Héctor Climente González
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 multidisciplinarity and collaboration and created synergies by combining engineering and basic research, biology and machine learning, academia and the private sector.

SELECTED WORK EXPERIENCE

Postdoctoral researcher
MAY 2020 – NOW
RIKEN AIP

▸ Development of feature selection methods for biological data, with emphasis on network regularization and interaction detection.

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

▸ Development of feature selection methods for high dimensional datasets, with emphasis on biological networks.
▸ Application of the aforementioned methods to biomarker discovery in GWAS datasets, both single-SNP and epistasis.
▸ R package *martini* published in Bioconductor, and Python packages *pyHSICLasso* and *spada* in PyPI.
▸ Conducted internships in Liège University and RIKEN AIP.

Research assistant
DEC 2013 – AUG 2016
Pompeu Fabra University

▸ Large-scale analysis of the involvement of alternative splicing in cancer.
▸ Integration of multi-omics data.

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

▸ Development and maintenance of pipelines for the statistical treatment of omics data.
▸ Supervision of intern, and collaboration with IT and Data analysis departments regarding database and software maintenance and product deployment.

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 10 articles, cited over 300 times.

Climente-González *et al.* (2020). **Boosting GWAS using biological networks: a study on susceptibility to familial breast cancer.** *PLoS Comp Bio* (in press)

Climente-González *et al.* (2019). **Block HSIC Lasso: model-free biomarker detection for ultra-high dimensional data.** *Bioinformatics*, 35 (15), i427–i435.

Climente-González *et al.* (2017). **The functional impact of alternative splicing in cancer.** *Cell reports*, 20 (9), 2215-2226.

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

▶ Experienced **communicator**: talks in international conferences, lead writer of articles and grant proposals, imparted workshops 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.