Chapter 1

Introduction

'A journey of a thousand miles begins with a single step.'

Confucius

The automatic recognition of images is an objective which is difficult to achieve. This issue has been analyzed and tackled in many different ways. Moreover, the automatic recognition of images is regarded as a complex field within the pattern recognition domain, as many questions such as the way of representing the knowledge and the way of adapting the knowledge representation to the changes in the images are essential for successful result and have to be analyzed with care.

Graph representations are widely used for dealing with structural information in different domains such as networks, psycho-sociology, image interpretation, pattern recognition, and many others. In a typical graph representation, regions of the image are represented by vertices in the graph. These vertices are related to each other by edges, which express structural relationships between objects. Vertices and edges are usually attributed.

One important problem to be solved when using such representations is graph matching, for instance to recognize image regions with the help of a model. The problem consists in searching for the best homomorphism between two graphs: the one that represents the model –the model graph[1]– and the other that represents the image –the data graph. The best graph homomorphism is determined regarding both the attributes of vertices and edges.

In order to achieve a good correspondence between the model and the data graphs, the most usual way is to search for a graph isomorphism. A lot of work is dedicated to the search for an exact isomorphism between two graphs or subgraphs. However, in many cases the bijective condition is too strong. Because of the schematic aspect of the model and of the difficulty to segment accurately the image into meaningful entities, no isomorphism can usually be expected between both graphs. Such problems call for inexact graph matching.

This type of problem occurs in different model-based image recognition domains. For instance, in the case of the recognition of brain images, the model (i.e. the anatomic atlas) is usually build as a representation of the regions that appear in a healthy human brain, and the data images are obtained using Magnetic Resonance images (MRi) of patients. In other application types such as cartography, the model is constructed from maps of the region of study, while the data images are obtained from aerial or satellite photographs. A last application to which this type of abstraction is applied is the recognition of facial features.

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[1] The model is sometimes also called *atlas* or *map* depending on the type of problem. Some authors in the literature also use the term *pattern graph* to refer to the model graph.

As the number of features in the image increases, the size of graphs increases too, and the matching process becomes more complex. This has been proved to be NP-hard. As a result, many different techniques have been applied to perform the matching between graphs, and among them we can find the use of relaxation techniques, the EM algorithm, combinatorial optimization techniques, etc.

This thesis proposes to solve this optimization problem using a class of evolutionary computation techniques called Estimation of Distribution Algorithms (EDAs), which are based on learning and simulation of probabilistic graphical models (i.e. Bayesian or Gaussian networks). The main drawback of other evolutionary computation techniques, such as Genetic Algorithms (GAs) in the discrete domain and Evolutionary Strategies (ESs) in the continuous domain, is that their behavior depends to a large extent on tuning appropriately associated parameters, and for this purpose the researcher requires experience in the resolution and use of these algorithms. EDAs do not have that many parameters and can be applied easily to complex problems. Furthermore, EDAs have already shown a better performance than GAs in many problems, specially in complex ones, but their use in graph matching has not been proposed previously. In addition, this thesis proposes the definition of a new type of attributes for creating the model and data graphs as well as related fitness functions, which are based on probability theory. Moreover, the parallelization of EDAs in the discrete domain is designed and tested in order to reduce the CPU cost of the most promising methods. Finally, two real problems are described and tested: the recognition of human brain structures and of facial features from images. The latter application has been developed in collaboration with Roberto Cesar from the University of São Paulo in Brazil.

This thesis is organized as follows. This introductory chapter summarizes the context, the motivation, and the main contributions of this PhD thesis. Chapter 2 explains the graph matching problem and its different types as found in the literature. Chapter 3 proposes to solve these problems as combinatorial optimization ones with constraints, and analyzes the modifications and adaptations that are required in any evolutionary computation technique when applied to graph matching problems. Chapter 4 explains the theoretical background behind the evolutionary computation approach of estimation of distribution algorithms for both the discrete and continuous domains. Chapter 5 reviews all the aspects that need to be considered for parallelizing EDAs in order to reduce the computation time that these require, and constitutes an overview of the main aspects that need to be taken into account for applying up-to-date parallelization techniques. Chapters 6 and 7 describe the experiments carried out with synthetic data and real problems respectively, and the performance and behavior of the different algorithms and the results obtained are presented. Finally, Chapter 8 presents the conclusions of this PhD thesis.