Héctor Climente González

Computational biologist & machine learning researcher



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 in creating synergies between engineering and basic research, biology and machine learning, academia and the private sector.

SELECTED WORK EXPERIENCE

Postdoctoral researcher

MAY 2020 - NOW

RIKEN AIP

- ▶ Developed machine learning methods for biological problems, including graph-based algorithms and deep learning
- 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 Paris Tech

- ▶ 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 10 articles, cited over 400 times.

Climente-González et al. (2020). 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), 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

оміся 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, workshop instructor on reproducible research
- ▶ **Project management** in teams and singleperson 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