Chapter 6

Conclusions

We proposed a parallel and fuzzy computer-aided diagnosis system to test if a subject takes disorders or not instead of an absolute diagnosis result. The whole method consists of feature selection, feature extraction and classification. Initially, a voxel-based morphometric analysis is performed to find the anatomical discrepancy between normal and abnormal groups where is considered as better feature for classification. Also, a customized template is obtained from the VBM analysis to construct a standard space for classification. Secondly, a principal component analysis is applied to find a proper representation for data without loss and two principal component selection methods, variance-based PC selection and significant-based PC selection, are then used to select more useful characteristics as features for classification. Thirdly, a probabilistic classification approach is implemented with Bayes' Theorem and the Parzen-window approach. Thus, two classifiers with different PC selection are established for a particular disease. Finally, the whole system is constructed by combining several classification models of the corresponding specific illness. A test subject will know how many possibilities he or she has of sicken with disorders.

According to the points of views addressed as follows, we decided to construct a classification system by using a probabilistic approach. First, a probabilistic classifier provides a test with a probability which reveals different degrees of being abnormal rather than discovers an absolute boundary to classify a test into a known group definitely. The higher the posterior probability is, the more similar to the specific group the unknown sample is. Secondly, due to the density-based approach, the probabilistic approach is more suitable and more intuitive to solve multi-class problems than the geometric approach is. Usually, geometric approaches are used in the two-category classification. Besides, in geometric methods, it is hard to use an analytic expression to represent the absolute boundary in a high dimensional classification space. Therefore, the dimensionality reduction must be done and may lead to data loss. Thus, we decide to construct a probabilistic classifier and estimate the density distribution of known groups to calculate posterior probabilities of an unknown sample in each known group in our work.

Here, we give some comparisons between the proposed evaluation system and some other geometric CAD systems mentioned in section 1.3. The most apparent characteristic of the proposed evaluation system is to provide a test sample with a fuzzy result instead of a definite result, yes or no. Moreover, only MR images of test subjects are analyzed in the evaluation system and GM/WM/CSF images segmented from original MR images are all used to construct individual classifiers. We put equal emphasis on various tissues and merge their results to have a final outcome. Furthermore, we classify two groups in a high dimensional space where is considered as a good classification space instead of only one dimensional space. Finally, we use an estimated density function to anticipate the probability of a sample to be in a specific category rather than find an absolute boundary to divide between groups.

Regarding comparisons between variance-based PC selection and significant-based PC selection, our experiments showed that a classifier with the latter method achieves a better and consistent performance than one with the former method. It conforms to our expectation because the method of significant-based PC selection takes account of the relation of different groups by applying a two sample *t*-test analysis on data projected into principal components. Moreover, data of two different groups may be mixed with each other after projected on principal component with the largest variance so that it is hard to separate. In short, it is recommended using the significant-based PC selection to construct a good classification space.

Yet, there are some flaws in our proposed system. Despite the difference in age, our classifier can examine people of all ages although the classifier was trained by using a study group with age in a specific range. Because of the limitation in the amount of training data, we were not able to construct different classifiers for different age groups. Fortunately, our experiment results showed that our classifier still can achieve good performance for all age groups. Thus, it might not be necessary to differentiate age groups when constructing classifiers.

Our evaluation system is a so-called VBM-based CAD system because features for classification depend on results of a voxel-based morphometric analysis. Therefore, the limitation of VBM would postpone to our proposed system. First, construct customized templates with Taiwanese templates instead of using ICBM152 template. Taiwanese templates are more similar with ours subjects and will lead to fewer normalization errors to have an accurate registration. Moreover, the improvement in segmentation and normalization may lead to an unbiased result. For example, all extracted partitions from BET2 will be segmented into one of GM, WM and CSF tissues. If some non-brain tissues are left, they will also be classified into one of them and cause incorrect segmentation and normalization. Furthermore, the significant level might influence the regions which are considered as good features for post-processings. In our experiments, we found that the significant level which is neither too strict nor too loose is a good choice to retain enough and suitable data information. In addition, it is much easier for the voxel-based morphometric approach to detect relatively localized differences than to discover relatively distributed differences involved with many brain structures because VBM analyzes the group discrepancy in a voxel-by-voxel manner. Thus, ROIs from VBM results may not contain the widely-distributed discrepancy located in a large area. In short, an unbiased voxel-based morphometric analysis may result in a robust classification system.

For a particular disease, there is a corresponding classification model which only distinguishes between the normal group and the disease group. We just give thought to the relation between normal and abnormal groups without thinking about the relation between distinct disease groups. Thus, it could happen that a subject is diagnosed to have more than one disorder though he or she has only one in reality. A fundamental solution to this problem is to consider multicategory at a time. Subjects of all diverse groups are projected into a common space and the density function of each group can be estimated with some estimation techniques. Therefore, it is easy to compute posterior probabilities of a test sample to be in each group. Besides, a classification model which classifies two similar

diseases can be built up by using our technological procedure and provides an index sign for physicians to assist them in diagnosing subjects.

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