

## Evaluation of segments reliability by means of cluster validity algorithms

Goal: This document illustrates the misuse of cluster analysis techniques due to the lack of cluster validity algorithms to evaluate the cluster analysis results. Note that the example presented here shows the drawbacks of the numerical strategy used to compute the segments but not about the theory behind the segments.

### Material and Methods

The data consisted on 4 grand means obtained from more than 10 healthy subjects recorded during 4 different conditions. Standard artifact rejection and/or electrode interpolation and filtering was used to create this data.

The segments were computed using the algorithm proposed in IEEE Trans Biomed Eng. 1995; 42:658-665 available also in CarTool, corresponding to a suboptimal solution of the cluster problem and thus, a solution that by construction, will hardly achieve an optimal partition of the data.

To evaluate the quality of the cluster provided by the algorithm we used the silhouette algorithm from the MATLAB statistics toolbox. The results are plotted using notched box plots.

### Results

Using the method referred in previous section we obtained the 9 clusters depicted in Figure 1.

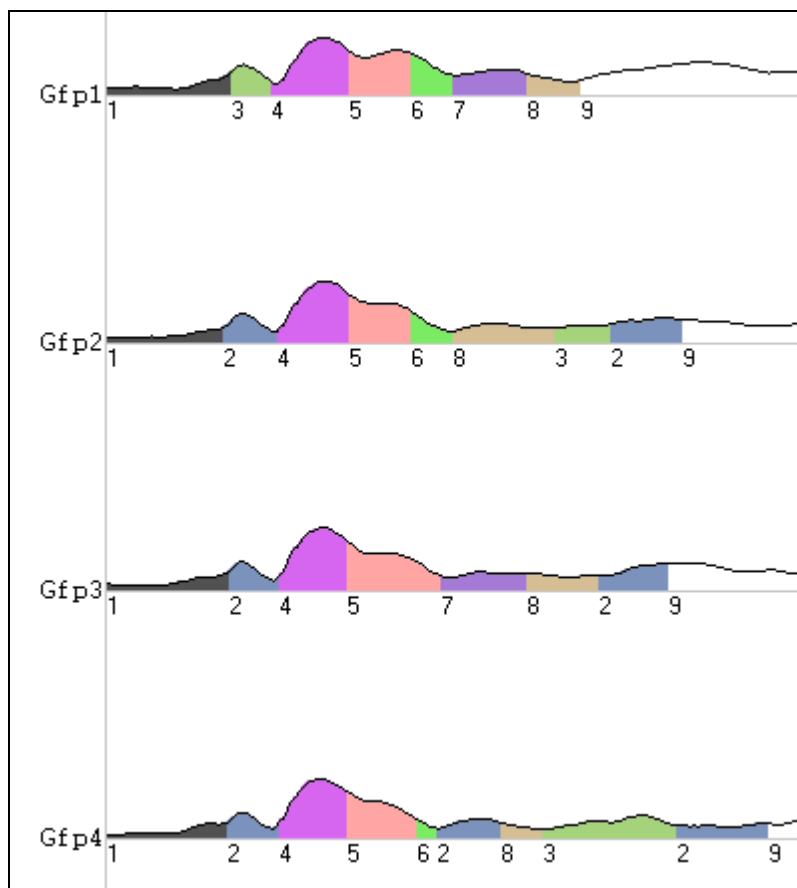
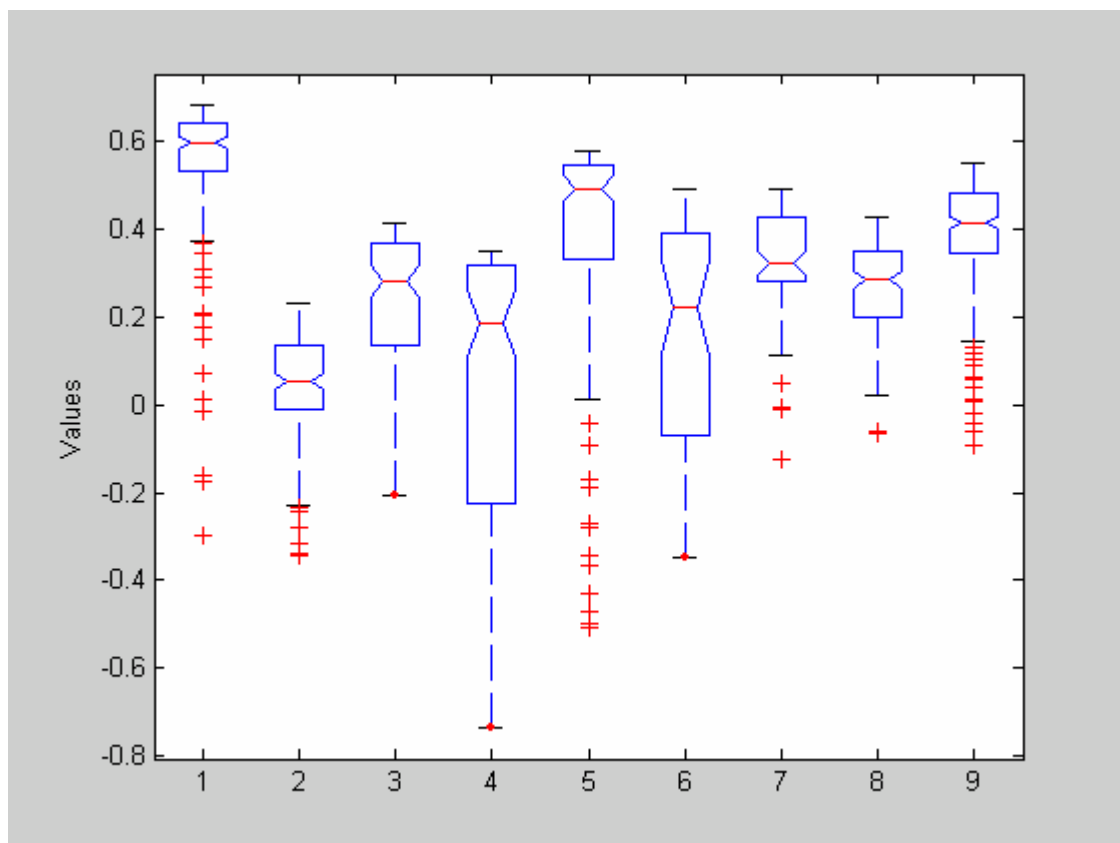


Figure 1. Segmentation results plotted on the global field power of each condition.

Condition 1 skips from segment 1 to segment 3 while Conditions 2, 3 and 4, change from segment 1 to segment 2.

To start analyzing the cluster results we compute for each map the silhouette value indicating the quality of the classification that assign one map to one particular segment. Values close to one indicate that the map has been correctly classified on that segment. Values about zero indicates that the map can be equally classified on any other segment. Values near  $-1$  suggest that the maps is clearly misclassified and that it better belongs to another segment. The average value for all the maps in one segment argues about the quality of the whole segment.

Figure 2, presents the silhouette results computed for all the maps of each segment. Each number in the horizontal axis denotes a segment. The vertical box plot represents the distribution of silhouette values in each segment. The middle line of the box represents the median and the notches allow for a direct paired comparison between group medians.



It results clear from figure 2 that clusters 2 and 4 and 6 contain maps (values near zero) that can be classified in any other segment as well as maps (negatives values) that are clearly misclassified. Then, conclusions about the generators, or the brain process based on those segments, are hardly acceptable. On that basis we encourage you to test the quality of your cluster before any posterior analysis. In fact we have never found a data set where all the maps have clearly positive ( $>0.25$ ) silhouette values. This is probably due to the following two facts: 1) The absence of a background segment, i.e., all the maps have to belong to one of the segments and 2) The suboptimal properties of the algorithm. Obviously, the ultimate solution, will be

the use of a different (non suboptimal !) algorithm that can “certify” the results together with the inclusion of background segment gathering all the “bad maps”.

As stated before this type of analysis, very well known by the statistical community, evaluates the algorithm used to obtain the clusters and not the particular hypothesis about the structure in the data. In other words, this analysis evaluates the quality of the results of the suboptimal K-means method used to obtain the segments and should not be interpreted as an evidence against the microstates theory itself.