

Vanessa Aguiar-Pulido, Ph.D.

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SUMMARY

Highly motivated individual with a penchant for problem solving in biomedical research, with a focus on understanding underlying genetic causes of neurological conditions, how these causes can be influenced by environmental factors, and how these findings can be applied to clinical practice. Background and interests include big data analytics, bioinformatics, neuroscience, machine learning, data mining, artificial intelligence, ontologies, biomedical data integration, health informatics, epigenetics and omics in general.

EDUCATION

April 2014	<i>Ph.D. in Computer Science</i> University of A Coruña, Spain Thesis: "Solving combinatorial optimization problems using evolutionary computation techniques. An application to biomedicine". Advisor: Prof. Julián Dorado
June 2013	<i>Postgraduate Diploma in Business Intelligence Technologies: Design and Implementation</i> Universitat Oberta de Catalunya, Spain
June 2010	<i>M.S. in Computer Science and Artificial Intelligence</i> University of A Coruña, Spain
October 2008	<i>B.S. in Computer Science</i> University of A Coruña, Spain

POSITIONS AND EMPLOYMENT

2016 – Present	<i>Senior Postdoctoral Research Associate</i> Center for Neurogenetics, Brain and Mind Research Institute. Weill Cornell Medicine, USA <ul style="list-style-type: none">• Research in bioinformatics. Participated in the creation of pipelines and tools for processing and analyzing Next Generation Sequencing (NGS) data from human samples for use to clinical settings and from mouse experimental models to further neuroscience research.• Research in neurogenetics and neuroscience. Analyzed data from patients with neurological disorders and neurodegenerative diseases to unravel their underlying genetic basis.• Supervised several rotation students from two different programs and tutored the journal club of the Brain and Behavior course.
2014 – 2016	<i>Postdoctoral Research Associate</i> School of Computing and Information Sciences. Florida International University, USA <ul style="list-style-type: none">• Research in bioinformatics. Participated in the creation of pipelines and tools for processing and analyzing Next Generation Sequencing (NGS) data. Worked on comparative genomics.• Contributed to devise 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 projects and mentoring students at the lab. Supervised one undergraduate thesis from the Computer Science degree.• Was responsible for coordinating and organizing computational and molecular biology seminars.

- 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.
- 2011 – 2014 *Predoctoral fellow. Research Assistant and Instructor*
Dept. Information and Communication Technologies. University of A Coruña, Spain
- Aided the instruction of 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 CHROMEVAL group from FIU. Collaborated to create CHROMEVALOA db (<http://chromevaloa.udc.es>), which was 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 (h-index = 8)

Peer reviewed journals

- 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).
- 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).
- 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).
- 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).
- 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).
6. 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).
 7. **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).
 8. 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.
 9. **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).
 10. Suárez-Ulloa V, Fernández-Tajes J, **Aguiar-Pulido V**, Rivera-Casas C, González-Romero R, Ausio J, Méndez J, Dorado J, Eirín-López 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).
 11. 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).
 12. **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).
 13. 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.
 14. 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).
 15. 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.
 16. **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).
 17. 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.
 18. **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).
 19. 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.

Peer reviewed conferences

1. **Aguiar-Pulido V**, Martin-Sanchez F (2016). From published examples to knowledge representation: an inductive approach for exposome data mapping (Invited talk & Poster). Emory Exposome Summer Course at Atlanta, GA (USA).

2. 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).
3. 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).
4. **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).
5. 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).
6. 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).
7. 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.
8. **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).
9. 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).
10. 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).
11. 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).
12. 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.
13. **Aguiar-Pulido V**, Suárez-Ulloa V, Rivero D, Eirín-López 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.
14. **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.
15. 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).
16. **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.
17. 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.
18. **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).

19. 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).
20. **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.
21. 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).

Peer reviewed 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. 197-219). Elsevier. *In press*
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**, 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.
5. 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.

TEACHING AND MENTORING EXPERIENCE

2017	Medical Education Weill Cornell College of Medicine, Cornell University Journal club tutor: Brain and Behavior
2017	Supervisor of 2 rotation students from Weill Cornell's Neuroscience and Physiology, Biophysics and Systems Biology (PBSB) Ph.D. programs
2016	Master of Science in Health Informatics Weill Cornell College of Medicine, Cornell University Invited lecture "'Omics' Informatics": Introduction to Health Informatics (HINF 5001)
2014 – 2015	Advisor of 1 undergraduate thesis from the Computer Science degree
2013 – 2014	Advisor of 1 undergraduate thesis from the Computer Science Engineer degree Specialty in Information and Communication Technologies for officers Antonio de Escaño Specialist School. Spanish Navy Instructor: Network Management Degree in Computer Science Dept. Information and Communication Technologies. University of A Coruña, Spain Instructor: Machine Learning

2013 – 2014	Degree in Computer Science Dept. Information and Communication Technologies. University of A Coruña, Spain Instructor: Security in Information Systems
2012 – 2013	Specialty in Information and Communication Technologies for officers Antonio de Escaño Specialist School. Spanish Navy Instructor: Network Management
	Degree in Computer Science Dept. Information and Communication Technologies. University of A Coruña, Spain Instructor: Machine Learning
	Degree in Industrial Design and Product Engineering Dept. Information and Communication Technologies. University of A Coruña, Spain Instructor: Basics of Informatics
	Degree in Information and Documentation Dept. Information and Communication Technologies. University of A Coruña, Spain Instructor: Informatics for Documentation
2011 – 2012	Advisor of 1 senior project from the Computer Science Technical Engineer degree

OTHER EXPERIENCE

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	Chair at IWANN’11 – Torremolinos, Spain Session: Data mining in biomedicine

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