

ALEJANDRO M CARRASCO

I am a bioinformatician and deep learning enthusiast with a strong background in biotechnology and genetics

View this CV online with links at
<https://amcalejandro.github.io/cv/>



WORK EXPERIENCE

present
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2021

● GP2 Cohort Integration Working Group member

📍 Remote

- Working group¹ to collect and harmonise clinical data from of sporadic PD cohorts from all around the world
- My role was to help collecting sample manifest from contributors as well as to perform the clinical data harmonization
- I developed an app² deployed in Google Cloud Platform to ease the sample manifest as well as the clinical data collection process



EDUCATION

2024
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2021

● PhD. in Bioinformatics

University College London

📍 London, United Kingdom

- **Thesis:** Using genomics to understand Parkinson's disease progression
- Developed and applied multiple pipelines to understand the biological impact of variants nominated in genetic studies

2020
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2019

● MSc in Bioinformatics

University of Murcia

📍 Murcia, Spain

- **Thesis:** Use of community detection algorithms to create co-expression and co-occurrence networks
- Tested the proposed pipeline over transcriptomics and genomics data sets from AMP-PD project

2018
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2014

● BSc in Biotechnology

University of Murcia

📍 Murcia, Spain

- **Thesis:** Review on the key role of inflammation in diabetes' disease etiology
- **Internship:** Studying the role of peritoneal macrophages in endometriosis
- **Internship:** Measuring the anti-inflammatory and antitumour activity of different drugs obtained by chemical synthesis

CONTACT



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[Github](#)

[LinkedIn](#)

[Google Scholar](#)

LANGUAGES

Python

R

Bash

TECHNOLOGIES

Git/GitHub

nextflow

docker

SQL

Made with the R package
[pagedown](#).

The source code is available
[GitHub](#).

Last updated on 2024-01-04.



TEACHING EXPERIENCE

2022



Introduction to Nextflow and longgwas tool

Virtual event

📍 London, United Kingdom

- Developed the content and the presentation
- Lectured a group of GP2 Trainees on Nextflow fundamentals, how to use the main Nextflow elements, and introduced longgwas tool³

2022



Bioinformatic analyses in Terra platform

Universidad Nacional Autónoma de México

📍 Queretaro

- Developed content and served as teaching assistant for this two day workshop⁴
- We covered Terra platform basic concepts as well as how to perform several analyses using GP2 data
- I taught on longitudinal GWAS and performing a cognitive decline PRS from GP2 Latino population data



SELECTED PUBLICATIONS

2023



Genome-wide Analysis of Motor Progression in Parkinson Disease

Neurology Genetics

- **Alejandro Martínez-Carrasco**, Raquel Real, Michael Lawton, Regina Hertfelder Reynolds, Manuela Tan, Lesley Wu, Nigel Williams, Camille Carroll, Jean-Christophe Corvol, Michele Hu, Donald Grosset, John Hardy, Mina Ryten, Yoav Ben-Shlomo, Maryam Shoai, Huw R Morris
- **Role:** First author
- **DOI:** <https://doi.org/10.1212/NXG.000000000200092>

2023



Genetic meta-analysis of levodopa induced dyskinesia in Parkinson's disease

NPJ parkinson's disease

- **Alejandro Martinez-Carrasco**, Raquel Real, Michael Lawton, Hirotaka Iwaki, Manuela M. X. Tan, Lesley Wu, Nigel M. Williams, Camille Carroll, Michele T. M. Hu, Donald G. Grosset, John Hardy, Mina Ryten, Tom Foltynie, Yoav Ben-Shlomo, Maryam Shoai & Huw R. Morris
- **Role:** First author
- **DOI:** <https://doi.org/10.1038/s41531-023-00573-2>

2023



Association between the LRP1B and APOE loci and the development of Parkinson's disease dementiaris

Brain

- Raquel Real, **Alejandro Martinez-Carrasco**, Regina H Reynolds, Michael A Lawton, Manuela MX Tan, Maryam Shoai, Jean-Christophe Corvol, Mina Ryten, Catherine Bresner, Leon Hubbard, Alexis Brice, Suzanne Lesage, Johann Faouzi, Alexis Elbaz, Fanny Artaud, Nigel Williams, Michele TM Hu, Yoav Ben-Shlomo, Donald G Grosset, John Hardy, Huw R Morris
- **Role:** Data analyst
- **DOI:** <https://doi.org/10.1093/brain/awac414>