Vanessa Aguiar-Pulido

Ph.D. in Computer Science, Postdoctoral Research Associate
Bioinformatics Research Group (BioRG), School of Computing and Information Sciences
Florida International University, USA

PERSONAL DETAILS

Date of birth: Jan-29-1985

Citizenships: Spain and France (visa required to work in the US; currently on a J1 visa)

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EDUCATION

April 2014	Ph.D. in Computer Science University of A Coruña, Spain
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 Science University of A Coruña, Spain

RESEARCH INTERESTS

Big data analytics, health informatics, ontologies, biomedical data integration, machine learning, data mining, bioinformatics, artificial intelligence, epigenetics and omics in general.

POSITIONS AND EMPLOYMENT

2014 – Present	Postdoctoral Research Associate School of Computing and Information Sciences. Florida International University, USA
2014	Research Associate Research Center on ICT. University of A Coruña, Spain
2013	Visiting Scholar Stanford Center for Biomedical Informatics Research. Stanford University, USA
2011 – 2014	Predoctoral fellow. Teaching and Research Assistant Dept. Information and Communication Technologies. University of A Coruña, Spain

2008 – 2011 Research Assistant
Dept. Information and Communication Technologies. University of A Coruña, Spain

2007 – 2008 Undergraduate Research Assistant
Dept. Information and Communication Technologies. University of A Coruña, Spain

PUBLICATIONS - h-index = 7, i10-index = 6

Peer reviewed journals

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).

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).

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).

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.

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).

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).

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).

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).

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.

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).

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.

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 Byosistems, 8(6):1716-1722 (JCR 3.534; 103/290; Q2).

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.

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).

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

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).

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).

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).

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).

Suarez-Ulloa V, **Aguiar-Pulido V**, 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).

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).

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).

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).

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).

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).

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.

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.

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.

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).

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.

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.

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).

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).

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.

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

Fernandez M, **Aguiar-Pulido V**, Riveros JD, Huang W, Segal J, Zeng E, Campos M, Mathee K, Narasimhan G (2015). Microbiome Analysis: State-of-the-Art and Future Trends. Computational Methods for Next Generation Sequencing Data Analysis (pp. 333-351). John Wiley and Sons.

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.

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.

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 EXPERIENCE

2014	Degree in Computer Science Dept. Information and Communication Technologies. University of A Coruña, Spain Teaching Assistant: Security in Information Systems
2013 – 2014	Specialty in Information and Communication Technologies for officers Antonio de Escaño Specialist School. Spanish Navy Co-lecturer: Network Management
	Degree in Computer Science Dept. Information and Communication Technologies. University of A Coruña, Spain Teaching Assistant: Machine Learning
2012 – 2013	Degree in Computer Science Dept. Information and Communication Technologies. University of A Coruña, Spain Teaching Assistant: Machine Learning
	Degree in Industrial Design and Product Engineering Dept. Information and Communication Technologies. University of A Coruña, Spain Teaching Assistant: Basics of Informatics
	Degree in Information and Documentation Dept. Information and Communication Technologies. University of A Coruña, Spain Teaching Assistant: Informatics for Documentation

SUPERVISORY EXPERIENCE

2014 – 2015	Co-supervision of 1 undergraduate thesis from the Computer Science degree
2013 – 2014	Supervision of 1 undergraduate thesis from the Computer Science Engineer degree
2011 – 2012	Co-supervision 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
2008 – 2014	Board member of the Information and Communication Technologies Department University of A Coruña, Spain
2008 – 2014	Board member of the Computer Science Faculty University of A Coruña, Spain
2008 – 2010	Member of the Computer Science Faculty Graduate Committee University of A Coruña, Spain

SKILLS

Programming Languages: R, C++, HTML, C, Java, MySQL, C#, MATLAB, PHP (prior experience)

(Coding sample at: https://github.com/vaguiarpulido/)

Frameworks and Tools: GitHub, Weka, VMWare, SPSS, Visual Studio, Eclipse, SVN

Languages: English, French, Spanish and Galician

COURSES

2014	Machine Learning. Prof. Andrew Ng (Stanford University). Coursera
2014	Making Sense of Data. Google
2014	Statistical Learning. Profs. Trevor Hastie and Rob Tibshirani. Stanford University Online

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