on Microbial Ecology (ISME-12)*, Cairns, Australia, 2008. Poster presentation.
112. **L. Rueda**, “Sub-grid Detection in DNA Microarray Images”, *IEEE Pacific-RIM Symposium on Image and Video Technology*, Santiago, Chile, 2007, LNCS 4872, pp. 248-259.
113. **L. Rueda** and A. Bari, “Clustering Temporal Gene Expression Data with Unequal Time Intervals”, *2nd International Conference on Bio-Inspired Models of Network, Information, and Computing Systems (BIONETICS 2007)*, *Bioinformatics Track*. Budapest, Hungary, 2007, ICST 978-963-9799-11-0, pp. 183-190.
114. **L. Rueda** and B.J. Oommen, “A New Approach to Adaptive Encoding Data using Self-organizing Data Structures”, *22nd International Symposium on Computer and Information Sciences*, Ankara, Turkey, 2007, pp.15-20.
115. **L. Rueda**, O. Uyarte, S. Valenzuela and J. Rodriguez, “Processing Random Amplified Polymorphism DNA Images Using the Radon Transform and Mathematical Morphology”, *4th International Conference on Image Analysis and Recognition*, Montreal, Canada, 2007, LNCS 4633, pp. 1071-1081.
116. T. Gutierrez, **L. Rueda**, J. Martinez, M. Bunster, “Finding Discriminant Features in Interaction Sites for Identifying Transient and Obligate Protein-protein Complexes”, *Bioinformatics 2007*, Joint Collaborative Workshop of the European Molecular Biology Network (EMBnet) and the Iberoamerican Bioinformatics Network (RIBIO), Malaga, Spain, 2007. Poster presentation.
117. **L. Rueda** and M. Herrera, “A New Approach to Multi-class Linear Dimensionality Reduction”, *11th Iberoamerican Congress on Pattern Recognition*, Cancun, Mexico, 2006, LNCS 4225, pp. 634-643.
118. **L. Rueda** and M. Herrera, “A Theoretical Comparison of Two Linear Dimensionality Reduction Techniques”, *11th Iberoamerican Congress on Pattern Recognition*, Cancun, Mexico, 2006, LNCS 4225, pp. 624-633.
119. **L. Rueda** and M. Herrera, “A New Linear Dimensionality Reduction Technique based on Chernoff Distance”, *10th Ibero-American Conference on Artificial Intelligence*, Ribeirao Preto, Brazil, 2006, LNAI 4140, pp. 299-308.
120. M. Ali, **L. Rueda**, and M. Herrera, “On the Performance of Chernoff-distance-based Linear Dimensionality Reduction Techniques”, *19th Canadian Conference on Artificial Intelligence*, Quebec, Canada, 2006, Springer, LNAI 4013, pp. 469-480.
121. A. Bari and **L. Rueda**, “A New Profile Alignment Method for Clustering Gene Expression Data”, *19th Canadian Conference on Artificial Intelligence*, Quebec, Canada, 2006, Springer, LNAI 4013, pp. 86-97.

122. M. Chopra, M. Vargas Martin, **L. Rueda**, P.C.K. Hung. Toward New Paradigms to Combating Internet Child Pornography. *IEEE Canadian Conference on Electrical and Computing Engineering (CCECE '06)*, Ottawa, Canada, 2006, pp. 471-474.
123. M. Chopra, M. Vargas-Martin, **L. Rueda** and P. Hung, "A Source Address Reputation System to Combating Child Pornography at the Network Level", *IADIS International Conference on Applied Computing*, San Sebastian, Spain, 2006, pp. 472-477.
124. **L. Rueda** and Y. Zhang, "A Geometric Framework to Visualize Fuzzy-clustered Data", *XXV International Conference of the Chilean Computer Science Society*, Valdivia, Chile, 2005, pp. 13-20.
125. W. Yang, **L. Rueda**, and A. Ngom, "A Simulated Annealing Approach to Find the Optimal Parameters for Fuzzy Clustering Microarray Data", *XXV International Conference of the Chilean Computer Science Society*, Valdivia, Chile, 2005, pp. 45-54.
126. **L. Rueda** and B. J. Oommen, "Efficient Adaptive Data Compression using Fano Binary Search Trees". *Proc. of the 20th International Symposium on Computer and Information Sciences*, Istanbul, Turkey, 2005, Springer, LNCS 3733, pp.768-779.
127. B. J. Oommen and **L. Rueda**, "On Utilizing Stochastic Learning Weak Estimators for Training and Classification of Patterns with Non-Stationary Distributions". *Proc. of the 28th German Conference on Artificial Intelligence (KI 2005)*, Koblenz, Germany, 2005, Springer, LNAI 3698, pp. 107-120.
128. **L. Rueda** and L. Qin, "A New Method for DNA Microarray Image Segmentation". *Proc. of the International Conference on Image Analysis and Recognition*, Toronto, Canada, 2005, Springer, LNCS 3656, pp. 886-893.
129. **L. Rueda** and V. Vidyadharan, "A New Approach to Automatically Detecting Grids in DNA Microarray Images". *Proc. of the International Conference on Image Analysis and Recognition*, Toronto, Canada, 2005, Springer, LNCS 3656, pp. 982-989.
130. L. French, A. Ngom and **L. Rueda**, "Fast Protein Superfamily Classification using Principal Component Null Space Analysis". *Proc. of the 18th Canadian Conference on Artificial Intelligence*, Victoria, Canada, 2005, LNCS 3501, Springer, pp. 158-169.
131. **L. Rueda** and L. Qin, "An Unsupervised Learning Scheme for DNA Microarray Image Spot Detection". *Proc. of the First International Conference on Complex Medical Engineering*, Takamatsu, Japan, 2005, pp. 996-1000.
132. **L. Rueda** and Y. Zhang, "A New Approach for Visualizing Fuzzy-clustered Microarray Data". *Proc. of the 6th International Conference on Mathematics and Computers in Biology and Chemistry*, Buenos Aires, Argentina, 2005, track No. 503-118.
133. **L. Rueda** and V. Vidyadharan, "A New Approach to Automatically Detecting Grids in DNA Microarray Images", *International Conference on Bioinformatics and its Applications (ICBA '04)*, Fort Lauderdale, Florida, 2004. Poster presentation.
134. **L. Rueda**, "New Bounds and Approximations for the Error of Linear Classifiers", *Proc. of the 8th Iberoamerican Congress on Pattern Recognition*, Puebla, Mexico, 2004, LNCS 3287, pp. 342-349.
135. **L. Rueda** and B. John Oommen, "On Families of New Adaptive Compression Algorithms Suitable for Time-varying Source Data", *Proc. of the Third Biennial International Conference on Advances in Information Systems*, Izmir, Turkey, 2004, LNCS 3261, Springer, pp. 234-244.
136. **L. Rueda** and L. Qin, "An Improved Clustering-based Approach for DNA Microarray Image Segmentation", *Proc. of the International Conference on Image Analysis and Recognition*, Porto, Portugal, September 2004, LNCS 3212, Springer, pp. 17-24.
137. B. J. Oommen and **L. Rueda**, "A New Family of Weak Estimators for Training in Non-Stationary Distributions", *Proc. of the Joint IAPR International Workshop on Statistical Pattern Recognition*, Lisbon, Portugal, August 2004, LNCS 3138, Springer, pp. 644-652.
138. **L. Rueda** and A. Ngom, "An Empirical Evaluation of the Classification Error of Two Thresholding Methods for Fisher's Classifier", *Proc. of the 2004 International Conference on Machine Learning, Model, Technology and its Applications*, Las Vegas, Nevada, USA, June 2004, pp. 837-842.
139. **L. Rueda**, "A New Approach that Selects a Single Hyperplane from the Optimal Pairwise Linear Classifier". *Proc. of the 8th Iberoamerican Congress on Pattern Recognition*, Havana, Cuba, November 26-29, 2003, LNCS 2905, Springer, pp. 521-528.

140. **L. Rueda**, “Two Schemes for Computing Thresholds in Linear Classifiers”. *Proc. of the 2003 International Conference on Natural Language Processing and Knowledge Engineering*, Beijing, China, October 2003, Track No. A24-05.
141. **L. Rueda**, “An Empirical Analysis of Traditional and Optimal Pairwise Linear Classifiers on Standard Benchmarks”. *Proc. of the Third International Workshop on Pattern Recognition in Information Systems*, Angers, France, April 2003, pp. 88-95.
142. B. J. Oommen and **L. Rueda**, “Using Pattern Recognition Techniques to Derive a Formal Analysis of Why Heuristic Functions Work”, *Proc. of the 2nd International Workshop on Pattern Recognition in Information Systems*, Alicante, Spain, April 2002, pp. 45-58.
143. **L. Rueda** and B.J. Oommen, “Greedy Adaptive Fano Coding”, *Proc. of the 2002 IEEE Aerospace Conference*, BigSky, MT, USA, March 2002, Track 10, No. 0407.
144. **L. Rueda** and B. J. Oommen, “Resolving Minsky's Paradox: The d -Dimensional Normal Distribution Case”, *Proc. of The 14th Australian Joint Conference on Artificial Intelligence (AI'01)*, Adelaide, Australia, December 2001, LNCS 2256, Springer, pp. 25-36.
145. **L. Rueda** and B.J. Oommen, “Enhanced Static Fano Coding”, *Proc. of the IEEE Conference on Systems, Man and Cybernetics*, Tucson, Arizona, USA, October 2001, pp. 2163-2169.
146. B.J. Oommen and **L. Rueda**, “Histogram Methods in Query Optimization: The Relation between Accuracy and Optimality”, *Proc. of the 7th International Conference on Database Systems for Advanced Applications*, Hong Kong, April 2001, pp. 320-326.
147. B.J. Oommen and **L. Rueda**, “An Empirical Comparison of Histogram-like Techniques for Query Optimization”, *Proc. of the 2nd International Conference on Enterprise Information Systems (ICEIS)*, Stafford, UK, 2000, pp. 71-78.
148. **L. Rueda** and B.J. Oommen, “The Foundational Theory of Optimal Bayesian Pairwise Linear Classifiers”, *Proc. of the Joint IAPR International Workshops SSPR'2000 and SPR'2000*, Alicante, Spain, 2000, LNCS 1876, Springer, pp. 581-590.

Patents

- B. J. Oommen and **L. Rueda**, *Encryption Possessing Statistical Perfect Secrecy and Stealth*. An overview can be found at <http://www.scs.carleton.ca/~oommen/papers/ReportIP3.pdf>. Canada (No. 2,358,048), Europe (No. 01975919.0-2415-CA0101429), US: filed.

Professional Activities

- Conference Chair – Organizing Committee:
 - Workshop on Machine Learning Models for Multi-omics Data Integration (MODI 2021), co-located with ACM-BCB 2021, Virtual.
 - Workshop on Machine Learning Models for Multi-omics Data Integration (MODI 2020), co-located with ACM-BCB 2020, Virtual.
 - Workshop Co-chair. Workshop on Machine Learning Models for Multi-omics Data Integration (MODI 2019), co-located with ACM-BCB 2019, Niagara Falls, USA. Workshop Co-chair.
 - Third IAPR International Conference on Pattern Recognition in Bioinformatics – PRIB 2008, Bioinformatics Session Chair.
 - XII Iberoamerican Congress on Pattern Recognition – CIARP 2007, Program Committee Co-Chair.
 - IEEE Pacific-Rim Symposium on Image and Video Technology – PSIVT 2007, General Co-Chair.
 - 17th Canadian Conference on Artificial Intelligence – AI'2004, Graduate Symposium Chair.
- Associate Editor:
 - IEEE Transactions on Computational Biology and Bioinformatics, 04/2020-present.
 - Network Modeling Analysis in Health Informatics and Bioinformatics, Springer, 07/2014-06/2021.
- Guest Editor:

- Special Issue "Pattern Recognition and Discovery Methods for Genomic and Proteomic Data", *Proteomes*, 2021.
- Special issue on Artificial Intelligence for Computational Biology, *Current Bioinformatics*, 2020.
- Special issue on Deep Neural Networks for Precision Medicine, *Neurocomputing*, 2020.
- Special Collection on Machine Learning Models for Multi-omics Data Integration, *Evolutionary Bioinformatics*, 2020.
- Review Panel:
 - NSERC, the Natural Sciences and Engineering Research Council of Canada. Member of the Discovery Grant Computer Science Evaluation Group 1507, 2019-2022.
 - NSERC, the Natural Sciences and Engineering Research Council of Canada. Session Chair of the Discovery Grant Computer Science Evaluation Group 1507, 2020-2022.
 - Prostate Cancer Canada. Member of the Review Panel for the Discovery Grants selection committee, 2019.
 - FONDECYT – Chile. Member of the Discovery Grant Computer Science Evaluation Group, 2006-2007.
- Program Committee Member:
 - International Conference on Bioinformatics and Biomedicine (BIBM 2021)
 - Workshop on Computational Biology (WCB) -- International Conference on Machine Learning (ICML 2019-2021)
 - 25th International Conference on Pattern Recognition (ICPR 2016-2021)
 - 4th International Conference on Biometric Engineering and Applications (ICBEA 2018-2020)
 - International Joint Conference on Artificial Intelligence – Bioinformatics in Artificial Intelligence (IJCAI/BAI 2016-2018)
 - IAPR Conference on Pattern Recognition in Bioinformatics (PRIB 2008-2016)
 - 11th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB 2014-2015)
 - Mexican Conference on Pattern Recognition (MCPR 2014-2018)
 - 5th International Conference on Image Analysis and Recognition – ICIAR 2005-2008.
 - 21st Canadian Conference on Artificial Intelligence – AI 2004-2008.
 - XIII Iberoamerican Congress on Pattern Recognition – CIARP 2007-2012.
 - International Symposium on Computational Models for Life Sciences – CMLS 2007.
 - IEEE Pacific-Rim Symposium on Image and Video Technology – PSIVT 2006-2007.
- Reviewer for Grant Applications:
 - NSERC Discovery Grants: 2009-2019.
 - NSERC - Collaborative Research and Development Grants, 2014.
 - Medical Research Council, UK, Research Fellowship Grant, 2014.
 - Collaboration Network Projects, Bicentennial Program for Science and Technology, Chile, 2007.
 - FONDECYT Operating Grants, Chilean Research Council for Science and Technology, 2005/2006.
 - FONDECYT Start-up Grants, Chilean Research Council for Science and Technology, 2006.
- Reviewer for Journals:
 - *Evolutionary Bioinformatics*, 2019-2020
 - *Bioinformatics*, 2005-2020
 - *Scientific Reports* (Nature Publishing Group), 2015-2020
 - *Neurocomputing*, 2009-2019
 - *Frontier in Genetics*, 2019
 - *Briefings in Bioinformatics*, 2018-2019
 - *Proteomics*, 2018

- Pattern Recognition, 2006-2018
- IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006-2016
- Nature Communications, 2014
- International Journal of Pattern Recognition and Artificial Intelligence, 2014
- Computational Biology and Chemistry, 2013
- IEEE Transactions on Image Processing, 2005-2012
- IEEE Transactions on Information Technology in Biomedicine, 2011
- IEEE Transactions on Nanobioscience, 2011
- BMC Bioinformatics, 2010
- IEEE Transactions on Neural Networks, 2006
- Information Processing Letters, 2006
- IEEE Transactions on Information Theory, 2004
- IEEE Transactions on Pattern Analysis and Machine Intelligence, 2004
- Pattern Recognition Letters, 2004-2006
- IEEE Transactions on Systems, Man and Cybernetics, 2002-2003
- Reviewer for Graduate Programs:
 - PhD in Computer Science, Catholic University of Chile, External Reviewer, 2016.
 - PhD in Computer Science, University of Chile, External Reviewer, 2010, 2017.
- Professional Memberships:
 - *Senior Member* of the Institute of Electrical and Electronic Engineers (IEEE), 2009-present.
 - *Member* of the American Association for the Advancement of Science (AAAS), 2014-present.
 - *Member* of the International Society for Computational Biology (ISCB), 2013-present.
 - *Member* of the Institute of Electrical and Electronic Engineers (IEEE), 2001-2008.
 - *Member* of the International Association for Pattern Recognition (IAPR), 2003-present.
 - *Member* of the Pattern Recognition Society, 2002-2008.