Villordo, Sergio Manuel

Personal Information:
Nationality: Argentine.
National Identification Number: 29886454
Marital status: single.
Date of birth: December 11, 1982.
Home address: Mariano Acha 1753 ,
Buenos Aires, Argentina.
Zip Code: 1430
Cell phone: +54-911-69616454
email:villordosergiomanuel@gmail.com
linkedin: https://ar.linkedin.com/pub/sergio-manuel-villordo/a6/4b0/715
researchgate: https://www.researchgate.net/profile/Sergio_Villordo
web: http://sergiovillordo.github.io/webpage/

Summary

   Bright, creative and enthusiastic scientist with more than ten years experience doing research at academia and private companies. Has a endless intellectual curiosity, and an ability to mine hidden gems from the deep of complex data sources.
   In addition to the strong Data Science and Molecular Biology background, other major strengths include, leadership, problem-solver and responsibility, as well as excellent communication skills and team work.

Education (most relevant schools or programmes):

- **"PhD in Biological Chemistry and Bioinformatics"**. Facultad de Ciencias Exactas. Universidad de Buenos Aires (UBA), Buenos Aires, Argentina. Graduation date : 2016/04/11.
- **"Specialist in Data Mining and Knowledge discovery"**. Facultad de Ciencias Exactas. Universidad de Buenos Aires (UBA), Buenos Aires, Argentina. Graduation date: 2014/02/10.
- **"Bachelor of Science in Genetics".** Facultad de ciencias Exactas, Químicas y Naturales. Universidad Nacional de Misiones, Misiones, Argentina. Graduation date: 2009/03/05.

Work Experience and skills

2017 - present:
Full-stack Data Scientist at Despegar.com (https://www.despegar.com.ar).
Responsibilities: At Despegar I'm working in an Artificial Intelligence Research Group focus on development of tools and microservices for image classification, content moderation and personalized customer recommendations. This group is strongly interested in the application of the state of the art Machine Learning and AI tools for the development of innovative solutions for the company.

Skills: Scene Image datasets generation and tagging, convolutional networks, image feature extraction. Cleansing and processing data, prototype ML model generation (python, keras, R). Research, development and deploy of descriptive and predictive models using cutting edge big data frameworks, environments and programming languages (java-scala, spark, presto, PostgreSQL, aws services, docker, tensorflow, opencv, etc.).

2016 - 2017:
Research Scientist at Etermax (https://www.etermax.com/en/home/):
Responsibilities: At Etermax, I lead two smalls groups, one focused on image and text classification for content moderation, and the other on customer lifetime value prediction.
Skills: Image and natural language processing for representation learning. Processing of big datasets (R,python). Research and development of descriptive and predictive models (R, python). Reporting and deploying of informative dashboards and visualizations (R, shiny).

2015 - 2016:
Data Scientist at Globant (https://www.globant.com)
Responsibilities: Working as Data Scientist consultant for Globant, I was involved with diverse clients and projects regarding: employees attrition, customer opinions and surveys text-analytics, time series modelling and sales forecasting, and operation research applied to products price optimization.
Skills: Processing of big datasets(R,excel, SPSS, SAS). Natural language processing. Processing of big datasets(R software, SAS). Research and development of descriptive and predictive models and linear programming (R,SPSS, SAS, Gurobi). Reporting and deploying of informative dashboards and visualizations (tableau, clickview).
References: Gonzalo Zarza, PhD, Technical Director in Big Data practice at Globant.
email:gonzalo.zarza@globant.com

2014-2015
Master Specialization Thesis at Laboratory of Molecular Virology, *Fundación Instituto Leloir*, Buenos Aires, Argentina (http://www.leloir.org.ar/gamarnik-en/).
Title: *"Use Statistical and deep learning approaches for multidimensional decomposition and noise reduction in high throughput sequencing".*
Responsibilities: This specialization work has been focused on the development of a new methodologies for RNA virus quasispecies analysis using NGS sequencing.
Skills: Planning, cost estimation, leading, execution and analysis of NGS sequencing experiments. Processing of sequencer device data outputs and quality checks. Mapping to reference and map-contig generation. Application of unsupervised machine learning (clustering, KNN), deep learning (autoencoders), statistics and maths for the development of bioinformatics pipelines for the noise reduction and viral variant characterization.
Molecular and cell biology, cell culture and laboratory bench work handling .
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).
References:Cristina Marino Buslje, PhD ,head of the Structural Bioinformatics Lab, Fundacion Instituto Leloir.
email: cmb@leloir.org.ar

2010-2015

PhD Thesis at Laboratory of Molecular Virology, Fundación Instituto Leloir. Buenos Aires, Argentina(http://www.leloir.org.ar/gamarnik-en/).

Title: *"Studies of RNA structures that regulate dengue virus replication in humans and mosquitoes".*

Responsibilities: The objective of this thesis was the discover of new insights about DENGUE virus replication and was focused on the study of genome RNA structures. As result of combining a plethora of biochemical, cell culture, deep sequencing and bioinformatics experiments tools we discovered new important insights about RNA virus replications. The result of the these findings were published at high impact indexed journals: https://www.ncbi.nlm.nih.gov/pubmed/?term=Villordo+SM%5BAuthor%5D

Skills: Wide experience working in Molecular and cell biology lab: cell culture and cell transfection, molecular cloning and recombinant technology, virus manipulation and reporter system manipulation, conventional and confocal microscopy, protein purification, biophysical devices (light-scattering, FPLC, EMSA, Biosensor, circular dichroism, mass spectrometry). RNA structure determination by biochemical probing and bioinformatics approaches. Sanger and NGS sequencing experiment and analysis (small and large reads). Long experience working with supervised and unsupervised machine learning (Clustering approaches, xgboost, gbm, random forest, svm, etc.) and deep learning (autoencoders, MLP, CNN). Proficient use of Bioinformatics tools and programming languages (Biopython, Biostring).

References:Andrea Gamarnik, PhD, head of the Molecular Virology Lab, Fundacion Instituto Leloir.
email: agamarnik@leloir.org.ar

Scientific Publications (most recent publications at pair review journals)

- de Borba L, **Villordo SM**, Marsico F, Carballeda J,Filomatori C, Gebhard L, Pallares H, Lequime S, Lambrechts L, Blair C, Sanchez-Vargas I and Gamarnik A. RNA Structure Duplication in the Dengue Virus 3'UTR: Redundancy or Host Specificity? mBio, 2019 (Accepted)
- Filomatori CV, Carballeda JM, **Villordo SM**, Aguirre S, Pallares H, Maestre A, Sánchez-Vargas I, Blair CD, Fabri C, Morales MA, Fernandez-Sesma A, Gamarnik A. "*Dengue Virus Genomic Variation Associated with Mosquito Adaptation Defines the Pattern of Viral Non-Coding RNAs and Fitness in Human Cells*". PLoS Pathog. 2017 Mar 6;13(3):e1006265. doi: 10.1371/journal.ppat.1006265.
- **Villordo S.M.**, Carballeda JM, Filomatori C., Gamarnik A.V. *"RNA Structure Duplications and Flavivirus Host Adaptation". Trends Microbiol. 2016. Apr;24(4):270-83.*
- **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.

more scientific publications at pubmed:
https://www.ncbi.nlm.nih.gov/pubmed/?term=Villordo+SM%5BAuthor%5D

Languages:

Spanish	Natural language
English	Intermediate to advanced level
Portuguese	Intermediate level

Trainings(most recents)**:**
Introduction to Functional Programing. Martin Odersky.
https://es.coursera.org/specializations/scala
Java test automatization. Marcelo Corpucci. EXO TRAINING CENTER. Buenos Aires (UBA), Buenos Aires, Argentina. Marzo, 2018.
An introduction to Big Data using Spark. Luis Argerich. Mulesoft Academy. Buenos Aires (UBA), Buenos Aires, Argentina. Julio, 2016.
Introduction to JAVA programming. Maria Vizoso. EXO TRAINING CENTER. Buenos Aires (UBA), Buenos Aires, Argentina. Noviembre, 2015.
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.

Teaching experience
2018/11
"An Introduction to Artificial Intelligence in the industry", Profesor. Universidad Argentina de la Empresa, UADE, Buenos Aires, Argentina.
"Clustering Approaches for Data Scientist", Profesor. Escuela Argentina de las Nuevas Tecnologías, EANT, Buenos Aires, Argentina.
2005/07-2006/07
2018/09
"Getting started with AI tools for viral variants characterization", Speaker , Winter School in Molecular Biology. Federal University of Latin-American Integration, Foz do Iguaçu ,Paraná, Brazil.
"A guide to start with RNA structure analysis". Speaker , Winter School in Molecular Biology. Federal University of Latin-American Integration, Foz do Iguaçu ,Paraná, Brazil.
2016/03-2018/12
"Statistics I and II",Teaching Assistant. Department of Genetics, Universidad Nacional de Misiones, Misiones, Argentina.
2006/07-2007/07
"Populations Genetics",Teaching Assistant. Department of Genetics, Universidad Nacional de Misiones, Misiones, Argentina.