

Italo M. Duran

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WORK HISTORY

Johnson & Johnson – Ethicon

Raritan, NJ

RDLD Engineer Data Science / Bioinformatician

02/2023-11/2024

- **Developed 'Janytor'**, a Python Dash application for automated data cleaning & transformation, reducing data processing time from 30 minutes to **7 seconds** per dataset.
 - Eliminated a 24-hour delay in data availability, enabling immediate post-experiment analysis.
 - Achieved annual time savings of over **3,600 hours**, equivalent to **\$183,000** in cost savings.
- Developed an **R Shiny app** for data transformation, summary statistics, and data visualization.
- Maintained and updated data analysis platforms, enhancing operational efficiency.
- Assisted in developing Python scripts for the NPDU Python course.

PROJECTS & RESEARCH EXPERIENCE

Biological Database web development for Mutational Accumulation of yeast

- Aiming to develop an open-source web interface that relocates and pools raw data files, cross references feature and performs

statistical aggregation to easily visualize queries against experimental data and automate workflows

- Worked in python and SQL to build a database focusing on identifying C to A mutational frequency in yeast strains containing msh2 mutations

Extended analysis of Dengue Virus-2 genome

- Assessed an extended analysis of Dengue Virus-2 genome by structure, domains, and phylogeny analyses
- Built an array package with several methods and attributes in python to perform calculations

Microarray based tumor classification

- Reproduced a colorectal cancer microarray analysis, focused on differentiating C3 and C4 tumor subtypes
- Developed a pipeline to process microarray data including normalization, batch correction, and scaling
- Employed Principal Component Analysis to reduce dimensionality and examine outliers using ggplot2

Analysis of transcriptional profile of murine cardiac regeneration using mRNA-Seq data

- Performed quality control on FASTQ files and recreated figures from O'Meara et. al., 2015
- Obtained mRNA-Seq datasets from GEO to generate estimates of transcript abundance/depletion in postnatal day 0 (P0) and adult (Ad) murine cardiomyocytes utilizing CuffLinks package
- Compared FPKM counts of genes involved in three biologically distinct functional processes using hierarchical clustering algorithm and heatmaps to interpret upregulation / downregulation between datasets

Analysis of neuraminidase and nucleoproteins of H1N1 influenza type A

- Conducted a multiple sequence alignment study to inspect and predict active target sites on neuraminidase and nucleoproteins of H1N1 influenza type A

EDUCATION

Boston University

Boston, MA

MS, Bioinformatics

2021-2023

Florida International University

Miami, FL

BS, Biology

2017 – 2019

SKILLS / CERTIFICATIONS

- **Programming:** Python, Html, CSS, SQL, mySQL, R, Rshiny, Excel, Dash, plotly
- **UX/UI:** HTML, Figma, CSS, Adobe (lightroom, Photoshop, InDesign)
- **Databases:** PDB, UniProt, Clustal Omega, SCOP, STRING, KEGG, GEO, GenBank
- Working experience with TCGA, protein, NCBI, Ensembl, EBI databases
- **Machine Learning:** K-means, K-Nearest Neighbor, Dimensionality reduction algorithm, PCAs
- Excellent communications and organizational skills across multiple fields.
- **Languages:** Fluent in English & Spanish; Elementary Japanese