Héctor Climente González

Computational biologist & machine learning researcher

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ABOUT ME

"Learn only to be content" – Inscription in Ryōan-ji, Kyōto.

The driving forces of my life are learning and personal growth. I strongly believe in collaboration, in boosting research with engineering solutions, and in the power of machine learning to improve our understanding of nature. Leveraging my formal background in machine learning and biotechnology, I develop algorithms to study the causes of complex diseases.

SELECTED WORK EXPERIENCE

Postdoctoral researcher   MAY 2020 – NOW
RIKEN AIP

▸ Developed machine learning methods for biological problems, including graph-based and deep learning algorithms
▸ Applied the algorithms above to discover new drug targets of leukemia (RNA-seq data) and breast cancer (imaging data)

Doctoral researcher   OCT 2016 – APR 2020
Institut Curie & Mines ParisTech

▸ Developed machine learning methods that leverage prior biological knowledge to study the genetics of complex diseases
▸ Applied the algorithms above to GWAS, to find both single-SNP associations and epistasis
▸ Authored an R package *martini* published in Bioconductor, and two Python packages, *pyHSICLasso* and *spada* in PyPI

Research assistant   DEC 2013 – AUG 2016
Pompeu Fabra University

▸ Conducted a highly-cited study on the functional implications of alternative splicing in cancer

Head of Biocomputing   SEP 2014 – MAY 2015
Anaxomics Biotech Ltd.

▸ Coordinated the company's bioinformatics activities, including decision-making, supervising an intern, and collaboration with IT to maintain the database and the framework
▸ Developed and maintained pipelines for the statistical analysis of bulk RNA-seq, microarray, WGS and MS/MS data

EDUCATION

2016 – 2020	**Ph.D. in Bioinformatics** *Paris Sciences & Lettres Univ.*
2012 – 2014	**M.Sc. in Bioinformatics** GPA 9/10 *Pompeu Fabra University*
2010 – 2013	**B.Sc. in Biochemistry** GPA 8.74/10, 1st Class Honors *Barcelona Autonomous Univ.*
2008 – 2012	**B.Sc. in Biotechnology** GPA 8.58/10 *Barcelona Autonomous Univ.*

SELECTED PUBLICATIONS

Co-author of 13 articles, cited over 500 times.

Poignard *et al.* (2022). **Feature Screening with Kernel Knockoffs.** *AISTATS 2022*.

Climente-González *et al.* (2021). **Boosting GWAS using biological networks: a study on susceptibility to familial breast cancer.** *PLoS Comp Bio*, 17 (3).

Climente-González *et al.* (2019). **Block HSIC Lasso: model-free biomarker detection for ultra-high dimensional data.** *Bioinformatics*, 35 (15).

SELECTED AWARDS

2020	**Special Postdoc. Researcher** RIKEN
2016 – 2019	**PhD EU Fellowship** MSCA COFUND

LANGUAGES

SPANISH	Native
ENGLISH	Fluent
FRENCH	Intermediate
JAPANESE	Beginner

TECHNICAL SKILLS

PROGRAMMING	Python, R, C++, Bash
PYTHON	pytorch, numpy, pandas, scikit-learn
R	tidyverse, igraph, Rcpp
BIG DATA	nextflow, HPC (PBS Torque, Slurm), SQL, Jupyter
OMICS	GWAS, RNA-Seq (single cell and bulk), MS–MS proteomics
ML/STATISTICS	Graph regularization, statistical interactions, nonlinear association deep learning
DEVOPS	Docker, conda, unit testing, continuous integration, git

SOFT SKILLS

▸ Motivated **self-learner**: took 10+ courses on **mathematics** and **machine learning** on my own initiative and time

▸ Experienced **communicator**: talks in international conferences, lead writer of articles and grant proposals, workshop instructor on reproducible research

▸ **Project management** in teams and single-person projects, **mentoring**, and coordination of **international collaborations**

▸ **Organization** of summer school on breast cancer, **teaching** assistant in large scale machine learning course

▸ Courses on critical thinking, ethics, project management, theater, and mindfulness