

Corina Duenas Roca

149 Coldhams Lane, Cambridge, United Kingdom
07599814854 • corina.bioinformatic@gmail.com • linkedin.com/in/corina-duenas-pharmaconetworks

Personal statement

A highly motivated and professional computational biologist with extensive experience in bioinformatic analysis with R and Python. Wet lab and dry lab experience and currently seeking a new position as Computational Biologist and Data Analyst. A self-taught, organised and with teamwork skills. Experience creating Python modules, GitHub, R, Octave and working with APIs to manage the biological data stored in several databases (GO, ChEMBL, Reactome).

Key Skills

- R, Octave and Python programming in Linux or Windows environment.
- Developing personalized extensions in Spotfire with Ironpython and R
- Experience in data analysis of biological datasets (course ongoing in advanced statistics using machine learning processes). Fluent in Microsoft Office tools (Excel, Word and PowerPoint) and alternatives as Libre office, and Prezi.
- Excellent communication skills, both written and verbal with experience in conferences and volunteer in scientific events for spreading science.
- Strong background in pharmacy and immunology (lab experience)

Employment History

Bioinformatician at REACTOME Team (Molecular networks Services), EBI-EMBL, Hinxton (Cambridgeshire) *(September 2016 – December 2017)*

My duties included statistical analysis of elements in our Protein-protein interaction network (PPI) (specialized in interleukins) 'Reactome'; weekly group discussion and extracting data from XML files, and graph database Neo4J (CYPHER). Managing Databases as Reactome, OpenTargets, ArrayExpress, AtlasExpression, ChEMBL, ENSEMBL by mean of GUI, REST API or Python.

As a final project, I developed an automatized way to see the metrics and coverage of the database.

Bioinformatician and curator of mathematical models at BIOMODELS Team (Molecular networks Services), EBI-EMBL, Hinxton (Cambridgeshire) *(March 2016 – September 2016)*

My duties included curation of some mathematical models and writing monthly abstracts about determined models. Simultaneously I worked in a research project of an autoimmune disease (literature mining, reanalysis of current data) with perspectives to merge existing Biological Quantitative models to help to understand the disease. Managing Databases as Reactome, OpenTargets, ArrayExpress, AtlasExpression, ChEMBL, ENSEMBL. I worked in a Linux environment with Python and R to manage big amounts of data.

I also use to write a mini review called 'The model of the month' to be published monthly in BioMed Central.

Bioinformatic Analyst, VIVIA Biotech SL, Tres Cantos (Madrid)

(September 2014 – February 2016)

My duties involve IronPython extension in the TIBCO software environment, R package development in NonLinearModel Analysis, Ironpython Spotfire customized extensions for Spotfire modeling, Data Analysis from immunological and pharmacodynamics experiments (from flow cytometry).

Education

Machine Learning, Coursera (Stanford University, Andrew Ng)

(July-September 2018)

Advanced machine learning algorithms to problems as anti-spam, image recognition, clustering, building recommender systems, and many other problems (using programming languages as Octave/Matlab). Algorithm selection depending of the task, 'debugging' and optimization of learning algorithm's performance.

Python 3 course, CodeAcademy (updated)

(July 2018)

Approaching and planning different genomic analysis based on type of data and assumptions, hypothesis testing, multivariate normal distributions and correlations, agreements and potential conclusions from the different outcomes.

HarvardX, Online course of Statistics and R

(May 2018 – June 2018)

Approaching and planning different genomic analysis based on type of data and assumptions, hypothesis testing, multivariate normal distributions and correlations, agreements and potential conclusions from the different outcomes.

University Complutense-ISCIII, Master in Biology and Computational Biology

(September 2015 – February 2016)

Modules include Phylogenetic analysis, Genetic analysis, Proteomic analysis, R for statistical analysis & Machine learning, Python for parsing databases, postgresQL database, Working in Ubuntu OS. Biochemistry and protein 3D structure description and interaction tools as Pymol are included.

University of Alcalá, Bachelor in Pharmacy

(September 2008 – June 2013)

Modules include Statistics, Biochemistry, Molecular biology.
Erasmus internship in Medical Institute of Warsaw, in the Tomasz Rygiel team (Immunology lab).

Hobbies & Interests

In my leisure time, I am improving my skills in programming. Also, I enjoy reading biology journals, and learning how to use bioinformatics tools for analysis. I like to actively participate in conferences related to my field (EBI-EMBL conferences) and spreading scientific knowledge (Cambridge Science Week as a volunteer). Also I like to keep me updated about biotechnology and biomedicine attending to conferences (Cambridge Therapeutic forum, EBI-EMBL workshops and Almazon-Alexa Workshops).