Elías Daniel Lopez

Curriculum Vitae

Fray Mamerto Esquiú 1067
Ingeniero Maschwitz-Buenos Aires
+54 911 39500631
elias@digitalhouse.com

"Success is the ability to go from failure to failure without losing your enthusiasm." – Winston Churchill

Professional Summary

I took my BSc in molecular biology at the University of Buenos Aires. After graduating, I accepted a PhD position in the faculty of exact science at the University of Buenos Aires, in the area of computational chemistry. Since 2012 I have specialised in the use and development of several tools in the field structural bioinformatics. During my stay at the University of Barcelona, I combine data science and computational chemistry to develop a new scoring function for drug development. Lastly, I'm a data science professor and responsible for the course in two important institutes of Argentine. I currently work in the systems department of a credit bureau developing different scoring functions and machine learning models. I have experience in several programming languages and Web technology (HTML, CSS, Javascript/ECMAScript), with excellent handling of python, Fortran and Linux OS.

keywords: team work, python, tensorflow, neural networks, sklearn, mssql, Tasks Automation, systems integration, machine learning, distributed processing, ms-sql,artificial intelligence and workflows.

Personal Data

Date of birth	12/1985
Nationality	Argentine
Civil status	Single
Web Page	`http://datadriven.tk`
LinkedIn	`https://www.linkedin.com/in/elias-lopez-data-scientist/`
GitHub	`https://https://github.com/biodatasciencearg/`
Google Scholar	`https://scholar.google.com/citations?user=dISuKoYAAAAJ&hl=es`
CUIL	23-31926494-9

Experience

Working experience

05/2019 present **Data scientist**, *Siisa*, Bs. As., Argentina.

The principal product of the company is a scoring service. The Score helps lenders make accurate and reliable credit risk decisions across the customer lifecycle.The credit risk score rank-orders consumers by how likely they are to pay their credit obligations as agreed. Major achievement:

- Implementation of an income predictor. Is a fundamental feature to determined if a customer will pay their credit obligations. To reach the goal I developed a model in mssql to predict their income and a confidence interval.
- Implementation of a model to predict if a customer gets a credit. Very often the information about customers is sensitive data. To to get around this lack of information about the credential history of a customer I developed a score using a ensamble model to determine if a certain client acquire a loan with a lender.
- Affordability score. The score computes the probability of default due to an over-indebtedness by the lender due to an incorrect credit limit. Implemented in mssql and developed in sklearn.
- Originations score improvement. Development of a new behaviour variable using a lstm neural network.

11/2018 01/2019 **Backend Developer**, *Bitgenia*, Bs. As., Argentina.

I'm was involved in the development of the bioinformatic pipeline for the analysis and interpretation of genomic data, handling large volumes of data to transform them into information. The pipeline implementation was done in bash, integrating GATK4 (a java program) with python scripts analysis to process genomic data. Major achievement:

- Addition of Bash modules calling Java programs that filter genomic reads applying Gaussian mixtures.
- Add support and compatibility for 23andme genomic file format.

04/2004 04/2006 **Production**, *Centro Diagnóstico veterinario*, Pilar - Bs. As., Argentina.

Biotechnology and production of bacterial antigens for the formulation of injectables for animal health. Some of the tasks developed were related to scaling up, identification and quality of bacterial antigens.

Academic experience

08/2017 12/2018 **PhD. Graduate-Postdoc position**, *Universidad de Buenos Aires*, CABA, Argentina.

Development of techniques for the study of conformational changes. Case study: "M. tuberculosis protein kinases". Development of libraries for the study of the effect of new drugs on molecules of interest of Mycobacterium tuberculosis. Major achievement:

- Addition of modules in FORTRAN that compute physical properties that are integrated into the molecular dynamics engine.

2015, 2017 **DEANN Exchange Visits**, *Barcelona University*, Barcelona, Spain.

I was selected to participate in DEEN exchange program between America and Europe funded by the European Union. Two stages and two trips of 3 months each at the University of Barcelona was my training in the drug design field. The ICREA Research Professor Xavier Barril's group is expert in aided computational drug design. My research was the development of a new scoring function derived from thermodynamics properties. Mixing data science and computational chemistry I was able to publish several papers with high-impact on international journals (see my scholar profile). Major achievement:

- I Developed a new scoring function adding thermodynamic information for drug design for mycobacterium tuberculosis

Teaching

09/2018 present **Data science Professor**, *Digital House*, Buenos Aires, Argentina.
Responsible for carrying out teaching duties related to data science tools and methods. Some of the topics discussed are: **decision trees, reduction of dimensionality, clustering, Regularization, regression and Bayesian techniques among others.** These machine learning algorithms automate the construction of analytical models allowing learn from data, identify patterns and make decisions, find frauds, etc. The course takes advantage of the python implementations of powerful libraries like scikit-learn, pandas and keras.

04/2019 09/2019 **Data science Mentor**, *Acámica*, Buenos Aires, Argentina.
Mentor in the online-career in data science.

08/2017 12/2017 **Professor**, *Universidad Nacional de Entre Ríos*, Paraná - Entre Ríos, Argentina.
Responsible for carrying out teaching duties related to discovery and drug design.

03/2017 08/2017 **Chief of Practical Applications**, *Universidad Nacional de Entre Ríos*, Paraná - Entre Ríos, Argentina.
In charge of the practices of the course "Modeling and Simulation of Macromolecules"

Education

2012-2017 **Computational Chemistry**, *Universidad de Buenos Aires*, Argentina.
PhD - Graduate. **Thesis title**: "Study of the structure-function relationship in protein kinases"

2006-2011 **Biological Sciences**, *Universidad de Buenos Aires*, Argentina.
BSc/MSc - graduate. Avg:7.43 **Orientation:** Molecular Biology and biotechnology.

Informatics

Programming languages	Fortran,C	Scripting	python, tcl, bash
Platforms	Unix, Windows, Open Source Software	DB	SQL
Tools	Data analysis, R, scikit learn, pandas, numpy, scipy, matplotlib, networkx	Programs	Office, Illustrator, GATK4, Amber, Origin.

Other courses / trainings

2017-Course "Protein Purification" - Facultad Farmacia y bioquímica-UBA. The course focuses on the purification of membrane proteins and the quality controls associated with the process.

2005-Course "Introduction to gas-chromatography (GC)" - Asociación Química Argentina. Introductory course where they explain the selectivity, phases of different columns and applications.

Languages

	comprehension	**Oral**	**reading**
English	*intermediate*	*intermediate*	*intermediate*

References

Adrían G. Turjanski
scientific director
Bitgenia
Alicia Moreau de Justo 1750 Piso 3H
CABA
✉ aturjans@gmail.com
☎ +549-11-24551001

Marcelo Martí
Department of Biological Chemistry
University of Buenos Aires
Int. Güiraldes, C1428 Buenos Aires
✉ marti.marcelo@gmail.com
☎ +549-11-57581800

Xavier Barril
Facultat de Farmacia
University of Barcelona
Barcelona,Spain
✉ xbarril@ub.edu

Mariano Sokal
IT Department
SIISA
Buenos Aires, CABA
✉ msokal@gmail.com

Publications

1. Elias D Lopez, Juan Pablo Arcon, Diego F Gauto, Ariel A Petruk, Carlos P Modenutti, Victoria G Dumas, Marcelo A Marti, and Adrian G Turjanski. Watclust: a tool for improving the design of drugs based on protein-water interactions. *Bioinformatics*, 31(22):3697–3699, 2015
2. Andrea C McReynolds, Aroon S Karra, Yan Li, Elias Daniel Lopez, Adrian G Turjanski, Elhadji Dioum, Kristina Lorenz, Elma Zaganjor, Steve Stippec, Kathleen McGlynn, et al. Phosphorylation or mutation of the erk2 activation loop alters oligonucleotide binding. *Biochemistry*, 55(12):1909–1917, 2016
3. Juan Pablo Arcon, Lucas A Defelipe, Carlos P Modenutti, Elias D Lo´pez, Daniel Alvarez-Garcia, Xavier Barril, Adria´n G Turjanski, and Marcelo A Martí. Molecular dynamics in mixed solvents reveals protein–ligand interactions, improves docking, and allows accurate binding free energy predictions. *Journal of chemical information and modeling*, 57(4):846–863, 2017
4. Franco Marsico, Osvaldo Burastero, Lucas A Defelipe, Elias Daniel Lopez, Mehrnoosh Arrar, Adrián G Turjanski, and Marcelo A Marti. Multiscale approach to the activation and phosphotransfer mechanism of cpxa histidine kinase reveals a tight coupling between conformational and chemical steps. *Biochemical and biophysical research communications*, 498(2):305–312, 2018
5. Elias Daniel Lopez and Juan Pablo Arcon. Water sites improve docking prediction for hydrophilic drugs. 2015
6. Juan Pablo Arcon, Lucas A Defelipe, Carlos P Modenutti, Elias D Lo´pez, Daniel Alvarez Garcia, Xavier Barril, Adria´n G Turjanski, and Marcelo A Martí. Correction to molecular dynamics in mixed solvents reveals protein–ligand interactions, improves docking and allows accurate binding free energy predictions. *Journal of chemical information and modeling*, 58(6):1312–1312, 2018
7. Osvaldo Burastero, Lucas Defelipe, Juan Arcon, Elias Lopez, Xavi Barril, Marcelo Marti, and Adrián Turjanski. Novel mycobacterium tuberculosis pkng inhibitors. a computational-experimental

study. *International Journal of Infectious Diseases*, 73:345–346, 2018

8. Juan Pablo Arcon, Carlos P Modenutti, Demian Avendaño, Elias D Lopez, Lucas A Defelipe, Francesca Alessandra Ambrosio, Adrian G Turjanski, Stefano Forli, and Marcelo A Marti. Autodock bias: improving binding mode prediction and virtual screening using known protein–ligand interactions. *Bioinformatics*, 35(19):3836–3838, 2019
9. Juan Pablo Arcon, Lucas A Defelipe, Elias D Lopez, Osvaldo Burastero, Carlos P Modenutti, Xavier Barril, Marcelo A Marti, and Adrian G Turjanski. Cosolvent-based protein pharmacophore for ligand enrichment in virtual screening. *Journal of chemical information and modeling*, 59(8):3572–3583, 2019
10. Elias D Lopez, Osvaldo Burastero, Juan P Arcon, Lucas A Defelipe, Natalie G Ahn, Marcelo A Marti, and Adrian G Turjanski. Kinase activation by small conformational changes. *Journal of chemical information and modeling*, 2019