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# María José Martínez

## Martínez

### Biologist - Bioinformatician

Biologist specialized in bioinformatics and biodiversity. My **goal** is to use my knowledge about **\*omic data analysis** and **AI** in evolutionary and biosystems research.

I graduated in Biology at Universidad Autónoma de Madrid (UAM), where I also did a Master's degree in Biodiversity. My biological educational background is in **identification of taxa** by combining molecular, morphological and ecological data. I carried out my Bachelor's and previous Master's Thesis about annelid taxonomy in the Marine Biology and Invertebrates Laboratory of the UAM. I also did an internship in the Nematology Laboratory of the National Museum of Natural Sciences (MNCN), identifying nematode species by **molecular techniques** (especially microsatellites). I also volunteered in the **Histology Laboratory** of the MNCN to learn complete processing of animal tissue (polyclads), including fixation, paraffin embedding, sectioning with microtome and cryotome, and routine staining.

I am currently enrolled in the Computational Biology Master's at Universidad Politécnica de Madrid (UPM), where I am learning different advanced methods and software tools for **data analytics** (dplyr, tidyr, ggplot2), **genomic analysis** (Samtools, Bowtie2, Bcftools, BWA, FASTQC, igv, Seurat), **lead discovery** (Chimera), **genomic assisted breeding** (rrBLUP, lme4), **evolutionary biology** (RDP, BEAST) and **machine learning** (scikit-learn) and biological systems modelling.

My particular interest in Single cell sequencing technologies and the origin and evolution of cell types led me to do my curricular internship and Master's Thesis in the department of Systems Biology at the CNB-CSIC with PhD Mónica Chagoyen and PhD Juan Poyatos. I analyse **single-cell RNAseq data** from human and model organisms and compile functional and morphological characteristics of cell types from **Cell Ontology** (obonet, ontologyX, SPARQLWrapper) with the aim of studying cell type evolution by clustering the data using **hierarchical unsupervised learning models**. I apply **dimensional reduction techniques** (UMAP, t-SNE, PCA, NMF) to analyse genes and functional systems specific to cell classes with common features. With this detailed information, I am also reviewing the concept of housekeeping gene. I am working in **R** and in a **Linux environment**, but I am also skilled in **Python** and **SQL**.

I enjoy **networking** and fostering good relationships with my colleagues. A keen personal interest in foreign cultures drives me to have a high level of **English (CAE)** and a basic one in German and French.

