

## Infinicyt 2.0 NGF (next generation flow):

In the field of chemistry, medicine and biology, biomedical devices are making increasingly complex measurements on a greater number of heterogeneous parameters. Multicolor flow cytometry (>10 parameters) has been used routinely in research and clinical laboratories for more than a decade and is not an exception to this trend of “Big Data” generation, management and analysis in biotechnology. Current flow cytometry technology generates much more information than ever from an increasing number of individual particles in a single assay; this allows, for example, for the detection of rare events with a sensitivity and a precision never reached before in the so-called NGF (Next Generation Flow), but at the same time, the amount and complexity of the data generated makes its analysis a tremendous challenge.

The methods traditionally used to solve this problem involve carrying out numerous manual steps for each population to be identified, such as selecting, debugging, sorting and reclassifying data, which drastically increases the number of steps depending on the number of parameters analyzed. In a n-parameter analysis we would have to analyze  $(n * (n-1) / 2)$  individual two-dimensional diagrams in which we can see the representation of all combinations of two parameters. In the great majority of cases, the user does not manually analyze all the populations present in the sample, but only takes into account the population that considers of interest, avoiding pieces of information that could be relevant, especially in diagnosis, prognosis or disease monitoring. In addition, the user performing the manual analysis must be skilled in the analysis technique to obtain reliable and reproducible results by another user. Even so, the analysis are not always totally objective, with the risks and inaccuracies that this implies.

Infinicyt 2.0 software incorporates mathematical algorithms for clustering of high dimensional data and a unique classification tool where groups of events are reclassified into cell populations according to a reference database. This classification is only possible when following rules previously established by flow cytometry experts.

The results is a true standardized and reproducible analysis methodology able to be applied in different places by different people without compromising the accuracy of the results in a clinical environment.

For this reason, the process of automatic clustering and classification of multidimensional information will change the paradigm of the flow cytometry data analysis and will play an important role in the clinical setting in the upcoming years. The combination of standardized sample processing protocols, reproducible reagents and automatic software tools will make flow cytometry a most robust, fast and reproducible technic which will increase its broad applicability.