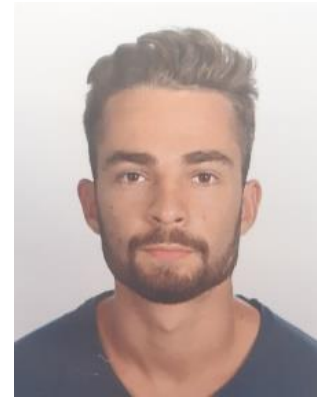

ALEJANDRO MELONES DELGADO

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Biologist graduate specialised in Computational Biology and Bioinformatics highly interested in the development of bioinformatic tools for protein structure prediction



PROFESSIONAL PROFILE

I am a Biology Graduate from Universidad Autónoma de Madrid, currently studying a Master's Degree in Computational Biology at the Universidad Politécnica de Madrid. In my last year of degree, I developed by Bachelor Thesis at the Centro de Biología Molecular Severo Ochoa (CBMSO-CSIC) on the "Study of the molecules involved in the adhesion between ovarian cancer cells and mesothelial cells", which gave me the possibility of knowing and learn some of the most used experimental techniques in the biology research field. During my Bachelor's Degree I spent one year abroad as an ERASMUS student at the University of Durham in England.

Some of the subjects I coursed during Bachelor introduced me some of the techniques and the databases used by professionals in computational biology nowadays. Therefore, I decided to change the course of my career and accept a new challenge to discover all the techniques and mechanisms underlying the bioinformatics area.

I consider myself an involved and proactive person that likes to learn new things and has no fear to accept new and complex challenges that take me to my limits as they will eventually help me to improve my professional skills.

While I have been enrolled in the Master course, I have been able to learn about machine learning and drug discovery techniques, or the analysis of genomic data. Moreover, it has enabled me to learn and fluently manage several programming languages such as python, R or Ruby. During my Master internship I have done a course in Biostatistics that have taught me the best and most important techniques for the validation and analysis of future results. Nowadays, I am doing my Master Thesis in the Department of Scientific Informatics at the Centro Nacional de Biotecnología (CNB-CSIC), supervised by Dr. José Ramón Valverde Carrillo, where I am using several algorithms for protein structure prediction.

I would like to develop my professional career in the field of protein structure prediction in the development of new and powerful tools that would, eventually assist biomedical studies such as drug discovery, ligand screening or protein function annotation.