Ana Delia Ramos Guerra

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**Overview**

Biotechnologist holding a Master of Computational Biology with interest in clinical and pharmaceutical bioinformatics. My major concern is the use of computational techniques for diagnosis and treatment improvement as well as drug development.

Biotechnologist holding a Master of Computational Biology from the Technical University of Madrid (UPM) with interest in clinical and pharmaceutical bioinformatics. As a self-starting professional, I work well independently but also collaboratively in a team setting. I am additionally creative and with a natural interest in learning, solving problems and helping. Carried out experimental work in the Aquaculture Research Group (GIA) of the University of Las Palmas de Gran Canaria (ULPGC), where participated in genetic sampling for SNPs analysis (group leader: Juan Manuel Afonso López). Also worked as structural biologist in the research group of molecular basis of allergenicity of plant food allergy (group leader: Araceli Díaz Perales) that belongs to the Centre for Plant Biotechnology and Genomics (CBGP). This involved the use of computational methods to study protein-ligand interactions in plant food allergens. Just working in the Biomedical Image Technologies’ research group of the UPM Higher Technical School of Engineers in Telecommunication (ETSIT) -group leader: Andrés Santos Lleó- for collecting and analyzing oncology-related molecular data in search of predictive biomarkers for immunotherapy.

Fluent in English and Spanish (native language) and with basic knowledge of German. Having a good grounding in Molecular Biology, acquired Python, Pearl, Ruby, SQL, R, MATLAB and Visual Basic programming languages and knowledge in machine learning methods through MLlib (PySpark), R and WEKA, in addition of Windows and Linux OS, Microsoft Office and LibreOffice. With basic experience in mathematical modeling for Computational Biology through MATLAB, also skilled at usage of bioinformatics programs such as structural biology software (Chimera, PyMol, VMD/NAMD), evolution bioinformatic tools (Mega, Beast, Beauti, Traces, BaTS, ClustalX, HyPhy, Mesquite, Spread. Path-O-Gen, PhyML, RDP) and genomics software (i.e. Samtools, Bowtie, HTSeq, SPAdes). With capabilities in creation and management of databases by MySQL, through workbench or driver for Python, and Resilient Distributed Datasets (RDDs), through the PySpark API of Spark, as well as Jupyter Notebook and GitHub handler.