

Francisco REQUENA

PERSONAL DATA

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WORK EXPERIENCE

- | | |
|----------------|---|
| MARCH-AUG 2017 | Kitchen assistant at KAFFI LAUGALEKUR, Reykjavik (Iceland) |
| JAN-SEP 2016 | <p>Internship at CENTRE FOR GENOMICS AND ONCOLOGICAL RESEARCH (GENYO), Granada</p> <p><i>Epigenetics in stem cells and cancer Group. David Landeira's lab</i></p> <p>Development of NOMEplot, a webtool which analyzes results obtained by novel technique NOME through NGS to observe methylation and nucleosome positioning in a region of DNA. The project is implemented on a server with a web interface user-friendly for any researcher in the world could use it, without the requirement of informatic knowledge. The tool is developed through three combined tools :</p> <ol style="list-style-type: none">1. R. The core mechanism has been developed with R language and packages such as Biostrings (Bioconductor), hclust, ggplot2, grid, base...2. Shiny. Connect R code (> 1.200 lines) with the user through a web interface and offer a reactive environment where the user can modify every variable and can see an instant modification with the updated graphic.3. Rmarkdown. This tool allows the generation of automated reports generated with user's data in format HTML. <p>The application NOMEplot is completed and will be published in 2018. Besides this project was presented at the national conference of spanish users of R (November - 2016) .</p> |
| SUMMER 2015 | <p>Internship at SPANISH NATIONAL CANCER RESEARCH CENTRE (CNIO), Madrid</p> <p><i>Translational Bioinformatics Group. Fatima Alsharour's lab</i></p> <p>Project oriented of repositionating of new drugs for prostate cancer with crossed transcriptional data of microarray obtained from public database (GEOdata) and project LINCS. Searching inverse gene expression data (prostate cancer) with respect drug response signature. Handling data with Bioconductor (packages: affy, limma, AnnotationDbi...), GSEA and pipelines (RUBIOSeq) of RNA-Seq data..</p> |
| FEB-MAY 2015 | <p>Internship at ENGINEERING INSTITUTE (I3A), Zaragoza</p> <p><i>Biomedical Engineering Group. Iñaki Ochoa's lab</i></p> <p>Development of biomimetic environments through microfluidic devices and cell culture using spheroids. Transfection, confocal microscopy, immunofluorescence, culture cell.</p> |

EDUCATION

- ACTUAL Master in BIOINFORMATICS and COMPUTATIONAL BIOLOGY
Autonomous University of Madrid, Madrid
Subjects: "R Language, Machine Learning, Python language, Databases, Linux, Data Mining, NoSQL databases
- SEPTEMBER 2016 Master in TRANSLATIONAL RESEARCH and PERSONALIZED MEDICINE
Granada University, Granada
Average mark: 9.6/10
Thesis: "Development of a webtool to analyze Sanger-sequencing NOME datasets" | Advisor: Prof. David LANDEIRA
GRADE: 10/10
- SEPTEMBER 2015 Degree in BIOTECHNOLOGY, **Francisco de Vitoria University, Madrid**
Average mark: 7/10
Thesis: "Generation of organotypic multicellular spheroids of HepaRG for microfluidic applications" | Advisor: Prof. Iñaki OCHOA
GRADE:9.5/10

LANGUAGES

SPANISH: Mother tongue
ENGLISH: B2 level

COMPUTER SKILLS

Statistical language: R (professional level)
Programming language: Python (basic level)
Database Management System : MySQL, NEO4j (basic level)
Operating system: Unix/Linux shell (basic level)

DATA SCIENCE SKILLS (USING R)

Machine learning: linear regression, logistic regression, decision tree, random forest, Naive Bayes, k-means and k-nn.
Data visualization: Shiny, plotly, ggplot, leaflet
Data manipulation: dplyr, tidy
Text Mining: tm, rtweet, tidytext

PRESENTATIONS

- NOVEMBER 2016 **VIII National Conference of spanish users of R. Albacete, Spain**
Title: "NOMePlot: web application developed with R/Shiny to visualize and analyze data from NOME-seq technique."
- NOVEMBER 2017 **IX National Conference of spanish users of R. Granada, Spain**
Title: "HealthPlot: Understanding public health in USA with Open data and R."
AWARD FOR THE BEST WORK PRESENTED BY A YOUNG RESEARCHER

PROJECTS OPEN-DATA

1. DRUGSPLOT: Web application which analyzes data from the European Monitoring Centre for Drugs and Drug Addiction (EMCDDA) with more than 500 variables through data visualization such as interactive boxplots, shapefile maps and automated reports. Developed with R and Shiny. Access: [Drugplot](#)

2. HEALTHPLOT: This app is conformed by a total of 40 datasets and more than 50 graphics divided into 13 categories (health, religion, politics, genre, security, ancestry, immigration, demography, economic, logistic, languages and population) that reflect some aspects of the American society. Every dataset was individually cleaned and prepare for the app. Access: [HealthPlot](#)

3. RSCIENCEEXPLORER2016: This application analyzes more than 12.000 articles and 22.000 tweets obtained through relevant scientific journals (and their twitter accounts). This app was built with R and Shiny. Access: [RSciencexplorer2016](#)