

Juan Cruz Rodriguez

Education

- PhD in Computer Science
FAMAF - National University of Córdoba (2014 - 2019)
- MSc in Applied Statistics
FCA, FCE and FAMAF - National University of Córdoba (2014 - 2019 *est.*)
- MSc in Computer Science
FAMAF - National University of Córdoba (2007 - 2012)
- BSc in Computer Science
FAMAF - National University of Córdoba (2007 - 2009)

Teaching Activities

- Teaching Assistant
FAMAF - National University of Córdoba (May 2014 - Present)
Algorithms and Data Structures
- Teaching Associate
Faculty of Engineering - Catholic University of Córdoba (2013 - 2014)
Programming in Python
- Student Assistant
FAMAF - National University of Córdoba (2011 - 2012)
Algorithms and Data Structures II & Databases

Industry Experience

- Software Engineer
Applied Research (INVAP; June 2013 - October 2013)
C ++ / Qt
- QA Engineer
HPC Group at Intel Corporation (June 2012 - June 2013)
C, Perl, Python, Bash

R Packages

Bioconductor

- MIGSA: Massive and Integrative Gene Set Analysis

CRAN

- rflights: Query Plane Tickets using the 'Kiwi' API

GitHub

- autokeras: R interface to Auto-Keras
- KerasModelCreator: Visually design Keras models for R language
- shinyWYSIWYG: Shiny What You See Is What You Get (WYSIWYG) editor

- shinyParallel: Run Shiny applications in a multi-session mode

--- Awards and Distinctions

- University Award
Diploma with Special Mention
National University of Córdoba to the second best average of 2011 graduates
- Substitute for First Escort
FAMAF - National University of Córdoba (2011)

--- Scholarships

- Fulbright exchange visiting scholarship
At the University of Florida (2018)
- Doctoral Scholarship
National Scientific and Technical Research Council, Argentina (CONICET; 2013 - 2019)
- Master's Scholarship
Government of Córdoba, Argentina (2007 - 2011)

--- Publications

2019

- Rodriguez, J. C., Luraschi J.
Auto-Keras: An R easily accessible deep learning library.
- Rodriguez, J. C., Merino, G. A., Llera A. S., Fernández, E. A.
Massive integrative gene set analysis enables functional characterization of breast cancer subtypes. **(Journal)**

2018

- Rodriguez, J. C., Vargas Rojas C., Fernández, E. A.
ShinyWYSIWYG: a Shiny What You See Is What You Get editor.

2017

- Rodriguez, J. C., Prato L., Llera A. S., Fernández, E. A.
Effects of RNA-Seq data gene analysis methods, on the over-representation analysis of gene sets.

2016

- Rodriguez, J. C., González, G. A., Fresno, C., Llera, A. S., Fernández, E. A.
Improving Information Retrieval in Functional Analysis. **(Journal)**
- Rodriguez, J. C., Merino, G. A., Prato L., Llera A. S., Fernández, E. A.
The impact of RNA-Seq differential expression algorithms on Over-Representation Analysis of Gene Sets.

2015

- Rodriguez, J. C., González, G., Fresno, C., & Fernández, E. A.
Integrative Functional Analysis Improves Information Retrieval in Breast Cancer.
- Fresno C., González G. A., Merino G. A., Rodriguez J. C., Balzarini M., Fernández E. A.
DNA Microarrays Quality Control by ANOVA-PCA / PLS decomposition.

--- Research Exchange

- At the Ana Conesa Lab.

University of Florida, USA (*October 2018 - December 2018*)

- At the Genomics of Gene Expression group.

Centro de Investigación Príncipe Felipe, Valencia, Spain (*October 2017 - December 2017*)

DEANN project (Marie Curie IRSES, European Commission, 2013)