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Abstract

Immunoinformatics is the branch of bioinformatics that studies the immune system. As a field, its gaining traction thanks to the rise of immunotherapies and the steadily increasing wealth of immunological data. In the context of cancer, immune cells are able to recognize tumors and fight them all across the body. Hence, the interest in reinvigorating the immune system via cancer immunotherapies. However, the response rate remains at 20-40%, which is remarkable in late-stage cancers (main patient group targeted) but still low. The only response biomarker for cancer immunotherapies is a high number of mutations or Tumor Mutational Burden High (TMB-H). During my placement at Tumour Immunogenomics and Immunesurveilance group (UCL Cancer Institute), we to refine using our immunoinformatic models (NetCleave, NOAH and PredIG) and a large patient dataset (UCL-CPI3000+) In addition, UCL Cancer Institute is devoted to early cancer detection and immunotherapy sensitization fields to improve response rates to cancer treatment. In this line, I have contributed to cancer detection with antibody predictions (Brewpitopes) and to immunotherapy sensitization with transcriptomic and proteomics analyses.



Roc Farriol-Duran is a 3rd-year Ph.D. affiliated both at Electronic and Atomic Protein Modelling and Cancer Immunogenomics groups. His background includes a BSc in Biomedical Sciences at UAB and MSc degrees in Translational Biomedical Research (Vall d'Hebron-UAB) and Omics Data Analysis (Universitat de Vic). During this period, he performed wet-lab internships in immunology and proteomics at UAB, Leiden University Medical Center and Vall d'Hebron Institute of Oncology. His main research interest is immunoinformatics and its applications to infectious disease and cancer. The latter has guided the 6 months placement at the UCL Cancer Institute, London.

Speakers

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Host: Victor Guallar, ELECTRONIC AND ATOMIC PROTEIN MODELLING GROUP MANAGER, Life Sciences, BSC.

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Source URL (retrieved on *30 Dic 2024 - 18:33***):** https://www.bsc.es/es/research-and-development/research-seminars/sors-our-immunoinformatics-guide-cancer-detection-biomarker-discovery-and-sensitization