ESOM Sampling as a Tool for Detection of Needles in the Haystack of Big Data in Medical Diagnostic Technologies

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In particular, within the context of molecular medical research data sets become larger and larger. High data volumes obtained with flow cytometric analyses of blood and tissue samples with real time multiparameter measurements were always a challenge for computer hard and software designers. Today, a regular Flow Cytometry \cite{1} data set for one single patient typically contains $d$ ($10 < d < 100$) variables for $n > 1,000,000$ single blood cells (counts) \cite{2}. A training period of many years is therefore prerequisite for biologists or physicians who perform the clinical data interpretation. It is, however, clear, that diagnostic structures in these files may be captured by an appropriate sampling procedure. In this work, we compare the advantages and disadvantages for three different sampling strategies producing a dataset consisting of $n_s < 5,000$ as a subset of the $n$ original data: simple random \cite{3}, Learning Vector Quantization (LVQ) \cite{4} and a novel proposal based on emergent self-organizing feature maps (ESOM) \cite{5}. For a short overview on sampling strategies, see \cite{3}. The approach is tested on different artificial and experimental datasets. Moreover, we validate our method by performing automated diagnosis of lymphomas employing diagnostic files from original flow cytometric patient lymphoma samples \cite{6}.

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References


