

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 7 articles, cited over 200 times.

Climente-González *et al.* (2019). **Combining network-guided GWAS to discover susceptibility mechanisms to breast cancer.** *In preparation.*

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 Postdoctoral Researchers Program**
RIKEN

2016 – 2019 **PhD EU Fellowship**
MSCA COFUND

LANGUAGES

SPANISH Native
ENGLISH Fluent
FRENCH Intermediate
JAPANESE Beginner

TECHNICAL SKILLS

PROGRAMMING	Python, R, C++/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, random forests consensus clustering
DEVOPS	Docker, conda, unit testing, git

SOFT SKILLS

- ▶ Experienced **communicator**: talks in international conferences, lead writer of articles and grants, imparted workshops on reproducible research.
- ▶ Proactive in seeking and coordinating **collaborations**.
- ▶ **Organization** of summer school on breast cancer, **teaching** assistant in large scale machine learning course.
- ▶ Courses on critical thinking, ethics, project management, and mindfulness.