

Vanessa Aguiar-Pulido

Ph.D. in Computer Science, Postdoctoral Research Associate
Center for Neurogenetics, Brain and Mind Research Institute
Weill Cornell Medicine, Cornell University, USA

PERSONAL DETAILS

Date of birth: Jan-29-1985

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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

2016 – Present	Postdoctoral Research Associate Center for Neurogenetics. Weill Cornell Medicine. Cornell University, USA
2014 – 2016	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 Biosystems*, 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**, 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).

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).

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.

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, Duado-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

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*

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.

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

MENTORING EXPERIENCE

- 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
- 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 (IJBDH)”
- 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

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

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