



# Pablo Garcia-Nieto

Product Manager  
Computational Biologist

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## Profile

Computational biologist with +7 years of experience in omics research. Product manager with 3 years of experience delivering products for access and analysis of large-scale single-cell data. I can effectively lead teams to identify high value research workflows and drive the delivery of products that accelerate them.

## Education

2009	<b>National University of Mexico</b>
—	B.Sc. in genomics.
2013	
2015	<b>Stanford University</b>
—	Ph.D. in molecular and computational
2020	biology.

## Key Skills

### Comp bio

- Strong statistics
- Python, R & shell
- AWS
- Git
- Single-cell analysis
- Multi-assay genomic analysis
- Genetics toolkits (BCFtools, etc)
- ML for bio (sklearn and PyTorch)

### PM

- Agile and waterfall
- Value-based prioritization
- Risk management
- Product launches
- Market analysis
- Leading cross-functional teams

## Employment

### Chan Zuckerberg Initiative

2020	<b>Computational Biologist</b>
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2022	Developed and prototyped algorithms for processing and analysis of single-cell data. Collaborated with engineers to bring the methods to production for 1000+ datasets (cellxgene.cziscience.com).
2022	<b>Product Manager</b>
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2024	Defined, developed, and launched single-cell software products for computational biologists. Led a team of engineers and UXR to deliver a service to access and analyze the largest repository of single-cell data. Implemented AI-based integration of data.

## Research highlights

For all publications see [pablo-gar.github.io](https://pablo-gar.github.io)

### Landscape of human somatic mutations

Developed computational methods to identify and analyze somatic mutations for 10,000+ samples from 500+ people.

Garcia-Nieto et al. Genome Biology, 2019.

### Carcinogen susceptibility in humans

Developed a sequencing technology to understand how DNA damage accumulates in the genome.

Garcia-Nieto PE et. al. EMBO J. 2017