Pablo Acera Mateos, PhD

Github: https://github.com/pabloacera
https://orcid.org/0000-0002-7599-6039
• E-mail: pabloacera91@gmail.com

Personal Statement

Computational biologist with 9+ years of experience applying deep learning, probability, and statistical models to RNA biology, genomics, and drug discovery. My expertise spans both academic and industry settings, where I have developed bioinformatics infrastructure, led machine learning projects, and collaborated across multidisciplinary teams. Passionate about algorithm development and therapeutic innovations, I aim to bridge computational methods with biological insights to drive breakthroughs in patient care.

Technical Skills

Bioinformatics & Computational Biology

- 8+ years of experience analyzing genomics data with focus on RNA-seq and Nanopore sequencing data.
- Built bioinformatics pipelines for differential expression, splicing, and RNA modifications from scratch in HPC environments.
- Expertise in transcriptome assembly, gene expression analysis for next and third generation sequencing technologies.
- Experience with protein structure prediction, molecular modeling and variant effect predition.
- 9+ years of experience with Python, Bash, SQL – Proficient in bioinformatics and data science pipelines.
- Experienced in HPC (SLURM, GPU-accelerated computing) and built Built scalable bioinformatics workflows using Docker & Snakemake.
- Optimized deep learning models for high-performance computing environments.

Machine Learning & AI

- 7+ years experience working and designing architecture with Deep learning frameworks: TensorFlow, PyTorch, Scikit-learn. Experience using and fine-tunning LLMs using LoRa.
- Designed and deployed end-to-end deep learning pipelines and created models from scratch for genomics, from concept to production.
- Built predictive models integrating statistical analysis and probabilistic programming for RNA-sequencing and splicing.
- Time-series and signal processing analysis for high-throughput sequencing (HTS) data with Nanopore Sequencing.
- Developed methods for dimensionality reduction and batch effect correction in genomics.

Drug Discovery and leadership

- Developed AI-driven ranking algorithms for **RNA** therapeutic target selection.
- Specialized in RNA splicing modulation & therapeutic target identification.
- Conference speaker at ISMB, London Calling Nanopore, ABACBS.
- Mentored & supervised 5+ graduate students (Master's, PhD, and Honours).
- Grant writing & funding acquisition, securing multiple research grants as a Principal Investigator.

Education and Work Experience

- **Postdoctoral researcher - Conjoint Lecturer, Computational Drug Discovery, Children's Cancer Institute.** 2022 -present.
  - **Main Supervisor:** Antoine de Weck
  - **Role:** I develop advanced statistical and machine learning methods using transcriptomics and protein structure data, to enhance the drug discovery process. My main focus is around developing new small molecule compounds that target mRNAs. My work also includes predicting and prioritizing genes for targeted intervention with RNA splicing modulators.

  - During my posdoc I had a commercial agreement with drug discovery company "Minimum Bio" were I was in charge of building the entire bioinformatics infrastructure of the company, involving the processing of Nanopore high throughput sequencing (HTS) data, statistical analysis of time series HTS data, RNA transcriptome assembly and peptide 3D structure prediction.

- **PhD. Bioinformatics. Australian National University.** 2019 - 2022.
  - **Main Supervisor:** Eduardo Eyras.
  - **Panel members:** Cheng Soon On, Benjamin Schwessinger and Nikolay Shirokikh.
  - **PhD thesis:** "Development of deep learning models for detection of RNA modifications using nanopore sequencing".
  - **Summary:** During my PhD, I developed a deep learning model that predicts RNA modifications at single-nucleotide and molecule resolution using RNA direct Nanopore sequencing. We also thoroughly benchmark our tool against other algorithms and apply it to several in-vitro, cell lines and mouse tissue sequencing datasets. My PhD work led to a first author publication in Nature Communications (https://doi.org/10.1038/s41467-024-47953-7).

- **Software developer - European Bioinformatics Institute, Cambridge.** March 2018 - March 2019.
  - **Supervisor:** Paul Flicek and Andy Yates.
  - **Project:** Development and implementation of capture Hi-C tools.
    - **Role**: While at EMBL-EBI, I worked at the Multi-Scale Complex Genomics (MuG) project. I developed and implemented algorithms to analyse capture-HiC datasets and integrate them into the Barcelona Supercomputer Center (BSC) HPC platform.

- **Bioinformatics Master's Degree with Erasmus + scholarship. Lund University and Utrecht University.** September 2016 - April 2018.
  - **Professor:** Jeroen de Ridder, Sara L. Pulit.
  - **Final project:** "Analyzing genome variation data using a 3D genome atlas".
  - **Summary:** In this project, we investigated the effects of single nucleotide polymorphisms (SNPs) epistasis and SNPs cumulative effects in the 3D genome on complex traits.

- **University of Seville. Biology Bachelor Degree.** 2009 - 2013.
  - **Professor:** Maria Tortolero
  - **Final bachelor project:** "Human microbiome in health and disease".

Awards and Grants

- **Anthony Rothe Memorial Trust:** Associate investigator, contributor to the idea and the written application 200,000$.

- **Future makers** grant from the Children's Cancer Institue. "Utilising splicing modulator-induced poison exons as a therapy for high-risk AML" Awarding 40,000$.

- **Principal investigator Bootes Foundation Grants award**. Principal investigator. "Dissecting the role of RNA modifications in onco-ribosomes to inform new anti-cancer therapies". Awarding 12.000$.

- **Provisional patent**: "A Computational Algorithm for Identifying chemical Modifications in nucleic acid Molecules". application number 2022900373.

- **National Computing infrastructure (NCI's) NCMAS.** merit grants. 2 years with 2M computing hours valued in ~$190k USD.

- **Innovation Research Projects Grant from Lumminesce alliance** (associated investigator) $125,000 ,$250,000 and $125,000 for 3 years.

- **“SBBq AWARD” for the best poster. 23rd International Congress of the International Union of Biochemistry and Molecular Biology (IUBMB). 2015. Parana, Brazil.**

- **The Cure starts now travel and accomodation grant** for the Brain Cancer symposium trip and seminar in Banff Canada 2025.

Work presented at conferences

- **Brain Cancer Symposium.** Invited speaker for the cure fund grant compatition, The Cure Start Now foundation.

- **Children’s Cancer Symposium. 2023.** CRYPTICO: Computational Discovery of Targetable Cryptic Exons for mRNA Modulation Therapy.

- **Intelligent Systems for Molecular Biology (ISMB) - 2021 - Oral presentation.** "Detection of RNA modifications at a single-molecule level using a two-stage deep learning model with Nanopore sequencing".

- **Australian Bioinformatics And Computational Biology Society (ABACBS).**
  - **2021** - "Detection of m6A and m5C RNA modifications at single-molecule resolution using Nanopore sequencing" Oral presentation.
  - **2020** - "PACIFIC: A lightweight deep-learning classifier of SARS-CoV-2 and co-infecting RNA viruses" Poster presentation.
  - **2019** - "Comprehensive identification of nucleotide biochemical modifications from nanopore signal data" Poster presentation.

- **London Calling Nanopore.**
  - **2021** - "Detection of m6A and m5C RNA modifications at single-molecule resolution using Nanopore sequencing". Poster presentation.
  - **2022** - RNA methylation detection at single-molecule resolution uncovers isoform-specific modifications during mouse brain development. Oral presentation.

- **Lorne 2022. Talk.** "Detection of m6A and m5C RNA modifications at single-molecule resolution using Nanopore sequencing".

Scientific Papers

- **P. Acera Mateos et al.** 2024. Prediction of m6A and m5C at single-molecule resolution reveals a transcriptome-wide co-occurrence of RNA modifications. *Nature Communications*. https://doi.org/10.1038/s41467-024-47953-7.

- **Pablo Acera Mateos et al.** 2023. Concepts and methods for transcriptome-wide prediction of chemical messenger RNA modifications with Machine Learning. *Briefings in Bioinformatics*.

- **Pablo Acera Mateos et al.** 2021. PACIFIC: a lightweight deep-learning classifier of SARS-CoV-2 and co-infecting RNA viruses. *Scientific reports*.

- A.J. Sethi, **PA Mateos**, R Hayashi, N Shirokikh, E Eyras. 2024. R2Dtool: Positional interpretation of RNA-centric information in the context of transcriptomic and genomic features. *Bioinformatics*.

- A. Sneddon, **P. A. Mateos**, N Shirokikh, E Eyras 2022. Language-Informed Basecalling Architecture for Nanopore Direct RNA Sequencing. *Machine Learning in Computational Biology*.

- Brown, L.M., Tax, G., **Acera Mateos, P.** et al. 2025. A novel TRKB-activating internal tandem duplication characterizes a new mechanism of receptor tyrosine kinase activation. npj Precis. Onc. 9, 137.

- Jonatas Erick Maimoni Campanella, Sergio Luiz Ramos Junior, Vanessa Thomaz Rodrigues Kiraly, Antoniel Augusto Severo Gomes, Andrea Coelho de Barros, **Pablo Acera Mateos**, Fernanda Zanolli Freitas, Marcos Roberto de Mattos Fontes, Júlio Cesar Borges, Maria Célia Bertolini 2021. Biochemical and biophysical characterization of the RVB-1/RVB-2 protein complex, the RuvBL/RVB homologues in Neurospora crassa. *Biochimie*.

Voluntary work and supervision

- Supervision of Master student Ryosuke Suzuki, PhD student Oyelami Favour and Bachelor student Lisi Chen, Honours student Ricky Nguyen.
- Representative higher degree by research (HDR) students for the Genome and Cancer department. John Curtin School of Medical Research (JCSMR), ANU.
- Organizer of JCSMR HDR seminars.
- Organizer of John Curtin School of Medical Research Social hour.
- I got interviewed by the University New South Wales Bioinformatic society, featured in their magazine https://unswbinfsoc.com/binfsights/binfsights24/.
- Organizer of the Children's Cancer Institute seminars. Coordinate seminars with over hundred people weekly.