Vanessa Aguiar-Pulido, Ph.D.

Assistant Professor, Dept. of Computer Science, University of Miami
Adjunct Assistant Prof. of Neuroscience, Weill Cornell Medicine
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SUMMARY

Highly motivated individual with a penchant for problem solving in biomedical research, with a focus on developing tools and algorithms that will impact diagnosis and therapeutics of rare and complex genetic disorders. Background and interests include big data analytics, machine learning, artificial intelligence, bioinformatics, neuroscience, data mining, ontologies, biomedical data integration, health informatics, epigenetics and omics in general.

EDUCATION

April 2014 *Ph.D. in Computer Science*
University of A Coruña, Spain
Thesis: "Solving combinatorial optimization problems using evolutionary computation techniques. An application to biomedicine"

June 2013 *Postgraduate Diploma in Business Intelligence Technologies: Design and Implementation*
Universitat Oberta de Catalunya, Spain

June 2010 *M.S. in Computer Science and Artificial Intelligence*
University of A Coruña, Spain

October 2008 *B.S. in Computer Engineering*
University of A Coruña, Spain

POSITIONS AND EMPLOYMENT

2020 – Present *Assistant Professor and head of the Computational Biology and Data Science Lab*
Department of Computer Science. University of Miami, USA
Adjunct Assistant Prof. of Neuroscience
Center for Neurogenetics, Brain and Mind Research Institute. Weill Cornell Medicine, USA

- Research on deep learning. Led the development of novel deep learning architectures for image data analysis. Collaborated on a study to analyze the internal behavior of convolutional neural networks (CNNs) in comparison with the human visual cortex.
- Directed the development of explainable AI approaches for the analysis of biomedical data.
- Spearheaded the machine learning component of a Center Without Walls U54 NIH grant for prediction of pathogenic variants in epilepsy.
- Directed the development of a machine learning approach for pathogenicity prediction of repeat expansions in rare genetic disorders.
- Participated in the development and application of methods for detecting structural variation.
- Directed the development of a machine learning framework for the simulation of genotype data and retrieval of genetic signatures.
- Research on COVID-19. Led an international group of researchers to design a novel, comprehensive bioinformatic strategy to study SARS-CoV-2 pathogenesis. Participated in devising novel anti-viral strategies against SARS-CoV-2 and other viruses.
- Supervised the creation of a machine learning approach for the analysis of recurrences in clinical respiratory pathologies.

2018 – 2020 *Instructor (Junior Faculty)*
Center for Neurogenetics, Brain and Mind Research Institute. Weill Cornell Medicine, USA

- Spearheaded the computational team at the Center for Neurogenetics (CNG), leading the development of approaches to prioritize potentially causative variants using Next Generation Sequencing (NGS). Worked in the development of new methods for improved (small and large) variant calling using long-read sequencing technologies and deep learning.
- Leader of the "Neural Tube Defects – International Data Consortium" (NTD-IDC) Computational Working Group, whose goal is to establish best practices to analyze distributed, heterogeneous genomic data.

- Devised machine learning-based approaches to reduce the genomic search space in the analysis of whole genome sequencing (WGS) data. Devised a comprehensive systems biology strategy to interrogate genomic data from a case/control study.
- Participated in the development of new methodologies for the analysis of single cell RNA-seq data from diploid and haploid samples.
- Coordinated joint projects with the Institute for Precision Medicine involving the analysis of genomic data.
- Mentored rotation and Ph.D. students at the CNG.

2016 – 2018 *Senior Postdoctoral Research Associate*

Center for Neurogenetics, Brain and Mind Research Institute. Weill Cornell Medicine, USA

- Research in bioinformatics. Devised strategies for processing and analyzing NGS data from human samples for use in clinical settings and from mouse experimental models to further neuroscience research.
- Research in neurogenetics and neuroscience. Established methodologies for the analysis of data from patients with neurological disorders and neurodegenerative diseases to unravel their underlying genetic basis.
- Was responsible for mentoring rotation students and volunteers at the CNG.

2014 – 2016 *Postdoctoral Research Associate*

School of Computing and Information Sciences. Florida International University, USA

- Research in bioinformatics. Participated in the creation of pipelines and tools for processing and analyzing NGS data. Worked on comparative genomics.
- Contributed to devising new metrics and algorithms for metagenomic data and network analysis.
- Worked on knowledge extraction from microbiome data.
- Collaborated with researchers in the fields of pharmacology, forensics, public health, molecular biology, marine sciences, microbiology and neuroscience to produce meaningful results.
- Was responsible for coordinating and organizing computational and molecular biology seminars. Was responsible for coordinating projects and mentoring students at the lab.

2014 *Research Associate*

Research Center on ICT. University of A Coruña, Spain

- Participated in the development of a platform for intelligent patient care based on cloud computing. The platform shows different content depending on the patient group (active aging or mental health). Integrated Fitbit data with the platform and developed an app for Android to monitor patient behavior.

2013 *Visiting Scholar* (From Sep-21-2013 to Dec-21-2013)

Stanford Center for Biomedical Informatics Research. Stanford University, USA

- Participated in the development of a scoring algorithm for biomedical ontology recommendation (Martínez-Romero M *et al* (2017). NCBO Ontology Recommender 2.0: An Enhanced Approach For Biomedical Ontology Recommendation. Journal of Biomedical Semantics, 8(21), 1-22).

2011 – 2014 *Predoctoral fellow. Research Assistant and Instructor*

Dept. Information and Communication Technologies. University of A Coruña, Spain

- Instructed different courses at the University of A Coruña from different degrees (Basics of Informatics, Degree in Industrial Design and Product Engineering; Informatics for Documentation, Degree in Information and Documentation; Machine Learning, Degree in Computer Science) and at the Spanish Navy (Network Management, Specialty in Information and Communication Technologies for officers). Supervised one undergraduate thesis and one senior project from two Computer Science degrees.
- Developed an artificial intelligence approach based on evolutionary computation as part of my Ph.D. thesis. Collaborated with several research groups, which implied working in a multidisciplinary environment.
- Gained experience in bioinformatics and epigenetics working with the CHROMEVOL group from FIU. Collaborated to create CHROMEVALOA db, which was originally developed using MySQL, Perl and HTML. Responsible for managing the Ubuntu Linux server in which this resource is stored. Also collaborated with the Gerontology Research Group from University of A Coruña and aided in the creation and maintenance of different PHP-based websites.
- Reviewer of “Neural Processing Letters” (2012 – present) and of “Database: The Journal of Biological Databases and Curation” (2013). Chair at ICAI’12, WORLDCOMP’12 (Las Vegas, USA) and at IWANN’11 (Torremolinos, Spain).

2008 – 2011 *Research Assistant*

Dept. Information and Communication Technologies. University of A Coruña, Spain

- Application and development of machine learning techniques to analyze biomedical and hydrological data.

2007 – 2008 *Undergraduate research assistant*

Dept. Information and Communication Technologies. University of A Coruña, Spain

- Application of genetic algorithms for classification rule mining.

PUBLICATIONS

Journal articles

1. Han X, Cao X, **Aguiar-Pulido V**, et al. (2022). CIC missense variants contribute to susceptibility for spina bifida. Hum Mutat. 2022;10.1002/humu.24460 (JCR 4.7).
2. **Aguiar-Pulido V**, Wolujewicz P, Martinez-Fundichely A, Elhaik E, Thareja G, Abdel Aleem A, Chalhoub N, Cuykendall T, Al-Zamer J, Lei Y, El-Bashir H, Musser JM, Al-Kaabi A, Shaw GM, Khurana E, Suhre K, Mason CE, Elemento O, Finnell RH, Ross ME (2021). Systems biology analysis of human genomes points to key pathways conferring spina bifida risk. Proc Natl Acad Sci USA (PNAS), 118(51):e2106844118 (JCR 12.779).
3. Ferrarini MG, Lal A, Rebollo R, Gruber A, Guarracino A, Martinez Gonzalez I, Floyd T, Siqueira de Oliveira D, Shanklin J, Beausoleil E, Pusa T, Pickett BE, **Aguiar-Pulido V** (2021). Genome-wide bioinformatic analyses predict key host and viral factors in SARS-CoV-2 pathogenesis. Communications Biology, 4:590 (Nature Publishing Group) (JCR: 6.548).
4. Wolujewicz P, **Aguiar-Pulido V**, Aleem AA, Nair V, Thareja G, Suhre K, Shaw GM, Finnell RH, Elemento O, Ross ME (2021). Genome-wide investigation identifies a rare copy number variant burden associated with human spina bifida. Genetics in Medicine, 23:1211-1218 (JCR 8.864).
5. Antunes J, Gauthier Q, **Aguiar-Pulido V**, Duncan G, McCord B (2021). A data-driven, high-throughput methodology to determine tissue-specific differentially methylated regions able to discriminate body fluids. Electrophoresis, 42(9-10):1168-1176 (JCR 3.595).
6. Tomoiaga D, **Aguiar-Pulido V**, Shrestha S, Feinstein P, Levy S, Mason C, Rosenfeld J (2020). Single-Cell Sperm Transcriptomes and Variants from Fathers of Children with and without Autism Spectrum Disorder. npj Genomic Medicine 5(14) (JCR 8.617).
7. Cao X, Tian T, Steele JW, Cabrera RM, **Aguiar-Pulido V**, Wadhwa S, Bhavani N, Bi P, Gargurevich NH, Hoffman EN, Cai CQ, Marini NJ, Yang W, Shaw GM, Ross ME, Finnell RH, Lei Y (2020). Loss of RAD9B impairs early neural development and contributes to the risk for human spina bifida. Human Mutation, 41(4):786-799 (JCR 4.878)
8. Cickovski T, **Aguiar-Pulido V**, Narasimhan G (2019). MATria: A unified centrality algorithm. BMC Bioinformatics. 20(11):278 (JCR 2.213).
9. Chen Z, Lei Y, Zheng Y, **Aguiar-Pulido V**, Ross ME, Peng R, Zou J, Wu J, Wang F, Zhang F, Jin L, Zhang T, Finnell RH, Wang H (2018). Threshold for Neural Tube Defect Risk by Accumulated Singleton Loss-of-function Variants. Cell Research (Nature Publishing Group) 28:1039-1041 (JCR 17.848).
10. Martin-Sanchez FJ, **Aguiar-Pulido V**, Lopez-Campos GH, Peek N, Sacchi L (2017). Secondary Use and Analysis of Big Data Collected for Patient Care. Contribution from the IMIA Working Group on Data Mining and Big Data Analytics. IMIA Yearbook of Medical Informatics, 26(1).
11. Cickovski T, Peake E, **Aguiar-Pulido V**, Narasimhan G (2017). ATria: A novel centrality algorithm applied to biological networks. BMC Bioinformatics 18(S8):239-248 (JCR 2.448).
12. **Aguiar-Pulido V**, Huang W, Suarez-Ulloa V, Cickovski T, Mathee K, Narasimhan G (2016). Metagenomics, metatranscriptomics, and metabolomics approaches for microbiome analysis. Evolutionary Bioinformatics, 12(Suppl 1):5-16 (JCR 1.452).
13. Huang W, Kazmierczak K, Zhou Z, **Aguiar-Pulido V**, Narasimhan G, Szczesna-Cordary D (2016). Gene expression patterns in transgenic mouse models of hypertrophic cardiomyopathy caused by mutations in myosin regulatory light chain Archives of Biochemistry and Biophysics, 601:121-32 (JCR 3.017).
14. Suarez-Ulloa V, Fernandez-Tajes J, **Aguiar-Pulido V**, Prego-Faraldo V, Florez-Barros F, Sexto-Iglesias A, Mendez J, Eirin-Lopez JM (2015). Unbiased high-throughput characterization of mussel transcriptomic responses to sublethal concentrations of the biotoxin okadaic acid. PeerJ, 3:e1429 (JCR 2.1).
15. Munteanu CR, **Aguiar-Pulido V**, Freire A, Martinez-Romero Marcos, Porto-Pazos AB, Pereira J, Dorado J (2015). Graph-Based Processing of Macromolecular Information. Current Bioinformatics, 10(5):606-631 (JCR 0.921; 43/57).

16. **Aguiar-Pulido V**, Gestal M, Cruz-Monteagudo M, Rabuñal JR, Dorado J, Munteanu CR (2013). Evolutionary computation and QSAR research. Current Computer-Aided Drug Design, 9(2):206-225 (JCR 1.54; 40/100; Q2).
17. Rivero D, **Aguiar-Pulido V**, Fernández Blanco E, Gestal M (2013). Using genetic algorithms for automatic recurrent ANN development: an application to EEG signal classification. International Journal of Data Mining, Modelling and Management, 5:182-191.
18. **Aguiar-Pulido V**, Gestal M, Fernandez-Lozano C, Rivero D, Munteanu CR (2013). Applied Computational Techniques on Schizophrenia using Genetic Mutations. Current Topics in Medicinal Chemistry, 13(5):675-84 (JCR 4.174; 5/59; Q1).
19. Suarez-Ulloa V, Fernandez-Tajes J, **Aguiar-Pulido V**, Rivera-Casas C, Gonzalez-Romero R, Ausio J, Mendez J, Dorado J, Eirin-Lopez JM (2013). The CHROMEVALOA Database: A Resource for the Evaluation of Okadaic Acid Contamination in the Marine Environment Based on the Chromatin-Associated Transcriptome of the Mussel Mytilus galloprovincialis. Marine Drugs, 11(3):830-841 (JCR 3.854; 7/59; Q1).
20. Seoane JA, **Aguiar-Pulido V**, Munteanu CR, Rivero D, Rabuñal JR, Dorado J, Pazos A (2013). Biomedical Data Integration in Computational Drug Design and Bioinformatics. Current Computer-Aided Drug Design, 9:108-117 (JCR 1.762; 31/99; Q2).
21. **Aguiar-Pulido V**, Seoane JA, Gestal M, Dorado J (2013). Exploring patterns of epigenetic information with data mining techniques. Current Pharmaceutical Design, Special Issue: Epigenetic and metabolic drug target for anticancer therapy:779-789 (JCR 3.870; 46/261; Q1).
22. Seoane J, **Aguiar-Pulido V**, Cabarcos A, Quintela S, Rabuñal J, Dorado J (2013). SNP Locator: a Candidate SNP Selection Tool. International Journal of Data Mining, Modeling and Management, 5(3):193-209.
23. Fernández Blanco E, **Aguiar-Pulido V**, Munteanu CR, Dorado J (2013). Random Forest Classification based on Star Graph Topological Indices for Antioxidant Proteins. Journal of Theoretical Biology, 317:331-337 (JCR 2.208; 11/47; Q1).
24. Seoane JA, Dorado J, **Aguiar-Pulido V**, Pazos A (2012). Data Integration in Genomic Medicine: Trends and Applications. IMIA Yearbook of Medical Informatics 2012: Personal Health Informatics, 7(1):117-125.
25. **Aguiar-Pulido V**, Munteanu CR, Seoane JA, Fernández-Blanco E, Pérez-Montoto LG, González-Díaz H, Dorado J (2012). Naïve Bayes QSDR classification based on spiral-graph Shannon entropies for protein biomarkers in human colon cancer. Molecular Biosystems, 8(6):1716-1722 (JCR 3.534; 103/290; Q2).
26. Cabarcos A, Sanchez T, Seoane JA, **Aguiar-Pulido V**, Freire A, Dorado J, Pazos A (2010). Retrieval and management of medical information from heterogeneous sources, for its integration in a medical record visualisation tool. International journal of electronic healthcare, 5(4):371-385.
27. **Aguiar-Pulido V**, Seoane JA, Rabuñal JR, Dorado J, Pazos A, Munteanu CR (2010). Machine learning techniques for single nucleotide polymorphism-disease classification models in schizophrenia. Molecules, 5(7):4875-4889 (JCR 1.988; 27/56; Q2).
28. Vázquez JM, **Aguiar V**, Seoane JA, Freire A, Serantes JA, Dorado J, Pazos A, Munteanu CR (2009). Star Graphs of Protein Sequences and Proteome Mass Spectra in Cancer Prediction. Current Proteomics, 6:275-288.

Conferences

1. Bonnell J, Xia M, Wall L, Eggleston Y, Ogihara M, **Aguiar-Pulido V** (2022). Machine learning in personalized skin care: A simulation scheme for pattern recognition in skin condition genome-wide association studies. 21st IEEE International Conference on Machine Learning and Applications (ICMLA) at Paradise Island (Bahamas).
2. Fazal S, Danzi M, Zuchner S, **Aguiar-Pulido V** (2022). RExPRT: a machine learning tool to rank repeat expansions by pathogenicity. American Society of Human Genetics (ASHG) annual meeting at Los Angeles, CA (USA).
3. Calhoun J, Mefford H, Schnell S, **Aguiar-Pulido V**, Ross ME, Parent J, Isom L, EpiMVP Consortium, Carvill G (2022). An integrated machine learning and functional analysis approach for resolution of variants of uncertain significance (VUS) in *PCDH19*. American Society of Human Genetics (ASHG) annual meeting at Los Angeles, CA (USA).
4. Claman A, Pan Xu, **Aguiar-Pulido V**, Schwartz O (2022). Comparing CNNs and the brain: sensitivity to images altered in the frequency domain. Neuromatch Conference (NMC).

5. Fazal S, Danzi M, Zuchner S, **Aguiar-Pulido V** (2022). Using machine learning to prioritize rare repeat expansions for pathogenicity. Journal of the Peripheral Nervous System 27, S47-S47. Peripheral Nerve Society (PNS) annual meeting at Miami, FL (USA).
6. Calhoun J, Gunti J, Mefford HC, Schnell S, **Aguiar-Pulido V**, Ross ME, Parent J, Isom LL, EpiMVP Consortium, Carvill GL (2021). An Integrated Machine Learning and Functional Analysis Approach for Resolution of Variants of Uncertain Significance (VUS) in STXBP1. Interrogating Biochemical Properties of STXBP1 Variant Proteins Using Immortalized Cell Lines and Neurons Differentiated from Human Pluripotent Stem Cells. American Epilepsy Society (AES) annual meeting at Chicago, IL (USA).
7. Parker W, Wang C, Pearson C, Niu W, Ji T, **Aguiar-Pulido V**, Mojica-Perez S, Parent J, Uhler M, Ross ME, EpiMVP Consortium (2021). Interrogating Biochemical Properties of STXBP1 Variant Proteins Using Immortalized Cell Lines and Neurons Differentiated from Human Pluripotent Stem Cells. American Epilepsy Society (AES) annual meeting at Chicago, IL (USA).
8. Calhoun J, Gunti J, Mefford HC, Schnell S, **Aguiar-Pulido V**, Ross ME, Parent J, Isom LL, EpiMVP Consortium, Carvill GL (2021). An integrated machine learning and functional analysis approach for resolution of variants of uncertain significance (VUS) in STXBP1. American Society of Human Genetics (ASHG) annual meeting.
9. Rodríguez AM, Guerra Tort C, Suárez-Ulloa V, López Gestal JM, Pereira J, **Aguiar-Pulido V** (2021). Training of Machine Learning Models for Recurrence Prediction in Patients with Respiratory Pathologies. Engineering Proceedings, 7(1):20. 4th XoveTIC Conference at A Coruña (Spain).
10. Ferrarini MG, Lal A, Rebollo R, Gruber A, Guarracino A, Martinez Gonzalez I, Floyd T, Siqueira de Oliveira D, Pickett BE, **Aguiar-Pulido V** (2020). Global analysis of human SARS-CoV-2 infection and host-virus interactions. CHSL COVID/SARS CoV2 Rapid Research Reports #3, Cold Spring Harbor Laboratory.
11. Ferrarini MG, Lal A, Rebollo R, Gruber A, Guarracino A, Martinez Gonzalez I, Floyd T, Siqueira de Oliveira D, Kanitz A, Pickett BE, **Aguiar-Pulido V** (2020). Comprehensive analysis of human SARS-CoV-2 infection and host-virus interaction (Poster). Intelligent Systems for Molecular Biology (ISMB).
12. **Aguiar-Pulido V**, Wolujewicz P, Finnell RH, Ross ME (2019). Data sharing and analysis in the Neural Tube Defects (NTDs) international community. International Neural Tube Defects Conference at Boston, MA (USA).
13. Floyd T, **Aguiar-Pulido V**, Collier P, Castaldo B, Abdel-Aleem A, Ross ME (2019). Assessing the impact of minor intron retention in mRNU12, a novel mouse model of recessive cerebellar ataxia, through high-throughput transcriptomics. Nature Next-Generation Genomics Conference at New York, NY (USA).
14. Wolujewicz P, **Aguiar-Pulido V**, Finnell RH, Mason CE, Elemento O, Ross ME (2018). Structural variation in neural tube defects: adding another layer to a complex genetic architecture (Poster). American Society of Human Genetics (ASHG) at San Diego, CA (USA).
15. **Aguiar-Pulido V**, Schlusche AK, Liu WA, Singh S, Shi S, Ross ME (2018). High-throughput single-cell transcriptomics profiling interneuron specification during brain development. Intelligent Systems for Molecular Biology (ISMB) at Chicago, IL (USA).
16. **Aguiar-Pulido V**, Lei Y, Gross SS, Shaw G, Finell RH, Ross ME (2017). Genome sequence insights into human predisposition to Spina Bifida. International Conference on Neural Tube Defects at Austin, TX (USA).
17. Cickovski T, **Aguiar-Pulido V**, Narasimhan G (2017). MATria: A unified centrality algorithm. IEEE 7th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS) at Miami, FL (USA).
18. **Aguiar-Pulido V**, Kim SE, Gross SS, Finnell RH, Ross ME (2017). Dominant Mutations in Primary Cilium Protein GPR161 are a Risk Factor for Human Spina Bifida. 11th Structural Birth Defects Meeting at Bethesda, MD (USA).
19. **Aguiar-Pulido V**, Martin-Sanchez F (2016). From published examples to knowledge representation: an inductive approach for exposome data mapping (Oral presentation & Poster). Emory Exposome Summer Course at Atlanta, GA (USA).
20. Martin-Sanchez F, Tran E, de Andrés-Galiana E, Benitez S, **Aguiar-Pulido V**, Lopez-Campos GH (2016). The Precision Medicine Game: an educational tool for understanding the Genome-Exposome interplay (Poster). Emory Exposome Summer Course at Atlanta, GA (USA).

21. Suarez-Ulloa V, **Aguiar-Pulido V**, Narasimhan G, Eirin-Lopez JM (2016). Network-inspired analysis of transcriptomic responses to environmental stressors in bivalve molluscs (Poster). Emory Exposome Summer Course at Atlanta, GA (USA).
22. **Aguiar-Pulido V**, Martin-Sanchez F (2016). Towards disease characterization: The Exposome as a new challenge for Bioinformatics (Poster). Intelligent Systems for Molecular Biology (ISMB) at Orlando, FL (USA).
23. Suarez-Ulloa V, **Aguiar-Pulido V**, Ruiz-Perez D, Narasimhan G, Eirin-Lopez JM (2016). Network-based analysis of chromatin-associated gene expression dynamics in response to environmental stress (Poster). Intelligent Systems for Molecular Biology (ISMB) at Orlando, FL (USA).
24. Valdes C, **Aguiar-Pulido V**, Narasimhan G, Clarke J (2016). Flint: A Distributed Surveying Tool for Metagenomic Samples (Poster). Intelligent Systems for Molecular Biology (ISMB) at Orlando, FL (USA).
25. Narasimhan M, Vietri G, **Aguiar-Pulido V**, Mehta A, Rajabli F, Mathee K, Narasimhan G (2016). Predicting Symptom Severity and Contagiousness of Respiratory Viral Infections. F1000Research 2016, 5(ISCB Comm J):1663 (poster). Best Poster Award ISMB-SCS.
26. **Aguiar-Pulido V**, Suarez-Ulloa V, Eirin-Lopez JM, Narasimhan G (2016). Network-inspired Approaches for Transcriptomic Analyses. International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO) at Granada (Spain).
27. Cickovski T, **Aguiar-Pulido V**, Huang W, Mahmud S, Narasimhan G (2016). Lightweight Microbiome Analysis Pipelines. International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO) at Granada (Spain).
28. Suarez-Ulloa V, **Aguiar-Pulido V**, Narasimhan G, Eirin-Lopez JM (2015). Framing epigenetic signatures of the Pacific oyster under environmental stress using network analysis. Asilomar Chromatin, Chromosomes and Epigenetics Conference (ACCEC) at Pacific Grove, CA (USA).
29. Cickovski T, Peake E, **Aguiar-Pulido V**, Narasimhan G (2015). ATria: A Novel Centrality Algorithm Applied To Biological Networks. International Conference on Computational Advances in Bio and Medical Sciences (ICCABS) at Miami, FL (USA).
30. Pedreira N, **Aguiar-Pulido V**, Dorado J, Pazos A, Pereira J (2014). Knowledge management for chronic patient control and monitoring. International Conference of Computational Methods in Sciences and Engineering (ICCMSE) at Athens (Greece). AIP Conference Proceedings, 1618:747-750.
31. **Aguiar-Pulido V**, Suarez-Ulloa V, Rivero D, Eirin-Lopez JM, Dorado J (2013). Clustering of gene expression profiles applied to marine research. International Work-Conference on Artificial Neural Networks (IWANN) at Tenerife (Spain). Lecture Notes in Computer Science, 7902:453-462.
32. **Aguiar-Pulido V**, Rivero D, Gestal M, Dorado J (2012). Weighting the Importance of Variables With Genetic Programming. International Conference on Artificial Intelligence (ICAI), WORLDCOMP'12 at Las Vegas, NV (USA), Vol II: 583-587.
33. Fernández Blanco E, **Aguiar-Pulido V**, Cabarcos A, Pazos A (2012). Un ADN artificial simplificado como método de clasificación. VIII Congreso Español sobre metaheurísticas, algoritmos evolutivos y bioinspirados (MAEB) at Albacete (Spain).
34. **Aguiar-Pulido V**, Seoane JA, Munteanu CR, Pazos A (2011). SNP-Schizo: A Web Tool for Schizophrenia SNP Sequence Classification. International Work-Conference on Artificial Neural Networks (IWANN) at Torremolinos (Spain). Lecture Notes in Computer Science, 6692:252-259.
35. Freire A, **Aguiar-Pulido V**, Rabuñal JR, Garrido M (2010). Genetic Algorithm based on Differential Evolution with variable length. Runoff prediction on an artificial basin. International Conference on Evolutionary Computation (ICEC) at Valencia (Spain), 207-212.
36. **Aguiar-Pulido V**, Seoane JA, Freire A, González-Díaz H, Duardo-Sánchez A, Dorado J, Pazos A, Munteanu CR (2010). New Markov-Randic Centralities for Computational Methods of Biology, Parasitology, Technology, Social and Law Networks. International Conference of Computational Methods in Sciences and Engineering (ICCMSE) at Island of Kos (Greece).
37. Freire A, **Aguiar-Pulido V**, Rabuñal JR, Garrido M (2010). Algoritmo genético de evolución diferencial con longitud variable para la predicción del caudal generado por lluvia en una cuenca artificial. VII Congreso Español sobre Metaheurísticas, Algoritmos Evolutivos y Bioinspirados (MAEB) at Valencia (Spain).

38. **Aguiar V**, Seoane JA, Freire A, Munteanu CR (2009). Data mining in complex diseases using Evolutionary Computation. International Work-Conference on Artificial Neural Networks (IWANN) at Salamanca (Spain). Lecture Notes in Computer Science, 5517:917-924.
39. Seoane JA, **Aguiar V**, Gestal M, Dorado J, Pazos A (2008). Association analysis in complex diseases using evolutionary computation (Poster). Intelligent Systems for Molecular Biology (ISMB) at Toronto (Canada).

Book chapters

1. Martin-Sanchez F, **Aguiar-Pulido V** (2017). Analytics and Decision Support Systems in Global Health Informatics. Global Health Informatics: How Information Technology Can Change Our Lives in a Globalized World (pp. 195-217). Elsevier.
2. Fernandez M, **Aguiar-Pulido V**, Riveros JD, Huang W, Segal J, Zeng E, Campos M, Mathee K, Narasimhan G (2016). Microbiome Analysis: State-of-the-Art and Future Trends. Computational Methods for Next Generation Sequencing Data Analysis (pp. 401-424). John Wiley and Sons.
3. **Aguiar-Pulido V**, Suarez-Ulloa V, Eirin-Lopez JM, Pereira J, Narasimhan G (2015). Computational Methods in Epigenetics. Personalized Epigenetics (pp. 153-180). Elsevier Academic Press..
4. **Aguiar-Pulido V**, Pazos A (2013). Informática biomédica: conceptos y aplicaciones. Investigación aplicada a Medicina Respiratoria. Un ABC para entender las innovaciones biomédicas. Andavira Editora.
5. Freire A, **Aguiar-Pulido V**, Rabuñal JR, Porto A, Pereira J (2011). Extracción de información mediante computación evolutiva. Nano, Bio, Info y Cogno (Convergencia de Tecnologías NBIC). Conceptos y aplicaciones. Redes CYTED NanoRoadmap e Ibero-NBIC. Ciencia y Tecnología para el Desarrollo (CYTED)
6. **Aguiar-Pulido V**, Seoane JA, Freire A, Guo L (2010). GA-based Data Mining applied to genetic data for the diagnosis of complex diseases. Soft Computing Methods for Practical Environmental Solutions: Techniques and Studies (pp. 220-240). IGI Global.
7. Munteanu CR, Fernández B, **Aguiar V**, Serantes J, Dorado J, Pazos A, González-Díaz H (2010). Directed Network Topological Indices for van der Waals complexes based on Coupled Cluster Interaction Energies. Topological Indices for Medicinal Chemistry, Biology, Parasitology, and Social Networks. Research Signpost.

PROFESSIONAL

Funded research

2022 – 2027	Genome Studies in Hereditary Spastic Paraplegia – Beyond the Exome. NIH (Co-Investigator)
2022 – 2023	IUCRC Phase I University of Miami: Center for Accelerated Real Time Analytics (CARTA). NSF Project: Genotype-aware Consumer Product Recommendation System (Project Leader)
2023	Machine learning to study and improve race-bias in the treatment of breast cancer. NanoString - GeoMx Whole Transcriptome Atlas Grant: University of Miami (PI)
2022 – 2023	Deep learning and explainable AI to improve race-bias in the treatment of breast cancer. University of Miami - iDSC "Expanding the Use of Collaborative Data Science at UM" (PI)
2020 – 2025	Epilepsy Multiplatform Variant Prediction (EpiMVP). NIH (Sub-award PI)
2019 – 2020	Hybrid sequencing for improved genetic diagnosis in clinical settings. Sackler Research Grant (Principal Investigator)
2018 – 2023	Progenitor regulation underlying cortical interneuron specification. NIH (Researcher)

Teaching experience

<u>Graduate level courses</u>

2021 – Present	Ph.D. in Computer Science, M.S. in Computer Science, M.S. in Data Science University of Miami Instructor: Statistical Learning with applications
2016	Master of Science in Health Informatics

Weill Cornell College of Medicine, Cornell University
Invited lecture "'Omics' Informatics": Introduction to Health Informatics (HINF 5001)

2016 Master in eHealth and Big Data
International University of La Rioja (UNIR), Spain
Syllabus development: "Health informatics: computational trends"

2012 – 2014 Specialty in Information and Communication Technologies for officers
Antonio de Escaño Specialist School. Spanish Navy
Instructor: Network Management

Bachelor level courses

2021 – Present Degree in Computer Science
University of Miami, USA
Instructor: Introduction to Software Engineering

2020 – Present Degree in Computer Science
University of Miami, USA
Instructor: Database systems

2013 – 2014 Degree in Computer Science
University of A Coruña, Spain
Instructor: Security in Information Systems

2012 – 2014 Degree in Computer Science
University of A Coruña, Spain
Instructor: Machine Learning

Degree in Industrial Design and Product Engineering
University of A Coruña, Spain
Instructor: Basics of Informatics

Degree in Information and Documentation
University of A Coruña, Spain
Instructor: Informatics for Documentation

Medical education level courses

2017 – 2019 Medical Doctor Degree
Weill Cornell College of Medicine, Cornell University
Journal club facilitator: Brain and Behavior

Thesis mentoring and evaluation experience

2021 – Present Ph.D. Thesis Advisor of two students
University of Miami. Program: Computer Science

2022 International Expert Evaluator of Ph.D. Thesis
"Methodology for the development of systems for the detection and tracking of fish using laser technology and computer vision with artificial intelligence"

2021 International Expert Evaluator of Ph.D. Thesis
"Study on the use of technological devices for the analysis and prevention of falls in nursing homes for the older adults from an occupational perspective"

2020 – Present Member of Ph.D. Thesis Committee
University of Miami. Program: Human Genetics and Genomics
"Identification and characterization of structural variants in neurological disorders"

2017 – 2022 Ph.D. Thesis Supervisor

	Cornell University. Program: Neuroscience “Development of new methodologies to assess the impact of minor intron retention in recessive cerebellar ataxia using high-throughput transcriptomics”
2017 – 2022	Ph.D. Thesis Supervisor Cornell University. Program: Physiology, Biophysics and Systems Biology (PBSB) “Development of new approaches for the detection of human structural variation using whole genome sequencing in research and clinical settings”
2015	International Expert Evaluator of Ph.D. Thesis “Impact of Information and Communication Technologies on daily life of children with Autism Spectrum Disorder”
2015	Member of Ph.D. Thesis Committee “Information processing by means of Artificial NeuroGlial Networks applied to classification and prediction”
2014 – 2015	Advisor of 1 undergraduate thesis from the Computer Engineer degree “Development of a bioinformatics platform for the storage and retrieval of NGS data in marine sciences, and its application to massive data processing and analysis”
2013 – 2014	Advisor of 1 undergraduate thesis from the Computer Science degree “Rule mining using genetic programming and data mining for medical purposes”
2011 – 2012	Advisor of 1 senior project from the Computer Engineer degree “Differential evolution: new approaches and an application to hydrology”

Editorial and other professional responsibilities

2021	Grant reviewer for the Swiss National Science Foundation
2021	Reviewer of “Scientific Reports” (Nature Publishing Group)
2020	Reviewer for the “Intelligent Systems for Molecular Biology (ISMB)” Conference
2019	Reviewer of “International Conference on Research in Computational Molecular Biology (RECOMB)”
2019	Reviewer of “ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM BCB)”
2018	Reviewer of “Communications Biology” (Nature Publishing Group)
2018	Reviewer of “ACS Chemical Neuroscience”
2018	Reviewer of “International Journal of Data Science and Analytics (JDSA)”
2018	Guest Editor of “Computational Intelligence and Neuroscience”
2017 – Present	Program Committee of the “IEEE Computer-Based Medical Systems” Conference
2017 – 2019	Reviewer for the “American Medical Informatics Association (AMIA)” Conference
2016 – Present	Member of the Editorial Review Board of “International Journal of Big Data and Analytics in Healthcare (IJBDAH)”
2013	Reviewer of “Database: The Journal of Biological Databases and Curation”
2012 – Present	Reviewer of “Neural Processing Letters”
2012	Chair at ICAI’12, WORLDCOMP’12 – Las Vegas, USA

	Session: Medical & Health Informatics + Related issues
2011 – Present	Program Committee of “International Work-Conference on Artificial Neural Networks (IWANN)”
2011	Chair at IWANN’11 – Torremolinos, Spain Session: Data mining in biomedicine

Professional organizations

2016 – Present	Member of the International Society for Computational Biology (ISCB)
2016 – Present	Member of the New York Academy of Sciences (NYAS)

Honors and awards

2013	Competitive grant supporting research stays. Inditex-UDC, Spain
2011	“Plan I2C” competitive Fellowship. Xunta de Galicia, Spain
2011	“Pre-doctoral” competitive Fellowship. University of A Coruña, Spain
2011	Competitive grant supporting travel. University of A Coruña, Spain
2009	Competitive research scholarship. Xunta de Galicia, Spain
2007	Competitive collaboration scholarship. Ministry of Science and Education, Spain