

Chapter 1 : CiteSeerX " Citation Query Graph Theoretic Techniques for Cluster Analysis Algorithms

cation of the graph theoretic outlook on multiagent systems is in the context of graph processes, where the network topology itself is given a dynamic role that lends itself to analysis via system theoretic methods (Chapter 12).

Show Context Citation Context We briefly review the approaches that are most related to our work. Definitions and terminology will be given in Section 2. This paper presents a generic method for perceptual grouping, and an analysis of its expected grouping quality. The grouping method is fairly general: The proposed method is divided into two parts: The first stage includes a cue enhancement procedure, which integrates the information available from multi-feature cues into very reliable bi-feature cues. The accompanying theoretical analysis of this grouping criterion quantifies intuitive expectations and predicts that the expected grouping quality increases with cue reliability. It also shows that investing more computational effort in the grouping algorithm leads to better grouping results. This analysis, which quantifies the grouping power of the Maximum Likelihood criterion, is independent of the grouping domain. To our best knowledge, such an analysis of a grouping process is given here for the first time. Three grouping algorithms, in three different domains, are synthesized as instances of the generic method, They demonstrate the applicability and generality of this grouping method. The perceptual information is represented by graphs, in which the vertices are the observed data elements edges, pixels, etc. In other work, 2 e. The grouping task is divided into two parts: For instance, the corrupted clique-graph model and the cluster affinity search technique CAST proposed by Ben-Dor and Yakhini 94 were successf In a typical content-based image retrieval CBIR system, query results are a set of images sorted by feature similarities with respect to the query. However, images with high feature similarities to the query may be very di erent from the query in terms of semantics. This discrepancy between low-le This discrepancy between low-level features and high-level concepts is known as the semantic gap. This paper introduces a novel image retrieval scheme, CLUster-based rEtrieval of images by unsupervised learning CLUE , which attempts to tackle the semantic gap problem based on a hypothesis that images of the same semantics are similar in a way, images of di erent semantics are di erent in their own ways. CLUE attempts to capture semantic concepts by learning the way that images of the same semantics are similar and retrieving image clusters instead of a set of ordered images. Clustering in CLUE is dynamic. In particular, clusters formed depend on which images are retrieved in response to the query. Therefore, the clusters give the algorithm as well as the users semantic relevant clues as to where to navigate. CLUE is a general approach that can be combined with any real-valued symmetric similarity measure metric or nonmetric. Thus it may be embedded in many current CBIR systems. An experimental image retrieval system using CLUE has been implemented. Empirical results demonstrate improved performance compared with a typical CBIR system using the same image similarity measure. One possible future direction is to integrate CLUE with keyword-based image retrieval approaches. CLUE may be combined with nonlinear dimensionality reduction techniques, such as the methods in [33] and [45], to provide a global visualizatio We have developed a novel algorithm for cluster analysis that is based on graph theoretic techniques. A similarity graph is defined and clusters in that graph correspond to highly connected subgraphs. A polynomial algorithm to compute them efficiently is presented. Our algorithm produces a clusterin Our algorithm produces a clustering with some provably good properties. The application that motivated this study was gene expression analysis, where a collection of cDNAs must be clustered based on their oligonucleotide fingerprints. The algorithm has been tested intensively on simulated libraries and was shown to outperform extant methods. It demonstrated robustness to high noise levels. In a blind test on real cDNA fingerprint data the algorithm obtained very good results. For a critique of these approaches see [16]. Both of these algorithms lack our important stopping criterion, with the ensuing provable results on the clustering quality. In particular these algorithms do not guarantee