

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 multidisciplinary 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

- Development of machine learning methods for biological problems, including graph-based algorithms and deep learning
- Application of the algorithms above to discover new drug targets of leukemia (transcriptome 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
- Application of the algorithms above to GWAS, to find both single-SNP associations 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 transcriptome analysis of the functional implications of alternative splicing in cancer

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 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
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