

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 multidisciplinary and collaboration, and created synergies by combining engineering and basic research, biology and machine learning, academia and private sector.

SELECTED WORK EXPERIENCE

Postdoctoral researcher

MAY 2020 – NOW

RIKEN AIP

- Development of feature selection methods for ultra-high dimensional datasets, with emphasis on network regularization and interaction detection.

Doctoral researcher

OCT 2016 – APR 2020

Institut Curie & Mines ParisTech

- Development of feature selection methods for ultra-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 package *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.
- Statistical interaction detection using mutual exclusion.

Head of Biocomputing

SEP 2014 – MAY 2015

Anaxomics Biotech Ltd.

- Responsible for the development and maintenance of pipelines for the statistical treatment of omics data.
- Collaboration with IT and Data analysis departments regarding database, software and infrastructure 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). **Comparing and combining network methods to understand the genetics of familial breast cancer susceptibility** *BiorXiv*

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	networkx, 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, kernels, statistical interaction, nonlinear association, selection inference, 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 coordinating **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.