Pablo Herrera Nieto

Researcher





(+34) 608 520 499



Profile summary

Five years of experience on basic research as data analyst focused on biological data. My professional goal is to apply precise and state-of-the-art data science approaches to real-world health problems.

Skills

Programming

python javascript R bash LATEX html, css sgl, mongodb

Software

numpy, pandas, matplotlib, scikit-learn tidyverse

Data analysis

clustering dimensionality reduction markov models

Operating systems

linux windows

Languages

spanish (native) english (advanced)

Experience

Universidad Autónoma de Madrid (Spain)

Postdoctoral Researcher | Supervisor: Ramón Díaz Uriarte

February 2021-Present

- Implemented simulations algorithms for cancer evolution.
- Supervised Master students.

Universitat Pompeu Fabra (Barcelona, Spain)

Data Analyst | PhD | Supervisor: Gianni de Fabritiis

June 2016-July 2020

- Authored 3 publications.
- Handled high-throughput computing resources.
- Built predictive models from time-series data sets using clustering, dimensionality reduction methods, and Markov state models.
- Assisted in the development of a novel reinforcement learning algorithm for conformational sampling of proteins.
- Studied complex biological processes related to intrinsically disordered proteins.

Janssen | Johnson & Johnson (Toledo, Spain) Junior Computational Chemistry Researcher

September 2015-May 2016

- Analyzed the structural role of water in GPCRs.
- Developed homology models.
- Completed virtual screening campaigns.

Universitat Autònoma de Barcelona (Spain) Master student

February 2015-September 2015

• Constructed homology models of GPCRs.

Education



Impact

Selected Publications

- Adrià Pérez, Pablo Herrera-Nieto, Stefan Doerr, and Gianni De Fabritiis. "AdaptiveBandit: A Multi-armed Bandit Framework for Adaptive Sampling in Molecular Simulations" Journal of Chemical Theory and Computation 16.7 (2020): 4685-4693.
- Pablo Herrera-Nieto, Adrià Pérez, and Gianni De Fabritiis. "Characterization of partially ordered states in the intrinsically disordered N-terminal domain of p53 using millisecond molecular dynamics simulations" Scientific reports (2020)