

This work focuses on finite mixture models and aims to introduce the maximum likelihood method as an approach of fitting finite mixtures. For that purpose the EM algorithm is adopted and derived in detail. Both the E and M steps of the EM algorithm are presented and performed for general finite mixture model. We derive new estimates for some of parameters defining the model. All updated estimates of the iteration of the EM algorithm are derived explicitly for the specific family of normal mixtures. The described theory is then applied to a model of the production of cytokine interleukin 10 in human periodontitis attack, which clearly demonstrates an application of the model in practice. Finally, we discuss the theory of clustering, which is based on our previous results. Like the previous theory, this one is also illustrated in the aforementioned model of cytokine IL10 production.