

HECTOR CLIMENTE-GONZALEZ

+44 07542 973135 ◊ Oxford, United Kingdom

hclimente@gmail.com ◊ [linkedin.com/in/hclimente](https://www.linkedin.com/in/hclimente) ◊ hclimente.eu

ABOUT ME

Applied machine learning researcher with 10+ years of experience in biology.
Leveraging genetics, epigenetics and genomics to tackle open questions in human health.

EDUCATION

Ph.D. in Bioinformatics , Paris Sciences & Lettres University	2016 - 2020
Master in Bioinformatics , Pompeu Fabra University	2012 - 2014
Bachelor of Biochemistry , Autonomous University of Barcelona	2010 - 2013
Bachelor of Biotechnology , Autonomous University of Barcelona	2008 - 2012

SELECTED WORK EXPERIENCES

Senior Data Scientist Novo Nordisk	Mar 2023 - Now Oxford, United Kingdom
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↔ **Key skills:** Human genetics, Sequence learning, Pipeline development

1. Developing machine learning models for SNP interpretation, drug target discovery and disease risk prediction
2. Data mining large scale datasets (UK Biobank, GTEx, GWAS Catalog)

Special Postdoctoral Researcher RIKEN AIP	May 2020 - Feb 2023 Kyoto, Japan
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↔ **Key skills:** Deep learning, Nonlinear feature selection, Graph regularization

1. Developed novel deep learning architectures for DNA sequence learning and computer vision
2. Developed graph methods to study RNA-seq gene expression profiles in leukemia
3. Developed strategies for FDR-controlled feature selection

Ph.D. student Institut Curie & Mines ParisTech	Oct 2016 - Apr 2020 Paris, France
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↔ **Key skills:** Machine learning, Human genetics, Statistical interactions, Kernel methods

1. Developed machine learning methods that leverage graphs to study the genetics of complex diseases
2. Applied them to discover cancer and autoimmune genetic markers in GWAS (single-SNP and epistasis)
3. Authored three software packages: martini (R, in Bioconductor), and pyHSICLasso and spada (Python, in PyPI)

Previously: ↔ Head of Biocomputing at Anaxomics Ltd. ↔ Research assistant at Pompeu Fabra University	Jun 2013 - Aug 2016 Barcelona, Spain
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TECHNICAL SKILLS

Programming	Python (numpy, pandas, scikit-learn), Deep learning (PyTorch), R, nextflow, C++, Bash
Big data	Accelerated computing (CUDA, HPC), Cloud computing (Azure), Databases (SQL)
Omics	GWAS, Epigenetics (ATAC-seq), RNA-seq (single cell and bulk), MS-MS proteomics
DevOps	Virtual environments (Docker, conda), Testing, CI/CD, Open source, git

PROFESSIONAL SKILLS

Communication	Lead writer of articles and proposals Speaker in international conferences Conductor of tech workshops
Project management	Management of projects within and across teams Coordination of AI-driven research project with external partner (Microsoft)
Interpersonal skills	Active listener, interested in sharing knowledge Initiated study groups and conversations to improve our coding practices

SELECTED COURSES AND CERTIFICATIONS

As an avid self-learner, I took dozens of courses on mathematics, machine learning, formal logic, cloud computing, ethics, project management, theater, and mindfulness. Selected ones:

- MicroMaster in Statistics and Data Science [MITx, Ongoing]
- Deep Learning specialization [Coursera, 2022]
- Oxford Machine Learning Summer School [AI for Global Goals, 2021]
- Data Science Summer School [École Polytechnique, 2017]

LATEST PUBLICATIONS

I have co-authored 14 articles (6 of them as first author), which have been cited more than 900 times.

Singh, D., Climente-González, H., Petrovich M., Kawakami E., & Yamada, M. (2023). Fsnet: Feature selection network on high-dimensional biological data. International Joint Conference on Neural Networks (IJCNN), 1-9.

Climente-González, H., Azencott, C., & Yamada, M. (2023). Network-guided GWAS using stability selection. STAR Protocols, 17;4(1).

Poignard, B., Naylor, P. J., Climente-González, H., & Yamada, M. (2022). Feature screening with kernel knockoffs. International Conference on Artificial Intelligence and Statistics, 1935–1974.

Duroux, D.[†], Climente-González, H.[†], Azencott, C.-A., & Van Steen, K. (2022). Interpretable network-guided epistasis detection. GigaScience, 11, giab093.

[†] Equal contribution

Freidling, T., Poignard, B., Climente-González, H., & Yamada, M. (2021). Post-selection inference with HSIC-Lasso. International Conference on Machine Learning, 3439–3448.

Climente-González, H., Lonjou, C., Lesueur, F., GENESIS study group, Stoppa-Lyonnet, D., Andrieu, N., & Azencott, C.-A. (2021). Boosting GWAS using biological networks: A study on susceptibility to familial breast cancer. PLOS Computational Biology, 17(3), e1008819.

AWARDS AND RECOGNITIONS

2024 Our model's results got highlighted in Novo Nordisk's [Capital Markets Day](#)

2022 Joined the [AIME registry's](#) steering committee

2020 Competitive postdoctoral fellowship from RIKEN: Special Postdoctoral Researcher (SPDR)
3-year salary and a yearly budget of 1,000,000 Japanese yen

2018 Scholarship to carry out a Ph.D. summer internship at RIKEN AIP
3-month stipend and travel

2016 Competitive Ph.D. fellowship from the European Union: Marie Skłodowska-Curie Actions COFUND
3-year funding

2013 Master internship fellowship from the Research Programme on Biomedical Informatics
7,800 euros

2013 First class honors of the 2013 graduating class of the B.Sc. in Biochemistry