

Pablo González de la Rosa

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Professional Summary

Analytical bioinformatician with over 10 years of experience in Python, R, and data visualization, specializing in genomic data analysis and pipeline development. Passionate about Generative AI, actively leveraging tools like Gemini AI to build innovative solutions such as Notion Explorer for self-discovery. Proven ability to create practical tools, including a Shiny R app used by colleagues, and a vision for AI's role in empowering entrepreneurs and creatives. Eager to contribute to Epoch AI's mission of understanding AI's trajectory through data-driven insights and collaborative research.

Projects

Notion Explorer: GenAI-Powered Self-Discovery Tool | April 14, 2025 – Present

- Designed and built a tool to analyze Notion notes using Gemini AI, targeting entrepreneurs, creatives, and lifelong learners to identify authentic values through systematic questioning.
- Developed a modular system with Python (CLI, FastAPI backend), React (GUI), and Gemini AI integration, including metadata fetching and question sets for analysis.
- Rapidly prototyped the project in one evening using Windsurf, showcasing agility in delivering AI-driven solutions.
- Early-stage project with potential to provide actionable insights for personal growth; currently iterating on core features like analysis depth and user interface.
- https://github.com/pgonzale60/Notion_explorer

Shiny R App for Genomic Visualization (vis_ALG) | April 14, 2025 – Present

- Built a Shiny R app in under 2 hours to visualize genomic data, enabling colleagues to rapidly distinguish the ancestral composition of nematode genomes.
- App usage persisted among team members, with network data showing consistent activity from other users over 3 months (Jan 24 – Apr 16, 2025).
- https://github.com/pgonzale60/vis_ALG

Education

PhD in Evolutionary Biology

University of Cambridge and Sanger Institute | January 2020 – September 2023

Thesis: *Chromosome evolution in Rhabditina (Nematoda) with a focus on programmed DNA elimination.*

- Discovered programmed DNA elimination in free living nematodes through long read sequencing.
- Identified conserved sequence motif at DNA break point in multiple free living nematodes.
- Assembled (long reads plus hi-c), decontaminated and annotated over 14 free living nematode genomes.
- Cultured nematodes and extracted long DNA for PacBio sequencing and RNA for Illumina RNA-seq.

Studies in Evolutionary Biology

University of Edinburgh, UK | January 2019 – December 2019

- Investigated chromosome evolution in Rhabditina nematodes.
- Assembled and annotated the monarch butterfly genome.

Master's in Integrative Biology

LANGEBIO-Cinvestav, Mexico | February 2016 – December 2018

Thesis: *Genes involved in host specificity of the monarch butterfly.*

- Differential expression of RNA-seq of monarch butterfly caterpillars fed on different hosts.
- Relative quantification of microRNAs through small RNA-seq.

Undergraduate Program in Genomic Sciences

Center for Genomic Sciences, UNAM, Mexico | August 2011 – August 2015

Thesis: *Estimating the true number of microRNA functional targets.*

- Automatised microarray differential expression analyses to identify the total number of targets of the most studied microRNAs.

Professional Experience

Bioinformatician

Oxford Nanopore Technologies, Oxford, UK | November 2023 – Present

- Developed Nextflow pipelines for genomic variant detection, processing large-scale datasets with Python and Rust.
- Created visualizations using matplotlib and Plotly to share insights with stakeholders, enhancing team understanding of complex data.
- Collaborated remotely with teams via Slack and Gitlab, ensuring reproducible workflows through version control.

Bioinformatics Intern

Winter Genomics, Mexico | August 2013 – November 2015

- Performed statistical analysis on microarray data using R, identifying genomic variants for research purposes.
- Developed a MySQL database with a web interface for genomic variants.

Skills

- **Programming & Tools:** Python (pandas, NumPy, matplotlib, Seaborn, FastAPI), R (tidyverse, Shiny), Rust, Bash, SQL, Nextflow, Git, Jupyter Notebooks, React
- **Data Analysis:** Statistical testing, data visualization, pipeline development
- **AI Familiarity:** GenAI tools (Gemini AI, LLMs, diffusion models), model integration
- **Cloud & Workflow:** AWS, containers, CI/CD, agile methodologies
- **Soft Skills:** Remote collaboration, communication, teamwork, adaptability
- **Languages:** Spanish (Native), English (Fluent), German (A2), Mandarin (A1)

Publications

Gonzalez de la Rosa, P., Stevens, L., Tracey, L., Kieninger, M., Moll, R., Launay, C., Wenger, E., Félix, M. A., Delattre, M. & Blaxter, M.. (Manuscript in preparation). Evolution of programmed DNA elimination in free-living *Oscheius* nematodes.

Gonzalez de la Rosa, P., Strand, L. G., Kieninger, M., Collins, J., Johansen, M., Villeneuve, A., Chan, B., Adams, S., Pires-daSilva, A. & Blaxter, M. (Manuscript in preparation). The germline genome of the nematode *Auanema rhodense* is edited to generate a much smaller somatic genome. (Manuscript in preparation).

Stevens, L., Kieninger, M., Chan, B., Wood, J. M., **Gonzalez de la Rosa, P.**, Allen, J., & Blaxter, M. (2024). The genome of *Litomosoides sigmodontis* illuminates the origins of Y chromosomes in filarial nematodes. *PLoS Genetics*, 20(1), e1011116.

Stevens, L., Kieninger, M., Chan, B., Wood, J. M., **Gonzalez de la Rosa, P.**, Allen, J., & Blaxter, M. (2024). The genome of *Litomosoides sigmodontis* illuminates the origins of Y chromosomes in filarial nematodes. *PLoS Genetics*, 20(1), e1011116.

Stevens, L., Martínez-Ugalde, I., King, E., Wagah, M., Absolon, D., Bancroft, R., **Gonzalez de la Rosa, P.**, ... & Blaxter, M. (2023). Ancient diversity in host-parasite interaction genes in a model parasitic nematode. *Nature Communications*, 14(1), 7776.

Ranz, J.M., Go, A.C., **González, P.M.**, Clifton, B.D., Gomes, S., Jaberyzadeh, A., Woodbury, A., Chan, C., Gandasetiawan, K.A., Jayasekera, S. & Gaudreau, C. (2023). Gene expression differentiation in the reproductive tissues of *Drosophila willistoni* subspecies and their hybrids. *Molecular Ecology*, 32(13), 3605-3623.

Villalobos-Escobedo, J. M., Martínez-Hernández, J. P., Pelagio-Flores, R., **González-De la Rosa, P. M.**, Carreras-Villaseñor, N., Abreu-Goodger, C., & Herrera-Estrella, A. H. (2022). *Trichoderma atroviride* hyphal regeneration and conidiation depend on cell-signaling processes regulated by a microRNA-like RNA. *Microbial Genomics*, 8(10), 000869.

Ranz, J. M., **González, P. M.**, Su, R. N., Bedford, S. J., Abreu-Goodger, C., & Markow, T. (2022). Multiscale analysis of the randomization limits of the chromosomal gene Organisation between Lepidoptera and Diptera. *Proceedings of the Royal Society B*, 289(1967), 20212183.

Ranz, J. M., **González, P. M.**, Clifton, B. D., Nazario-Yepiz, N. O., Hernández-Cervantes, P. L., Palma-Martínez, M. J., ... & Abreu-Goodger, C. (2021). A de novo transcriptional atlas in *Danaus plexippus* reveals variability in dosage compensation across tissues. *Communications biology*, 4(1), 1-13.

Gonzalez de la Rosa, P. M., Thomson, M., Trivedi, U., Tracey, A., Tandonnet, S., & Blaxter, M. (2021). A telomere-to-telomere assembly of *Oscheius tipulae* and the evolution of rhabditid nematode chromosomes. *G3*, 11(1), jkaa020.

Gonzalez-De-la-Rosa, P. M., Loustalot-Laclette, M. R., Abreu-Goodger, C., & Markow, T. A. (2020). Differential gene expression reflects larval development and survival of monarch butterflies on different milkweed hosts. *bioRxiv*.

De-La-Cruz-Montoya, A. H., Ramírez-Salazar, E. G., Martínez-Aguilar, M. M., **González-de-la-Rosa, P. M.**, Quiterio, M., Abreu-Goodger, C., ... & Velázquez-Cruz, R. (2018). Identification of miR-708-5p in peripheral blood monocytes: Potential marker for postmenopausal osteoporosis in Mexican-Mestizo population. *Experimental Biology and Medicine*, 243(13), 1027-1036.