Universitat Pompeu Fabra Barcelona

Master in Bioinformatics for Health Sciences

Master project 2024-2025

Personal Information

Supervisor	Víctor Guallar
Email	victor.guallar@bsc.es
Institution	Barcelona Supercomputing Center
Website	https://www.bsc.es/es/discover-bsc/organisation/scientific-structure/electronic-and-atomic-protein-modeling-eapm
Group	Electronic and Atomic Protein Modelling

Project

Structural bioinformatics

Project Title:

Development of an ML-based predictor of antigen processing and presentation for vaccine design

Keywords:

Immunology, Immunoinformatics, Machine Learning, Vaccine, Structural Biology

Summary:

Background: T-cells are crucial actors in the human immune response to cancer and infection. Computational immunology has studied extensively the proteins and pathways that enable T-cell reactivity and the activation of the subsequent immune response. These include predictors of antigen processing as the proteasome and cathepsin cleavage, antigen transport via TAP, specially HLA-I binding and most recently T-cell immunogenicity and TCRpHLA pairing. Such methods have been implemented to guide vaccine design and biomarker discovery projects. Project Summary: The immunoinformatics research line of the group includes method development using AI techniques and implementation to real vaccine development projects. In this project you will be given the choice to get involved in the different immunology projects of the lab with the goal develop an ML-based predictor to complement our immunoinformatics pipeline. The range of topics to choose from include: - developing a TAP predictor; a crucial protein for HLA-I peptide transport quite unexplored bioinformatically, - contributing to an updated version of NOAH; the structural HLA-I binding predictor of the lab and to include recent MHC crystals and AlphaFold models. - contributing to HLA-II immunogenicity prediction tools, a gap in the immunoinformatics field of relevance for vaccine design. - exploring the most challenging problem in immunoinformatics by contributing to the TCRpHLA pairing prediction. Learning outcomes and methods involved in the project: • Learn about AI and develop an ML-based immunoinformatic method to contribute to the lab's research line in computational immunology. • Usage of immunoinformatic state-of-the-art methods: MHC Binding, Immunogenicity, Antigen processing methods) to learn about bioinformatic vaccine design. • Learn structural bioinformatics by using AlphaFold 2.3 Multimer and other methods available at BSC. • Usage of the HPC facilities of the Barcelona Supercomputing Center (Marenostrum 5)

References:

Amengual-Rigo, P. & Guallar, V. NetCleave: an open-source algorithm for predicting C-terminal antigen processing for MHC-I and MHC-II. Scientific Reports 2021 11:1 11, 1–8 (2021). Aguilar-Gurrieri, C. et al. NOAH: High immunogenic VLP-based vaccines elicit new T cell specificities against melanoma neoantigens in mice. J Immunother Cancer 9, (2021). Carrillo, Guallar et al. Immunization with V987H-stabilized Spike glycoprotein protects K18-hACE2 and golden Syrian hamster upon SARS-CoV-2 infection. Nature Communications (2023) Farriol-Duran, R., Vallejo-Vallés, M., Amengual-Rigo, P., Floor, M. & Guallar, V. NetCleave: An Open-Source Algorithm for Predicting C-Terminal Antigen Processing for MHC-I and MHC-II. Methods in Molecular Biology - in Computational Vaccine Design (2023) Farriol-Duran, R. et al. PredIG: an interpretable ML-based predictor of CD8+ T-cell (neo)epitope immunogenicity [unpublished] Farriol-Duran, R. et al. iTMB: an immunogenicity TMB biomarker for immune checkpoint inhibitor response [UCL – unpublished] VRSVAC: Misiones hRSV Vaccine Project – Hipra, Nostrum Biodiscovery & Spanish Government LWWNVIVAT: Limiting West Nile Virus impact by novel vaccines and therapeutics approaches – HORIZON-HLTH-2023-DISEASE-03

Expected skills:

Basic programming skills (R and/or Python, Bash, Git ...). Basic immunology is preferable but can be gained during the project.

Possibility of funding:

Yes

Possible continuity with PhD:

To be discussed

Comments:

Application note: Please, to enquire for this position send us an email (in english) briefly introducing yourself and include an updated CV and a motivation letter. If you have them, include reference letters from previous research experience. Motivation for research and eagerness to learn will be valued the most. If interested in the topic, the group may have PhD positions coming up in the future (to be discussed). Hybrid work model possible. Profile of the candidate: Interested in vaccine design, structural bioinformatics and computational immunology. Motivation for the project, eagerness to learn and proof of independence to develop their own will be highly valued. Basic programming skills are expected (R, Python, Bash...) but basic background in immunology can be gained during the project. The student’s profile characteristics are preferable but not necessarily mandatory to apply. Research context and lab environment: Our group on Electronic and Atomic Protein Modelling led by Prof Víctor Guallar, at the Life Sciences Department of the Barcelona Supercomputing Center, is a multidisciplinary laboratory that applies protein modelling to various research lines in enzyme engineering, protein design, AI and immunoinformatics. This latter has experienced an important boost in the recent years with the participation in vaccine development projects such as LNWIVAT (European Project to develop a vaccine against West Nile Virus) and VRSVAC (National Project in collaboration with HIPRA to develop a vaccine against Human Respiratory Syncytial Virus). In these projects we lead the bioinformatic design of the immunogen molecules that are tested for vaccination. In addition, we have recently published a list of immunoinformatic methods in collaboration with experimental and pharmaceutical partners. As for lab environment, our group is now formed by more than 20 people well balanced between post-docs, PhDs, technicians and master students. Our day to day in the lab is social and everyone is helpful with each other.