

Flow cytometry is a method for measuring chemical characteristics of single cells in a solution, with applications in biological and clinical research. Recent advances in the technology of flow cytometers make it exceedingly easy to produce larger datasets that describe more interesting phenomena, which creates new challenges for data processing and analysis software. This thesis describes and implements a proof-of-concept software that simplifies the data processing by implementing an interactive analysis pipeline editor designed to efficiently handle huge datasets. The functionality of the software is demonstrated by implementing a recent data analysis algorithm, and by comparing the resource efficiency to a typical R analysis tool. Future use of the software by biologists and medics is facilitated by providing a simple interface for including new algorithms, thus arbitrarily extending the functionality.