Villordo, Sergio Manuel

Personal Information

Nationality: Argentine. DNI: 29886454

Age: 32

Date of birth: December 11, 1982.

Marital status: single.

Home address: Julian Alvarez 691, 2 "A", CABA, Argentina. 1414

Cell phone: 54-911-69616454

webpage: http://sergiovillordo.github.io/webpage/

email:villordosergiomanuel@gmail.com

Personal Summary

Bright, creative and enthusiastic scientist with a wide experience in data mining and knowledge discovery. With an endless intellectual curiosity, and ability to mine hidden gems on the deep of complex datasets.

Major strengths include strong leadership, problem-solver and responsibility, as well as excellent communicational skills and teamwork. Proactive, adaptable, quick learner and open to new ideas.

Education

- "PhD of the University of Buenos Aires" (in course). Facultad de Ciencias Exactas. Universidad de Buenos Aires (UBA), Buenos Aires, Argentina. Start date: 09/20/10.
- "Master in Data Mining and Knowledge discovery" (in course). Facultad de Ciencias Exactas. Universidad de Buenos Aires (UBA), Buenos Aires, Argentina. 12/04/13.
- "Specialist in Data Analysis". Facultad de Ciencias Exactas. Universidad de Buenos Aires (UBA), Buenos Aires, Argentina. Graduation date: 02/10/14.
- "Master of science in Journalism". Instituto de Educación Continua, Universitat Pompeu Fabra. Buenos Aires, Argentina. Graduation date: 07/14/12.
- "Bachelor of Science. Genetics". Facultad de ciencias Exactas, Químicas y Naturales. Universidad Nacional de Misiones, Misiones, Argentina. Graduation date: 03/05/09
- "Agronomy technician". Instituto Agrotécnico Salesiano Pascual Gentilini, San José, Misiones Argentina. Graduation date: 11/30/01.

Key Skills

- Experience in searching, cleansing and processing crude data. (Using tools: Social networks API, R, Python, OpenRefine, Tesseract).
- Research and development of descriptive and predictive models using cutting edge softwares (R, SPSS, Weka, Matlab, Pyhton, RapidMiner, JMP, Infostat) and gold standard algorithms (Regression techniques, Decision Trees, Random Forest, Machine Learning approaches, survival analysis, neural networks, SVM, Naïve Bayes, KNN.
- Development of creative data visualizations using suitable tools (Ggplot2, D3, Tableau, Illustrator, Inkscape).
- Design, development and management of DBs systems (Postgresql, SQLserver, MySQL, SQLdf).
- Proficient use of Geographic information systems tools (R-GIS, Qgis, gvGIS, PostGIS).
- Large experience in Biological Data Analysis (R, Biostrings, BioPerl, BioPython, Blast, Bioinformatics databases and genome sequencing analysis tools).
- Reporting.
- Wide experience in Molecular and cell Biology laboratory and virus manipulation.



Honors

- Hackaton Verde 2014. Buenos Aires May, 16th and 17th, 2014. Organized by the government of Buenos Aires. Honorable Mention: "Development of an accuracy regression model to predict solid waste levels produced around the city".
- Hackaton AgroDatos 2014. Buenos Aires, October 25, 2014, Organized by Sadosky Foundation and the National Ministry of Science and Technology. Honorable Mention: "Predictive Analysis of crop fields in small soil areas".
- Facultad de ciencias Exactas, Químicas y Naturales. Universidad Nacional de Misiones, Misiones, Argentina. March, 2009 "Honorable Mention for Outstanding Students".

Professional Experience	
2014-2015.	Master student : Laboratorio de Virología Molecular, Fundación Instituto Leloir. Buenos Aires, Argentina. Research Topic : "Use of multidimensional decomposition and density based clustering analysis to detect low frequency viral variants".
2011-2012	International Internship: Department of Microbiology and Immunology, University of California, San Francisco, USA. Research Topic: "Studies of viral population using ultra-deepsequencig techniques". Funding: Defense Advanced Research Projects Agency (DARPA).
2010-2015.	PhD Student : Laboratorio de Virología Molecular, Fundación Instituto Leloir. Buenos Aires, Argentina. Research Topic : "Studies of RNA structures that regulate dengue virus replication in humans and mosquitoes".
2008-2009	Undergraduate Research Assistant: Laboratorio de Inmunología Estructural. Fundación Instituto Leloir. Buenos Aires, Argentina. Research Topic: "Genetics and structural studies on primary antibody response against proteins".
2006-2008	Undergraduate Research Assistant: Laboratorio Biología Molecular Aplicada. Universidad Nacional de Misiones, Misiones, Argentina. Research Topic: "Studies on the circulation of reemerging arboviruses transmitted by mosquitoes".
2001-2002	Agronomy technician: Instituto Agrotécnico Pascual Gentilini, Misiones, Argentina. Research Topic : "Use of hydro-absorbent polimers in agriculture":

English Intermediate to advance level **Portuguese** Intermediate level.

Publications

- Villordo S.M., Filomatori C., Sanchez-Vargas I., Blair C., Gamarnik A.V. "Dengue Virus RNA Structure Specialization Facilitates Host Adaptation". PLoS Pathog. 2015 Jan 30;11(1):e1004604. doi: 10.1371/journal.ppat.1004604.
- De Borba L., Villordo S.M., Iglesias N., Filomatori C., Gebhard L., Gamarnik A. "Overlapping Local and Long Range RNA-RNA Interactions Modulate Dengue Virus Genome Cyclization and Replication". J Virol. 2015 Mar 15;89 (6):3430-7.
- **Villordo S.M.** And Gamarnik A.V. "Differential RNA sequence Requeriment fo Dengue Virus Replication in Mosquito and Mammalian Cells" J Virol. 2013 Aug;87(16):9365-72.
- Leal MC, Magnani N, Villordo S.M., Marino Buslje C, Evelson P, Castano EM, Morelli L."Transcriptional regulation of Insulin Degrading Enzyme modulates mitochondrial A[beta] catabolism and functionality". J Biol Chem. 2013 May 3;288(18):12920-31.

- Filomatori C.V., Iglesias N.G., **Villordo S.M.**, Alvarez D.E., Gamarnik A.V. "RNA sequences and structures required for the recruitment and activity of dengue virus polymerase". J Biol Chem (2011), 286, 6929-6939.
- **Villordo S.M.**, Alvarez D.E., Gamarnik A.V. "A balance between circular and linear forms of the dengue virus genome are crucial for viral replication". RNA (2010) 16, 2325-35.
- **Villordo S.M.**, Gamarnik A.V. "Genome cyclization as strategy for flavivirus RNA replication". Virus Research (2009) 139, 230-239.

Courses

Current Methods in Machine Learning. Pablo Granito & Lucas Uzal. Escuela de Ciencias Informáticas (ECI). Facultad de Ciencias Exactas. Universidad de Buenos Aires (UBA), Buenos Aires, Argentina. July, 2014.

Machine Learning. Coursera, free online courses, 2014. Andrew Ng. Stanford University, USA.

Neural Network and Machine Learning. *Coursera, free online courses*, 2014. Geoffrey Hinton. Toronto University, Canada.

Intensive Introductory Perl Programming course. Edita Karosiene. Department of Systems Biology. Technical University of Denmark. June, 2012.

Introduction to Bioinformatics. Fernán Agüero. Instituto de Investigaciones Biotecnológicas, Universidad de San Martín, Buenos Aires, Argentina. September, 2010.

Teaching experience		
07/2005-07/2006	Teaching Assistant. Subject: "Statics I and II", Department of Genetics,	
	Universidad Nacional de Misiones, Misiones, Argentina.	
08/2006-08/2007	Teaching Assistant. Subject: "Populations Genetics", Department of Genetics,	
	Universidad Nacional de Misiones, Misiones, Argentina.	

Presentations at international scientific meetings

Villordo, S.M., Alvarez D.E., Gamarnik, A.V. "A Balance between Circular and Linear Forms of the Dengue Virus Genome is Crucial for Viral Replication". III ICGEB Workshop on Human RNA Viruses. Buenos Aires, Argentina. April, 2012

Villordo, S.M., Alvarez D.E., Gamarnik, A.V. "Different Conformations of Dengue Virus RNA Genome Are Crucial for Infectivity". A Re-Emerging Challenge in the Americas: Opportunities for Dengue Research Collaboration, National Institute of Allergy and Infectious Diseases (NIAID) National Institutes of Health (NIH). San Juan, Puerto Rico, USA. February, 2011.

Villordo S.M., Filomatori C.V., Alvarez D.E., Iglesias N.G., and Gamarnik A.V. "Dynamic RNA Structures Involved in Dengue Virus Genome Amplification". 6th Mexican National Congress of Virology. Merida, Mexico. November, 2009.

Villordo S.M., Alvarez D.E., Filomatori C.V., Gamarnik A.V. "Circular and Linear Conformations of the Dengue Virus Genome Are Necessary for Viral RNA Amplification" Workshop on Replication and Recombination of RNA Virus Genomes, Juan March Foundation. Madrid, Spain. October, 2009.

Villordo S.M., Filomatori C.V., Alvarez D.E., Mondotte J.A., Gamarnik A.V., Location and Function of Dengue Virus Cyclization Sequences. 28th Annual Meeting, American Society for Virology, Vancouver, Canada. July, 2009.