Mass spectrometry based identification of neoantigens for development of personalized cancer immunotherapy

Open PhD position in bioinformatics –

A PhD position is availablel at the Immunopeptidomics Unit headed by Dr. Michal Bassani-Sternberg at the Oncology Department of the University Hospital of Lausanne (CHUV/UNIL). The Immunopeptidomics Unit is incorporated into the Hi-TIDe (human integrated tumor immunology discovery engine) translational research group led by Prof. George Coukos. The unit is affiliated to the Center of Experimental Therapeutics (CHUV) and to the Ludwig Cancer Research Institute. In addition,

The unit has close collaboration with the Swiss Institute of Bioinformatics (SIB), specifically with Markus Muller, expert in mass spectrometry related bioinformatics, who will be directly involved in the supervision of the PhD candidate.

The Immunopeptidomics Unit implements advanced experimental and computational mass-spectrometry based antigen discovery workflows to support development of personalized cancer immunotherapy. We are involved in first-in-man phase I clinical trials where we are responsible for identifying neoantigens individually from tumor samples, which are further used to identify tumor neoantigen-specific T cells for adoptive T cell therapies. In collaboration with the Vital-IT group at the SIB, we have established a continuous proteo-genomics bioinformatic pipeline enabling direct identification of neoantigens by combining genomic information derived from RNA-seq and exome-seq with measured immunopeptidomics mass spectrometry data. In addition, we pursue fundamental discovery work to elucidate how tumour cells present antigens, and what are the molecular bases of tumour immunogenicity.

We are looking for a highly motivated researcher with strong background in bioinformatics, statistics and programming. The candidate should have excellent skills in one or several programming languages such as Java, Python, or C/C++ and statistical scripting languages such as R. He/she must have experience in high level statistics and must be motivated to use advanced statistical methods. The project will produce large volumes of heterogeneous data (immunopeptidomics, proteomics, transcriptomics and genomics) from cancer models in mice, which need to be organized and made retrievable and accessible for the queries of lab biologists. Furthermore, statistical models will have to be developed in order to improve the prediction of immunogenic peptides, which is of great importance for cancer immunotherapy.

We are looking for a self-motivated, interactive and flexible researcher, who likes to work in the diverse and challenging field of cancer immunotherapy on a broad range of subjects such as databases, visualization, and statistical modelling. The project will take place in close collaboration with a wet lab scientist and will require good communication skills. The researcher will be embedded in an interdisciplinary team consisting of biologists, mass spectrometry experts and bioinformaticians, who will provide guidance and supervision.

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