Abstract

Acute lymphoblastic leukaemia (ALL) is the most frequent childhood malignancy. One of the recent improvements in ALL treatment was the introduction of minimal residual disease (MRD) monitoring that enables risk stratification based treatment adaptation. The same MRD monitoring helps to choose relapse treatment, to guide indication for stem cell transplantation (SCT) and allows for a more personalized management of patients undergoing SCT. One of the main routes of MRD levels detection is characterisation of leukemic blasts using flow cytometry.

However, flow cytometry is limited by its mainly manual expertise-based analysis. Such analysis is subjective and clearly insufficient for current complex data. While new computational tools are available for multidimensional flow cytometry data, there is an urgent need to test and adapt them for the use in clinical environment.

The goal of this thesis is to detect immunophenotypes associated with leukaemia and their development by leveraging machine-assisted analysis of a set of diagnostic files selected based on information about more than three hundred thousand of multiparameter flow cytometry datasets. Advanced bioinformatic tools will help to detect blast and healthy haematopoietic populations, to derive their immunophenotypes and to identify individual CD marker contributions. Resulting leukemic immunophenotypes will be compared to the clinically reported immunophenotypes.

Keywords: Acute lymphoblastic leukaemia, immunophenotype, flow cytometry, bioinformatics