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Statistical learning approaches to modelling T cell response at the molecular level

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The immune response to an infection and to cancer is based on the 'recognition'of small portions of pathogen or cancer-related proteins (antigens) by cells of the immune system, for instance T cells. The specific binding of T-cell receptors (surface proteins of T cells) to antigens is the key step leading to effective immune responses. Identifying antigens that can be recognized by T cells, as well as antigen-specific T-cell receptors, is therefore crucial to vaccine and cancer immunotherapy design. In this talk, I will discuss a set of flexible and easily interpretable models that we have recently developed based on the machine learning scheme of Restricted Boltzmann Machines (RBM) and that are learnt from large protein sequence datasets. Such scheme allowed us first to build models of the process of antigen presentation to the immune system, which can be used to reconstruct the underlying molecular motifs and as predictors of viral and cancer antigens. I will next introduce RBM-based models of the complementary process of recognition by T cells of presented antigens, which are able to discriminate responses specific to different antigens and to detect signatures of response at the T-cell repertoire level.

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