

DATA EFFICIENT SUPPORT VECTOR MACHINE TRAINING USING THE MINIMUM DESCRIPTION LENGTH PRINCIPLE

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ABSTRACT

Support vector machines (SVMs) are established as highly successful classifiers in a broad range of applications, including numerous medical ones. Nevertheless, their current employment is restricted by a limitation in the manner in which they are trained, most often the training-validation-test or k -fold cross-validation approaches, which are wasteful both in terms of the use of the available data as well as computational resources. This is a particularly important consideration in many medical problems, in which data availability is low (be it because of the inherent difficulty in obtaining sufficient data, or because of practical reasons, e.g. pertaining to privacy and data sharing). In this paper we propose a novel approach to training SVMs which does not suffer from the aforementioned limitation, which is at the same time much more rigorous in nature, being built upon solid information theoretic grounds. Specifically, we show how the training process, that is the process of hyperparameter inference, can be formulated as a search for the optimal model under the minimum description length (MDL) criterion, allowing for theory rather than empiricism driven selection and removing the need for validation data. The effectiveness and superiority of our approach are demonstrated on the Wisconsin Diagnostic Breast Cancer Data Set.

Index Terms— cancer, breast, pathology, application

1. INTRODUCTION

Support vector machines (SVMs) are supervised machine learning models which have been used extensively in medical and biomedical applications [1, 2, 3]. This popularity of SVMs stems, first and foremost, from their often highly competitive performance, but also their mathematically well-understood behaviour and explainability, contrasting many types of neural networks. The major methodological limitation associated with SVMs concerns the setting of their hyperparameters. All research to date employs one of the following approaches as regards the setting of the hyperparameter values: (i) they are set to default values which are sensible in the absence of any domain specific knowledge, or (ii) they are adopted from previous successful work on similar problems, or (iii) they are learnt using the standard

training-validation-test protocol [4] so as to ensure model specificity while preventing overfitting [4]. All of these approaches are rather unsatisfactory. Specifically, the first two are failing to make any use of training data and adapt to the particular problem at hand. The last, most principled one, is unattractive in that it is purely empirical (though this may seem to be practically unavoidable in some instances, herein we show that it is not) and wasteful both in terms of data, as a validation data set, separate from the training and test data sets, has to be set aside. This is particularly problematic in applications where data is scarce, which is often the case in medical applications [5].

In this paper we propose a novel approach of training support vector machines and setting their hyperparameter values which avoids the aforementioned problems. In particular, our idea is to make use of the minimum description length (MDL) principle which can be seen as a formalization of Occam's razor. MDL allows for the quality of fit to be assessed and balanced against the complexity of a model (in our case the number of support vectors of a trained model, given the values of hyperparameters) on principled, theoretical grounds, i.e. without the need for follow-up empirical assessment [6, 7]. Thus, using a publicly available Breast Cancer Wisconsin (Diagnostic) Data Set [8], we show how MDL can be employed in the training of SVMs and demonstrate that the outcome is not only more methodologically appealing and principled, but due to its more efficient use of data that it also achieves superior results when compared with the traditional training-validation-test approach.

2. SVM MODEL SELECTION APPROACHES

Selecting the appropriate model from a large pool of models trained with different hyperparameters values is a difficult task. Yet, it is important to get a sense of the model's reliability and generalization ability before it is applied in practice. A naïve selection approach can result in the adoption of models which exhibit overfitting or indeed underfitting [9]. Unsurprisingly, there has been plenty of previous work [10, 11, 12, 9] in this realm and the techniques proposed vary somewhat based on the type of problem considered, that is on whether one is dealing with classification or regression.

In the context of regression, the ‘hold out’ technique [13] estimates the empirical error of a model using unseen data, and uses the estimate to make the best model choice. In contrast, the Model Selection Curve [14] method involves drawing predicted points of trained models on the training and validation set, and the model which exhibits the best consistency between the two sets is selected as the best one.

In the context of classification, the training-validation-test approach is probably the most widely used one [15]. The available data is split into three subsets – namely training, validation, and test, with the size of the first of these usually being much larger than that of the other two. Models with different hyperparameter values (or indeed models using different learning algorithms altogether) are trained on the training data set. The trained model is then queried to predict the output of all data in the validation set. The best model is selected based on the trained models’ performances on the validation set, whereas the performance of the said selected model is finally assessed on the test data set (thus ensuring a lack of bias).

The k -fold validation approach can be seen as a modified version of training-validation-test. It involves firstly the splitting of the available data into k subsets, referred to as *folds* in this context [16]. In each iteration, one particular fold is selected and kept aside (withheld) while the model is trained on the union of all others. The trained model is assessed on the withheld fold. The process is iterated with a different fold being withheld in each iteration. The overall validation performance is computed as the average of the performances obtained at each fold. The process is applied to different hyperparameter values or learning algorithms. The best performing model under the aforementioned criterion is selected as the best choice model. As before, it is ultimately assessed on the test data set.

3. PROPOSED METHOD

As we briefly noted earlier, there are two major drawbacks to the existing model selection methods. The first of these lies in the inefficient use of data. In particular, since validation and test sets need to be entirely disjoint from the training data set (and of course with one another), less data is available to actually train the model, and the lesser amount of training data translates to less well trained models. This is particularly important in many medical applications wherein data scarcity poses a significant challenge. This scarcity may be inherent, e.g. because a specific condition of interest is rare, or it may be of a practical nature, e.g. because relevant data cannot be easily accessed or shared due to privacy concerns or regulations.

Our approach surmounts the drawbacks of these limitations by preserving the validation/test sets and using them for training. In particular, we are interested in the MDL [17] criterion, which can be thought of as a formalization of Occam’s razor [18], allowing one to make a principled compromise be-

tween the complexity of a model and the explanatory power of the model in the context of training data. This means that no validation data is needed, which can instead be used for training, thus improving the model.

3.1. Description length and the MDL, and SVMs

In the context of the present work the description length is the length in bits needed to encode the parameters of a model and the data given the model. Formally:

$$DL(M, D) = L(M) + L(D|M) \quad (1)$$

where $DL(M, D)$ is the description length corresponding to the model M and data D . For a statistical model defined as a parametrized family of probability distributions, as in the case of SVMs, the description length can be further written as:

$$DL(M, D) = \frac{1}{2} N_M \log_2 N - \sum_{i=0}^{N-1} \log_2 P(d_i) \quad (2)$$

where d_i are individual data points from D , N their count, and N_M the number of free model parameters.

3.1.1. Support vector based learning

Support vector machines perform classification through linear separation in a high (possibly infinitely) dimensional space into which the original input data is mapped [19]. Importantly, the seemingly intractable task of mapping data into the high dimensional space is achieved efficiently by performing the aforesaid mapping implicitly rather than explicitly. This is done by employing the so-called ‘kernel trick’ which ensures that dot products in the high dimensional space can be readily computed using the variables in the original space. Given labelled training data (input vectors and the associated labels) in the form $\{(x_1, y_1), \dots, (x_n, y_n)\}$, a support vector machine aims to find a mapping which minimizes the number of misclassified training instances, in a regularized fashion. The mapping $x \rightarrow \Phi(x)$ is performed implicitly by employing a Mercer-admissible kernel [19] $k(x_i, x_j)$ which allows for the dot products between mapped data to be computed in the input space: $\Phi(x_i) \cdot \Phi(x_j) = k(x_i, x_j)$. The classification vector in the transformed, high dimensional space of the form

$$w = \sum_{i=1}^n q_i y_i \Phi(x_i) \quad (3)$$

is sought by minimizing

$$\sum_{i=1}^n q_i - \frac{1}{2} \sum_{i=1}^n \sum_{j=1}^n y_i q_i k(x_i, x_j) y_j q_j \quad (4)$$

subject to the constraints $\sum_{i=1}^n q_i y_i = 0$ and $0 \leq q_i \leq 1/(2nc)$, with the parameter c penalizing prediction errors.

The key insight we introduce lies in the modelling of the distribution of data in the target high dimensional space of a SVM. In particular, we assume that class data points are normally distributed, which is an assumption consistent with the linear separability goal of support vector based learning:

$$P(\hat{d}_i) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x_i - \mu)^2}{2\sigma^2}} \quad (5)$$

where μ and σ are respectively the mean and the standard deviation of the normal distribution, and \hat{d}_i the data, all in the target high dimensional space of the SVM. Then, the data description length term in (2) becomes:

$$\sum_{i=0}^{N-1} \log_2 P(\hat{d}_i) = \sum_{i=0}^{N-1} \log_2 \left[\frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(\hat{d}_i - \mu)^2}{2\sigma^2}} \right] \quad (6)$$

$$= \log_2 \left[\left(\frac{1}{\sqrt{2\pi\sigma^2}} \right)^N e^{\sum_{i=0}^{N-1} -\frac{(\hat{d}_i - \mu)^2}{2\sigma^2}} \right] \quad (7)$$

$$= -\frac{N}{2} \log_2(2\pi\sigma^2) - \frac{1}{2\sigma^2 \ln 2} \sum_{i=0}^{N-1} (x_i - \mu)^2 \quad (8)$$

and since $\sum_{i=0}^{N-1} (\hat{d}_i - \mu)^2 = \sigma^2 N$:

$$\sum_{i=0}^{N-1} \log_2 P(\hat{d}_i) = -\frac{N}{2} \log_2(2\pi\sigma^2) - \frac{N}{2 \ln 2} \quad (9)$$

$$= -\frac{N}{2} (\log_2 2\pi\sigma^2 + \log_2 e) \quad (10)$$

$$= -\frac{N}{2} \log_2(2\pi e \sigma^2) \quad (11)$$

Thus in our case the description length in (2) becomes:

$$DL(M, D) = \frac{1}{2} N_M \log_2 N + \frac{1}{2} N \log_2(2\pi\sigma^2 e) \quad (12)$$

where N_M , the number of free model parameters, is equal to the number of support vectors of the trained model.

4. EXPERIMENTAL ANALYSIS

4.1. Experimental data

We carried out our experiments on the Breast Cancer Wisconsin (Diagnostic) Data Set [8] – a popular and publicly freely available corpus. By way of summary, the data set comprises exemplars (569 in total) of two classes corresponding to the two diagnostic decisions as regards cancer malignancy (malignant or benign), characterized by 30 features extracted from images of fine-needle aspirates of breast masses. These features describe the characteristics of the cell nuclei morphology (captured through the mean and extreme values, and standard deviations of relevant characteristics across a slide) present in the images and are obtained after performing cytological analysis and simple image processing (curve-fitting for cell delineation) [20, 21].

Table 1. Summary of experimental parameters.

Parameter	Value
Number of features	30
Number of samples	569
Min c	1
Max c	1000
Min γ	0.001
Max γ	1.000
Number of equidistant c samples	100
Number of equidistant γ samples	100

4.2. Methodology

The following summarizes the process used to apply the proposed method and compute the corresponding performance metrics:

1. The data was divided into two subsets, training and test, with the split ratio (in terms of data sample counts) of 4:1.
2. Radial basis function (RBF) SVM models were trained using 10,000 combinations of c and γ (100 c and 100 γ) as per Table 1, where γ is the reciprocal of the RBF standard deviation.
3. Using the training set only, description lengths were computed for models trained with different values of hyperparameters. The performance of the model selected according to the MDL criterion was assessed on the test data.

Comparison was made with the standard k -fold based approach:

1. The data was divided into training, validation, and test set with split ratio 3:1:1. Then, k -fold cross-validation was applied with 4 folds on the union of training and validation sets. As before, the performance of the final selected model was assessed on the test data.

4.3. Results and discussion

We start our discussion with the baseline approach first, that is the k -fold cross-validation based model selection. The plot in Fig. 1 shows the dependency of the final, trained classifier accuracy on the values of the parameters γ and c , which is useful in demonstrating that the model actually selected is indeed sound i.e. one which does not exhibit over- or under-training. It is worth observing that expectedly the accuracy

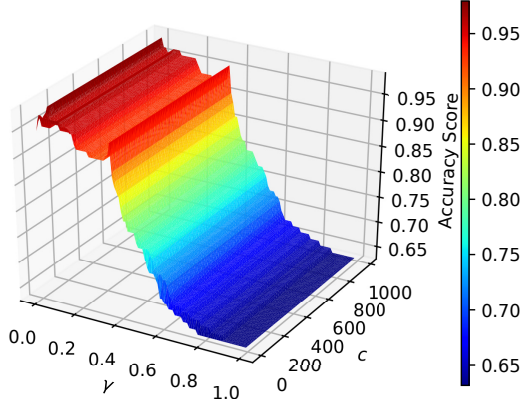


Fig. 1. Trained classifier accuracy as a function of the parameters γ & c , using k -fold cross-validation.

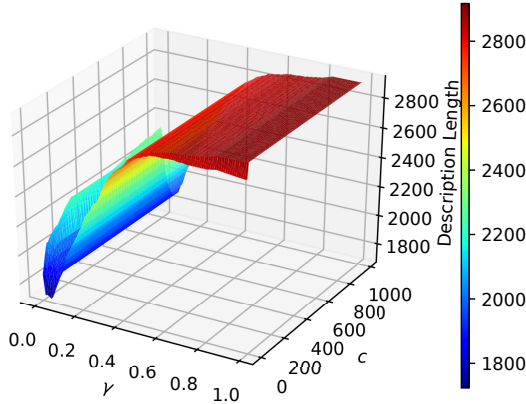


Fig. 2. Description length as a function of SVM parameters γ & c .

is greatly affected by varying γ but not by the regularizing penalty parameter c . The latter suggests good separability of classes in the implicit high dimensional space of the trained SVMs.

Turning our attention to the proposed method now, the variation in the description length attained with the models trained with different values of the hyperparameters γ and c is shown in Fig. 2. As anticipated based on the behaviour observed using k -fold cross-validation training, here too we observe that in this case the description length is highly affected by γ but not by c . Importantly, it is also the case that a clear local minimum is present in the plot, corresponding to the ultimately selected model i.e. the ‘best’ model under the minimum description length criterion.

Having ensured that both approaches are making sensible decisions in the context of the given data, we proceeded by evaluating the two selected models – one using k -fold cross-validation and another with the proposed approach – and comparing them with one another. A summary is shown in Table 2, demonstrating that the proposed method achieves supe-

Table 2. Comparison of the models selected using traditional k -fold cross-validation (xV) and the proposed method.

Method	Accuracy	Recall	F1-Score	Precision
k -fold xV	0.9649	0.9286	0.9512	0.9750
Proposed	0.9737	0.9524	0.9639	0.9756

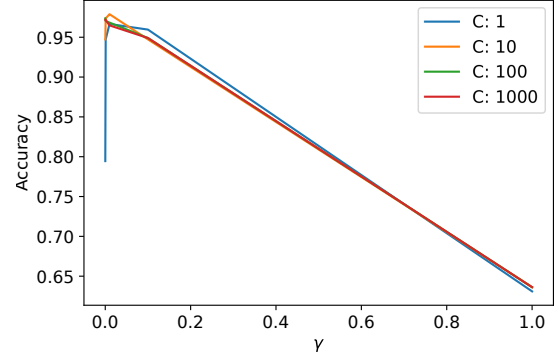


Fig. 3. Accuracy as a function of γ for fixed values of the penalty c , namely $c = 1, 10, 100, 1000$.

rior results according to all metrics considered. This is despite the absence of empirically, verification guided model selection – or rather, precisely because of, as we have argued, with our approach being based on fundamental theoretical grounds which allows for a more efficient use of available data.

For completeness, we also include the plot showing the variation of classification accuracy of different trained models compared in terms of their description length in Fig. 3, which shows that the parameter combination selected by our MDL guided selection process indeed does achieve best performance too.

5. SUMMARY AND FUTURE WORK

In this paper we introduced a novel, theoretically rigorous framework for SVM model selection which overcomes the inefficiencies of the current, empirically driven approaches used in practice. This contribution is especially important in numerous medical applications, where the effect of the aforementioned inefficiencies can be a limiting factors in applicability of machine learning (e.g. due to limited data). The effectiveness of the proposed approach was demonstrated on the Wisconsin Diagnostic Breast Cancer Data Set, on which it is shown to outperform the existing alternatives.

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