

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 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 (GWAS and transcriptome), with emphasis on biological networks and detection of interactions.

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 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.