

HECTOR CLIMENTE-GONZALEZ

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ABOUT ME

Lead scientist with 12+ years of experience in computational biology & bioML

Leverages genetics, epigenetics and genomics to inform early target discovery and precision medicine

EDUCATION

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| 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

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| Novo Nordisk , Research & Early Development | London, United Kingdom |
| Lead Scientist | Nov 2024 - Now |
| <i>Promoted from Senior Scientist</i> | Mar 2023 - Nov 2024 |

↪ **Key skills:** Human genetics, AI/ML, Pipeline development, Real-world data

1. Develop, deploy and mine AI/ML models for SNP interpretation, early target discovery and precision medicine. Influenced decisions on target progression.
2. Developed the 2-year VP area strategy on AI/ML for genetics-based target discovery
3. Developed Nextflow pipelines for large-scale genetics analysis (e.g., colocalization, Mendelian randomization) following best nf-core practices. Massively decreased compute time and human effort for common workflows.

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| RIKEN , Center for AI Project | Kyoto, Japan |
| Special Postdoctoral Researcher | May 2020 - Feb 2023 |

↪ **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 using kernel knockoffs

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| Institut Curie & Mines ParisTech , Centre for Computational Biology | Paris, France |
| Ph.D. student | Oct 2016 - Apr 2020 |

↪ **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)

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

TECHNICAL SKILLS

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| Programming | Python (numpy, pandas, scikit-learn), Deep learning (PyTorch), nextflow (nf-core, nf-test), R |
| 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), MLOps (Azure ML, MLFlow), Testing, CI/CD, git |

PROFESSIONAL SKILLS

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| Communication | Lead writer of articles, project proposals & documentation Engaging speaker at global conferences & senior leadership briefings Proactive at seeking and disseminating best practices |
| Project management | Management of projects within and between teams, and across companies Experience with Scrum, including sprint planning, stand-ups and retrospectives |
| Interpersonal skills | Active listener, interested in sharing knowledge Onboarding and mentoring of junior colleagues |

SELECTED COURSES AND CERTIFICATIONS

As an avid self-learner, I took dozens of courses in 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 16 articles (7 of them as first author), which have been cited more than 1 000 times.

Zhu, T., Ghose, U., Climente-González, H., Howson, J.M.M., Hu, S. & Nevado Holgado, A (2025). Multimodal deep learning enhances genomic risk prediction for cardiometabolic diseases in UK Biobank. medRxiv.

Climente-González, H.[†], Oh, M.[†], Chajewska, U., Hosseini, R., Mukherjee, S., Gan, W., Traylor, M., Hu, S., Fatemifar, G., Del Villar, P.P., Vernet, E., Koelling, N., Du, L., Abraham, R., Li, C. & Howson, J.M.M (2025). Interpretable Machine Learning Leverages Proteomics to Improve Cardiovascular Disease Risk Prediction and Biomarker Identification. Accepted in Communications Medicine.

Hoffman, M., . . . , Climente-González, H., . . . , List, M. & Blumenthal, D.B. (2024) Network medicine-based epistasis detection in complex diseases: ready for quantum computing. Nucleic Acids Research 52 (17), 10144-10160.

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.

[†] Equal contribution

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