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Annoyed Turnout Ability Transmittal Using Heap-Structure

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ABSTRACT—In machine learning, support vector machines are supervised learning models with associated learning algorithms that analyze data used for classification and regression analysis. Given a set of training examples, each marked as belonging to one or the other of two categories, an SVM training algorithm builds a model that assigns new examples to one category or the other. SVMs are able to deal with datasets with imbalanced class frequencies. Many implementations allow you to have a different value for the slack penalty for positive and negative classes (which is asymptotically equivalent to changing the class frequencies). I would recommend setting the values of these parameters in order maximize generalization performance on a test set where the class frequencies are those you expect to see in operational use. Dealing with imbalanced datasets entails strategies such as improving classification algorithms or balancing classes in the training data (data preprocessing) before providing the data as input to the machine learning algorithm. The later technique is preferred as it has wider application. In this paper an effective method of using SVM classifier for multiple feature classification is proposed. Compared with traditional combination methods where all needed base classifiers should be trained before the decision combination, the proposed approach is to train individual classifiers and combine the decisions of these base classifiers at the same time. Thus the complexity of the training can be reduced because our proposed method involves solving only one optimization problem while several optimization problems should be solved for traditional methods. Furthermore, during the combination, our proposed approach takes into account both a base classifier's performance on the training data and its generalization ability while traditional combination approaches consider only a base classifier's performance on the training data. The experiments proved the efficiency of our proposed approach.

I. INTRODUCTION

Imbalanced datasets are frequently found in many real applications. Resampling is one of the effective solutions due to generating a relatively balanced class distribution.

In this paper, a hybrid sampling SVM approach is proposed combining an oversampling technique and an

undersampling technique for addressing the imbalanced data classification problem. The proposed approach first uses an undersampling technique to delete some samples

of the majority class with less classification information and then applies an oversampling technique to gradually create some new positive samples. Thus, a balanced training dataset is generated to replace the original imbalanced training dataset. Finally, through experimental results on the real-world datasets, our proposed approach has the ability to identify informative samples and deal with the imbalanced data classification problem.Dealing with imbalanced datasets entails strategies such as improving classification algorithms or balancing classes in the training data (data pre-processing) before providing the data as input to the machine learning algorithm. The later technique is preferred as it has wider application. In this paper an effective method of using SVM classifier for multiple feature classification is proposed. Compared with traditional combination methods where all needed base classifiers should be trained before the decision combination, the proposed approach is to train individual classifiers and combine the decisions of these base classifiers at the same time. Thus the complexity of the training can be reduced because our proposed method involves solving only one optimization problem while several optimization problems should be solved for traditional methods. Furthermore, during the combination, our proposed approach takes into

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II. LITERATURE REVIEW

In this section, let us survey some major contributions towards LS-SVM, DCOT-LS-SVM and its successful applications in various fields.

Giorgio Valentini[19] have proposed classification methods, based on non-linear SVM with polynomial and Gaussian kernels, and output coding (OC), ensembles of learning machines to separate normal from malignant tissues, to classify different types of lymphoma and to analyze the role of sets of coordinately expressed genes in carcinogenic processes of lymphoid tissues. By using gene expression data from ''Lymphochip'', he has shown that SVM can correctly separate the tumoural tissues, and OC ensembles can be successfully used to classify different types of lymphoma.

Kemal Polat[3] has developed a medical decision making system based on Least Square Support Vector Machine (LSSVM) which was applied on the task of diagnosing breast cancer and the most accurate learning methods was evaluated. He conducted the experiment on the WBCD dataset to diagnose breast cancer in a fully automatic manner using LSSVM. The results strongly suggest that LSSVM can aid in the diagnosis of breast cancer. In his conclusion he has claimed that on the exploration of large data sets the accuracy level may increase.

GuanjinWang[20] developed a new deep cross-output knowl edge transfer approach based on least-squares support vector machines, called DCOT-LS-SVMs. Its aim is to improve the gen eralizability of least-squares support vector machines (LS-SVMs) while avoiding the complicated parameter tuning process that occurs in many kernel machines. DCOT-LS-SVMs is able to autonomously and quickly decide the extent of the cross-output knowledge transfer between adjacent modules through a fast leave-one-out cross-validation strategy. She presented an imbalanced version of DCOT-LS-SVMs, called IDCOT-LS-SVMs, given that imbalanced datasets are common in real-world scenarios. The effectiveness of the proposed approaches is demonstrated through a comparison with five comparative methods on UCI datasets and with a case study on the diagnosis of prostate cancer**.**

D. P. Ankerst[16] modified the Prostate Cancer Prevention Trial risk calculator (PCPTRC) to predict low- vs high-grade (Gleason grade ≥7) prostate cancer and incorporate percent free-prostate-specific antigen (PSA). Methods Data from 6664 Prostate Cancer Prevention Trial placebo arm biopsies (5826 individuals), where prostate-specific antigen and digital rectal examination results were available within 1 year before the biopsy and PSA was ≤10 ng/mL, were used to develop a nominal logistic regression model to predict the risk of no vs low-grade (Gleason grade ;lt&7) vs high-grade cancer (Gleason grade ≥7). Percent free-PSA was incorporated into the model based on likelihood ratio analysis of a San Antonio Biomarkers of Risk cohort. Models were externally validated on 10 Prostate Biopsy Collaborative Group cohorts and 1 Early Detection Research Network reference set.

III. RELATED WORKS

In this section, we introduce background studies that are relevant to the transfer learning and deep architectures used in the proposed approaches.

Shallow and Deep Architecture:

The deep architecture adopted in this work was motivated by the DCN proposed by Deng and Yu. The DCN contains multiple layers of modules where each module is an independent neural network containing a single hidden layer. These modules are stacked together and the outputs from a lower module become an additional subset of the new inputs in the higher module immediately next to it. Therefore, through this type of deep architecture, the original data manifolds are forced to expand, which can help to improve generalization performance. The mechanism for constructing this deep architecture shares the same philosophy as stacked generalization. There are two approaches to expand the feature space with the growth of the deep architecture. In one approach, the new feature space is created by concatenating the original feature space with an additional feature that only uses the previous module's predictions. In the other approach, the new feature space for a higher module is created by concatenating the original feature space and additional features that use the predictions from all previous modules. Our models exploit the second approach to recursively leverage previous predictions and better separate the manifolds in the original data.

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Transfer Learning:

Traditional machine-learning methods follow the assumption that the training and testing datasets have the same distribution. If this assumption is not satisfied, the prediction models have to be reconstructed from scratch using the newly collected training data. This idealized assumption limits the feasibility of traditional machine-learning technologies in many real-world applications. Therefore, we propose transfer learning with the aim of leveraging the knowledge from a source domain in a different, but related, target domain of interest to improve learning performance.

Cross-Output Knowledge Transfer Under Stacked Architecture:

This section provides details of how the proposed approach DCOT-LS-SVMs works. Both versions of the approach for balanced and imbalanced datasets are discussed. All the modules in the proposed approach are based on LS-SVMs. Unlike traditional SVMs, there are two updates. The first update replaces the inequality constraints in SVMs with equality constraints. The second update replaces the hinge loss function with a squared loss function in the objective function. This simplifies the optimization problem of the LS-SVMs to a problem that can be solved with a linear system instead of the quadratic programming required by SVMs.

Empirical studies have shown that the generalization performance of LS-SVMs is comparable to SVMs, which is one of the reasons we chose this method. Another reason is that LS-SVMs produce analytical solutions that can be used to formulate a fast leave-one-out cross-validation strategy for parameter tuning.

IV. MODULE DESCRIPTION

Modules:
1) Treatment
2) Diseases
3) Payment
4) Medicine

- Treatment:

This module describes the treatment taken by the user. If the user new to the application means they want to register to this application after they can access this application easily. The user can register the details with proper validation and all the fields will be required for the registration process. The user can search the treatment according to their disease occurs and it will guide by the step by step symptoms. So the user monitored the treatment easily and makes it more efficient to take treatment.

- Diseases:

This module describes the identification of the disease from the user. It refers to any one of a large number of diseases characterized by the development of abnormal cells that divide uncontrollably and have the ability to infiltrate and destroy normal body tissue. It often can spread throughout your body. It is the second-leading cause of death in the world. It is caused by changes to the DNA within cells. The DNA inside a cell is packaged into a large number of individual genes, each of which contains a set of instructions telling the cell what functions to perform, as well as how to grow and divide.

- Payment:

This module describes the online payment for the treatment. Payment is the transfer of one form of good, service, or financial asset in exchange for another form of good, service, or financial asset in proportions that have been previously agreed upon by all parties involved. Payment can be made in the form of funds, assets, or services.

Payment is the trade of value from one party (such as a person or company) to another for goods or services, or to fulfill a legal obligation. Payment can take a variety of forms. Barter, the exchange of one good or service for another, is a form of payment. The most common means of payment involve the use of money, cheque, or debit, credit, or bank transfers. Payments may also take complicated forms, such as stock issues or the transfer of anything of value or benefit to the parties. In US law, the payer is the party making a payment while the payee is the party receiving the payment. In trade, payments are frequently preceded by an invoice or bill.

- Medicine:

This module provides information about the prescription for the treatment. The user had caused the disease and they will prefer the prescription according to the treatment taken. The treatment prescription will show in the layer by layer prescription to the user. For the first time, user medicine will be shown in the first layer regarding the user symptoms. In case is not cured in the first layer of symptoms means automatically moves to the next layer of the symptoms. There is a chance to cure the disease within the layer and make it more useful to the user.

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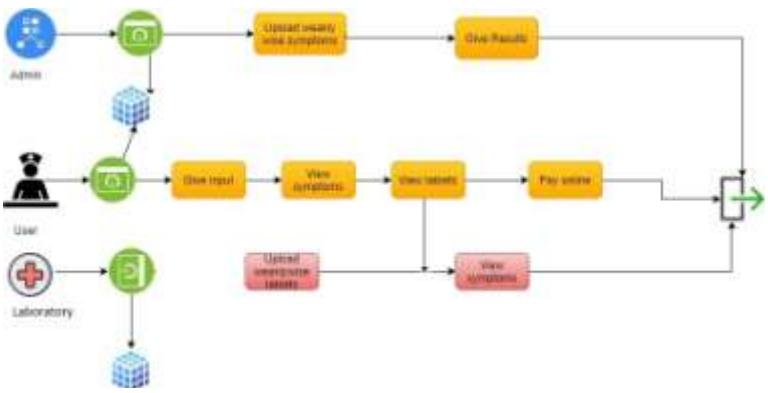
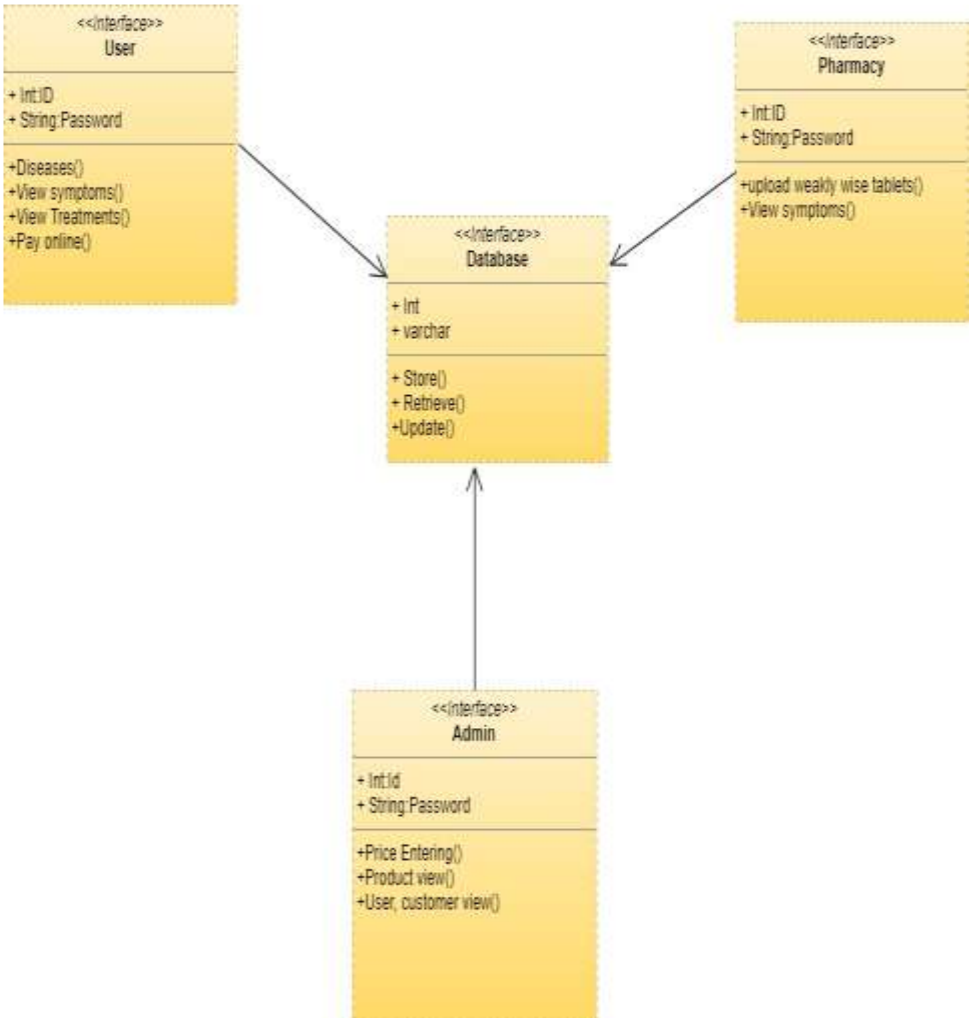
V. SYSTEM ARCHITECTED



VI. CLASS DIAGRAM



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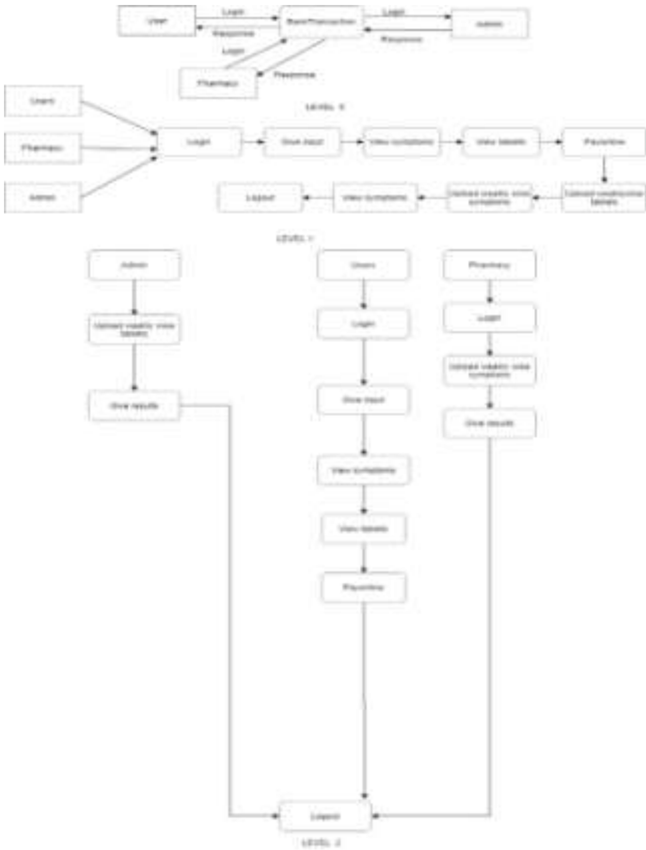
VII. DATA FLOW DIAGRAM



VIII. RESULTS

IX. CONCLUSION

In this application of medical diagnosis, we presented a deep cross-output knowledge transfer approach using stacked-structure LS-SVMs called DCOT-LS-SVMs and its imbalanced version IDCOTLS-SVMs. The proposed approaches not only show good classification performance on both balanced and imbalanced datasets but they also effectively avoid the complicated process of parameter tuning C and δ, which significantly simplifies the learning process this process are based on a stacked hierarchical architecture where several-SVMs modules are stacked together. Cross-output knowledge transfer is embedded between adjacent layers to leverage prediction knowledge from the previous module(s) to improve the learning process in the current module. We show experimentally that both approaches are robust against different levels of noise in contrast to five comparative methods. In future studies, we intend to extend the proposed approaches to a wider range of applications to further demonstrate their feasibility for practical use.

X. FUTURE WORK

In future we can developed new feature and techniques by using neural networks it is high accuracy compare to machine learning.

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