Modification of replication analysis for cluster validation

Formally, replicating clusters proceeds as follows (see Breckenridge [2000], 262-263; Milligan [1996], 368-369; Gordon [1999], 184; Walesiak [2008]):

- 1. The data are randomly divided into two samples: sample A (arbitrarily primary) and sample B (replication). Data must exist on the same set of variables in both samples.
- 2. Sample A is clustered (via kmeans, pam or any hierarchical agglomerative method: single, complete, average, mcquitty, median, centroid, Ward) into u clusters $A = \{A_1, \ldots, A_u\}$. Decisions regarding variable normalization, distance measure, and selection of the number of clusters are to be completed. Once clusters have been identified, the centroids of u clusters are computed (for metric data) or u representative objects (often called centrotypes or medoids) are selected (for metric or nonmetric data).
- 3. Sample *B* is clustered, using the same clustering procedure, into *u* clusters $B = \{B_1, ..., B_u\}$.
- - 5. Repeat steps 1-4 S times (S the number of simulations).
- 6. Compute a measure of agreement (mean corrected Rand index see Hubert and Arabie [1985]) between two clusterings B and B^* for S simulations. The level of agreement between the two partitions reflects the stability of the clustering in the data.

References

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