Application of Machine Learning in Computer Vision and Cancer Bioinformatics

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Abstract. This article focuses on some of the problems of machine learning in computer vision and cancer bioinformatics. Separately, in computer vision, this paper adopts the method based on machine learning to study the face recognition, natural environment image classification, Static Image Behavior Recognition Algorithm; in the bioinformatics, questions relating to the classification of subtypes and stages of breast cancer are explored.

Keywords: Machine Learning, Computer Vision, Cancer Bioinformatics

1. Introduction

Computer Vision Technology is a hot and difficult problem in many research fields nowadays. It is the focus and goal that human beings devote themselves to the research of computer vision technology. In the real world, however, this task is not easy. Bioinformatics is an interdisciplinary subject between computer science and biology, and the use of machine learning and other computer technologies to solve cancer related problems is a hot research area. Computer Vision is a secondary discipline in computer science, and cancer bioinformatics is a secondary discipline in the bioinformatics[1]. These two research contents because the research object is not quite same, therefore will have certain span. Computer Vision deals with image data, whereas cancer bioinformatics deals with genetic data, so the emphasis of the machine learning approach will vary, however, both of them have common in classifier learning and feature representation. So this paper chooses computer vision and cancer bioinformatics as the main research contents, and takes machine learning method as the main line to establish the internal relationship between the two main research contents.

2. Static image behavior recognition algorithm based on non-sequential convolution neural network model

In this chapter, we focus on the research of robust human behavior recognition model based on static image, which can avoid the tedious work of Feature Engineering, explicit body posture estimation and reasoning, and part-based representation. Therefore, this chapter presents a new non sequential
convolutional neural network model, NCNN, to automatically analyze body posture and sense the surrounding environment[2]. It can avoid the trivial tasks such as manual feature design, modeling based on body part, representation based on gesture and behavior.

![Figure 1. Sample images on Li Action database](image1)

![Figure 2. Willow behavior dataset sample images](image2)

2.1. Data processing

When it comes to training classification models in image recognition, it is common to have very little data. In order to alleviate the over-fitting problem, this chapter uses powerful "data enhancement" technology to improve the performance of CNN network model. The random transformations in this study include rotation, width offset, height offset, clipping, scaling, horizontal flipping and vertical flipping. The average value of each chapter of each image is set to 0.

2.2. CNN model proposed

This section gives a detailed description of the CNN models proposed in this chapter, including baseline CNN and NCNN models. Firstly, the CNN model proposed in this chapter is suitable for small sample set. [3] Secondly, it simplifies memory consumption through batch operations, making it possible to train your CNN model on CPU-only pcs. Finally, the new CNN model has a non-sequential network topology by introducing a separable convolution module. It makes the NCNN model proposed in this chapter lighter and improves the generalization ability of the model. In order to better explain the specific model structure, this section first introduces the constructed baseline CNN model, then shows the NCNN model proposed in this chapter, and finally illustrates the combined model.
2.3. Summary of the chapter

This chapter proposes a non-sequential CNN model that NCNN, the model can automatically complete feature extraction and recognition of human behavior. Some human behaviors, such as "phone calls ", "horseback riding" and "running ", are determined by their nature by methods that require static cues. Video-based behavior recognition is done by analyzing continuous frames of specified behavior in the video, so when identifying behavior with "static" characteristics, if the same is done by default, on the one hand, the computational overhead is increased, on the other hand, satisfactory recognition effect can not be obtained. This To some extent, static image-based human behavior recognition is a supplement to video-based behavior recognition. how to mitigate overfitting has been one of the most challenging tasks in computer vision and machine learning. The overfitting problem becomes more intractable when it is necessary to train deep learning models on small sample sets. therefore, how to mitigate overfitting well in training their own models is another important issue.

3. Natural environment image classification algorithm based on two-layer visual dictionary

This chapter presents a data-driven learning framework for a two-layer visual dictionary structure. DTSVDL algorithm can not only be proposed The overfitting problem can also be avoided when learning the components of the model. More importantly, the natural ring. The success of image classification task in environment can further guide other computer vision tasks, such as target detection and target tracking tasks, etc., cars are more likely to appear in the street than in the bedroom[4].

3.1. Layer Vision Dictionary Learning Algorithm

After constructing the visual dictionary, local features are extracted for each image, and the distribution of codewords on the visual dictionary is collected to generate the K-DIMENSIONAL BOF vector. K-means method is a non-probabilistic method, which is one of the most commonly used clustering methods. This section first describes the data-driven attribute-level information learning process for image datasets, and then introduces each attribute Weighting strategy for detail information extraction.
3.2. Build details information

In the attribute information learned by the pure bayesian model is high-level information, where there must be more descriptive details around each attribute. Therefore, details can be further explored for each attribute. For simplicity, K-means techniques are used to explore the details of each attribute. After building the details of all properties, this subsection will eventually obtain a histogram with L dimension length.

4. Classification of cancer stages in significant differential co-expression networks

Determining the stage of cancer is the key to cancer diagnosis and drug discovery. In such cases, appropriate and accurate specific treatment can be provided. Physicians usually determine the stage of cancer based on the AJCC tumor-lymph node-metastasis (TNM) system guidelines. When providing a diagnosis, the doctor can use TNM's description to determine the stage or stage of the cancer. However, doctors do not use gene expression data, such as data based on RNA-Seq, to determine the stage of cancer in this way. Gene expression data can visually reveal the inherent change information of the data. Therefore, cancer staging research based on gene expression data can greatly promote the discovery and reveal the mechanism of cancer development and evolution.
The use of gene expression data for cancer staging is a challenging task. So far, as far as I know, there is no report of cancer staging based on gene expression data. Although trained classifiers performed well using gene expression data for cancer classification and subtype identification, the performance of cancer staging was not satisfactory. Although more and more computational methods use RNA-seq data for cancer subtype identification, there are few studies related to cancer staging. Using machine learning-based techniques and methods to model cancer staging data and train powerful classifiers will help to understand what factors are at play in the development and evolution of cancer, in order to further explore the biological function changes of different stages of cancer. In this case, better treatment options can be chosen for different patients. Because it is difficult to use gene expression data to model the stages of cancer, the research on the mechanism of cancer evolution and the appropriate treatment is limited.

For Cancer Classification and subtype identification, differential expression genes (DEGs) based on expression profile data are used for classification learning and to measure biological functional differences. However, this primitive method can not reveal the molecular (genetic) interaction mechanism. Complex diseases are often the result of molecular interactions. Therefore, we conclude that the replacement of DEGs by molecular interaction network (coexpression network) can better characterize the different stages of cancer.

4.1. Building SDCN and SDCNS

The SDCNS for control and experimental groups were first constructed and then fed into the fusion network to form SDCNs models. The SDCNS are designed to extract sparse features for each sample, which will demonstrate strong classification capabilities. Pearson Correlation Coefficient is used to construct the reference network RN, in which the reference sample is composed of the control group with RC sample and the experimental group with Re sample. The differential coexpression networks of the control group and the experimental group were obtained. Significant difference co-expression networks were obtained between the control group and the experimental group. At last, network convergence to obtain the final convergence SDCN network.
4.2. Analysis of pathway enrichment using PEUCGP

The different SDCN structures between the control group and the experimental group can not only verify the validity of the model, but also prompt the development of a new path enrichment method in this chapter. The up-or down-regulated expression was measured using significantly different gene pairs rather than different expression genes between the two groups. The PEUCGP proposed in this chapter can explore the changes of biological function based on the co-expression pairs of generalized up-regulation and down-regulation.

5. Conclusion

In this paper, machine learning method is used to study the computer vision problems of face recognition, natural environment image classification and static image behavior recognition, in the bioinformatics of cancer staging and classification. In this paper, we discuss the common problems in machine learning. Including feature extraction methods, such as subspace features, hand-designed features such as HOG and SIFT, and depth features; Solution to model overfitting problem. For example, Bayesian non-parametric model, depth CNN model; Unbalanced sample problems, such as the use of SMOTE and ROSE methods to sample breast cancer subtypes, cancer staging data. Through the study of these problems, this paper puts forward the corresponding algorithm, model and solution, experimental results verify its effectiveness.
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