

Abstract No: utku520

Data Analysis by Clustering for the IR Microspectroscopy

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Beamline(s): U10B

The principal function of clustering is to reveal the protein structures in an infected tissue, and to display so that the influences or causes in arriving a pathogenic state might be predicted. The IR data is reduced to a relatively compact description through cluster analysis by which an IR image of protein secondary structure can be generated. Figure 1 illustrates the basic operations performed in the cluster algorithm utilized by the developed software. Result of the cluster analysis can contribute directly to classification schemes. If the grouping suggested by the cluster analysis is to be adopted for operational use, then it may become the basis for classifying new observations. The developed software provides Linear Discriminant Analysis (LDA) option to perform classification based on the output of the cluster analysis. Since the cluster analysis is an unsupervised method, LDA as being supervised method serves as a computational checklist to provide a degree of confidence for the whole analysis.

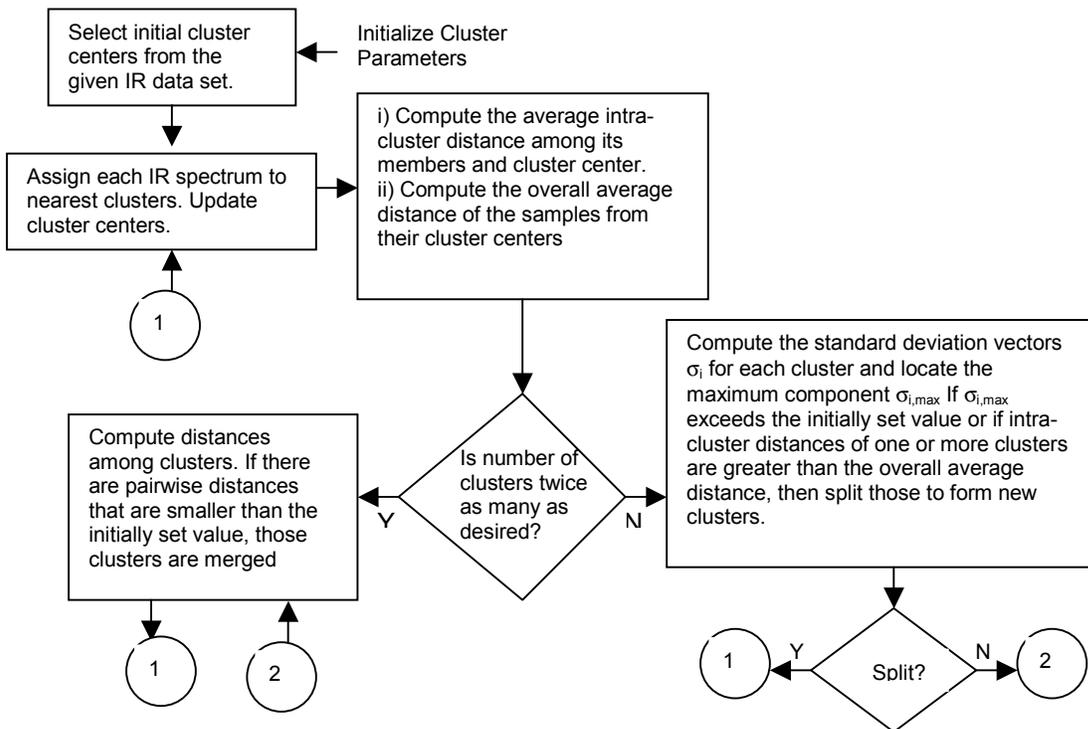


Figure 1. Basic operations performed in ISODAT cluster algorithm.