A Granular Parakeratosis Classification using SVM Hinge and Cross Validation

Sheetal Janthakal[1*] and Girisha Hosalli[1]

[1] Department of Computer Science and Engineering Rao Bahadur Y. Mahabaleswarappa Engineering College, Bellary, Karnataka, India

[*] Corresponding author. E-mail: sjanthakal@yahoo.co.in

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Now-a-days, a challenging task in the medical field is the diagnosis of skin illness considering numerous characteristics such as color, size, and the lesion region. Dermoscopy is a technique that has been frequently used to diagnose skin lesions. Researchers have recently demonstrated a keen interest in building an automated diagnosis system, and a satisfying result can be achieved with a high degree of skill, as skin lesion classification necessitates a great deal of knowledge and expertise. Automated skin lesion classification in dermoscopy images is an essential way to improve diagnostic performance. This paper presents the power of convolutional neural networks in classifying the skin lesions into two different categories, namely Granular Parakeratosis and Paraneoplastic Pemphigus. The proposed method includes implementation of Support Vector Machine with hinge loss and linear activation function for classification of lesions and this output is fed to the 10-fold cross validation model, yielding an accuracy of 94%, sensitivity of 93%, and specificity of 91%. The proposed strategy outperforms the SVM kernel Radial basis function (RBF), which was created specifically for binary classification problems.

Keywords: 10-fold Cross Validation, Convolutional Neural Networks, Hinge Loss, Linear Activation Function, Support Vector Machine

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1. Introduction

Granular parakeratosis is a disease characterised by thickening of the outer layer of the skin, presence of keratinocytes and retainment of keratohyalin dots in the horny layer. It has the characteristics of histopathological findings [1, 2].

Paraneoplastic pemphigus (PNP) is a newly recognized autoimmune blistering disease associated with an underlying malignancy. The diagnosis is based on clinical, histological, and immune-fluorescent findings. It most commonly affects people between the ages of 45 and 70, but it can also affect youngsters [3].

'Early diagnosis and treatment of skin diseases increases the rate of recovery'. However, the traditional procedures that depend on manual examination face several difficulties due to the high similarity of lesions. In some cases, samples may cause complications in the spread of the disease. The conjunction of contemporary imaging techniques and computer vision algorithms provides a better result related to accuracy and processing speed. Generally, a computer-aided diagnostic system consists of four steps, including pre-processing, segmentation, feature extraction, and, finally, lesion classification.

As seen in the dermatology area for skin lesion classification, particularly for differentiating melanoma and nevus, digital image processing techniques are gaining relevance in various computer tools that assist in diagnostic conclusion [4]. The techniques used in such tasks span

from Deep Learning, which determines the sorts of features to be used for classification automatically, to more traditional Machine Learning (ML) algorithms that require hand-crafted features. The application of the deep learning algorithm has yielded impressive results [5]. Those techniques, however, necessitate large, precisely annotated datasets, which are rarely available.

Dermoscopy, a technique for removing the skin's surface reflection and examining the structures, is an important tool for improving diagnostic performance and assisting experts in determining whether a lesion is harmful or harmless. To enhance the appearance of features like color, this procedure uses a dermatoscope, which is a device that includes a light source and an amplification lens.

Over the years, convolutional neural network (CNN) has been considered as a tool for biomedical image classification. It works effectively in a variety of medical fields, including histology and dermatology [6]. The rapid expansion of deep neural networks, such as CNN, allows non-professionals to become acquainted with the sophisticated tools and understand them.

In the early 1990s, computer-aided diagnosis (CAD) systems were developed for the detection of skin lesions. Since then, various approaches have been published to handle the challenge of lesion categorization. The majority of the algorithms (e.g. [7]) employ a manual evaluation process based on Nachbar et al.'s ABCD principle [8]. This rule encompasses an asymmetry (A), border (B), color (C), and differential structure (D). Alquran Hiam [9] introduced the Support Vector Machine (SVM) with Principal component analysis (PCA) approach, which correctly categorized the retrieved lesion ROI with 92.1% accuracy. SVM [10] is able to classify samples containing melanoma and non-melanoma lesions and showed that accuracy goes up with the larger number of samples.

Due to the following reasons, this research offers an ensemble approach of SVM with hinge loss function and 10–fold cross validation for detecting and classifying granular parakeratosis and paraneoplastic pemphigus.

- Hinge loss is computationally effective and provides better accuracy.
- Compared to log loss, hinge loss is easier and processes faster.
- 10–fold cross validation improves the performance of a machine learning model by reducing computation time and bias.
- The variance of the result is reduced as k increases.
- Cross-validation can make predictions about each of the samples.

The paper consists of the following sections. Section 2 includes a review about the classification of skin lesion. Further, section 3 focuses on methodology and section 4 produces the results obtained after the implementation and finally, the paper is concluded.

2. Literature review

CAD tools for skin lesions are studied in many disciplines and at various levels of the diagnostic system. Natale Cascinelli [11] reported the first study on the automatic classification of pigmented lesions. Following that, different methods for pre-processing, segmentation, feature extraction, and classification were shown. The publications on CAD systems for skin problems are reviewed below.

According to Pereira et al., improved segmentation accuracy leads to better classification results. It improved the classification of skin lesions into Nevus and Melanoma by automating the process. Adding border-line characteristics to automatic classification algorithms enhanced their performance by more than 90%.

The work of [12] proposed an automatic method for skin lesion classification that employs pre-trained deep learning models and combines the features from several layers or from several CNNs to yield a better classification performance of 97.55%.

To categorize moles and melanoma, Rohan Gaonkar used two classifiers: Radial Basis Function Network (RBFN) and SVM in [13]. The accuracy of SVM and RBFN for the K10 protocol was 87% and 91%, respectively. Specificity and sensitivity for SVM were 82% and 92%, respectively, for the K10 protocol, whereas specificity and sensitivity for RBFN were 90% and 93%, respectively. As a result, the technique maintains a balance between specificity and sensitivity.

The work of [14] performed automatic lesion segmentation using encoder-decoder architecture, MobileNetV3-UNet that achieved high accuracy with a limited number of resources. The approach was tested on three datasets: ISIC-2017, ISIC-2018, and PH2, yielding dice coefficient and Jaccard index values of 87.74%, 80.25%, 91.01%, 83.44%, and 95.18%, 91.08%, respectively, for ISIC-2017, ISIC-2018, and PH2.

A deep neural network framework was proposed in [15] for classifying the lesion images into multiple classes. This framework applies balanced multi-class accuracy (BMA), a measure available in multi-class classification problems, to the ISIC 2018 dataset and obtained an accuracy of 60%.

The work of [16] proposes 2D super-pixels and the deep learning system to improve classification accuracy. The features extracted from the PH2, ISBI 2016, and HAM1000 datasets are optimized using the grasshopper optimization algorithm and then classified using the Naive Bayes classifier. This hierarchical framework achieved an accuracy of 95.40%, 91.1%, and 85.50%, on the three datasets, respectively.

The work of [17] Ghasem Shakourian Ghalejoogh (2020) proposed a hybrid model consisting of Structure Based on Stacking (SBS) and Hierarchical Structure Based on Stacking (HSBS) that were implemented on PH2 and Ganster datasets and found that HSBS method classified lesions as benign, dysplastic, and melanoma in a better manner compared to the SBS. For the PH2 dataset, an accuracy of 98.5% is obtained, and for the Ganster Dataset, it is 97.78%.

Table 1 summarizes all of the previous studies that are connected. In reviewed research, most of the studies concentrate on differentiating melanoma from non-melanoma. Granular parakeratosis and paraneoplastic pemphigus are the emphasis of the suggested technique.

The algorithms utilized by different authors in classifying skin lesions have not been demonstrated to be extremely accurate and effective, according to literature. This made us step into an efficient ensemble technique, SVM-hinge loss and 10-fold cross validation. This method is able to train, test, and classify the dataset of granular parakeratosis and paraneoplastic pemphigus images and will be very helpful in the diagnosis of these lesions efficiently.

3. Methodology

3.1. Our contribution

The contributions of proposed work are summarized as follows.

- A dense layer with an L2 regularizer and linear activation function is chosen as the last layer of the CNN model, leading to the implementation of the SVM classifier.
- The loss function plays a vital role in the optimization process, and a proper selection of the loss function helps improve the training process. Here, Hinge loss that eases the process of training with small datasets is adapted. Thus, a method to automatically classify the lesions of granular parakeratosis is proposed.
- The output of the proposed SVM classifier is fed to 10-fold cross validation, thereby increasing the accuracy.

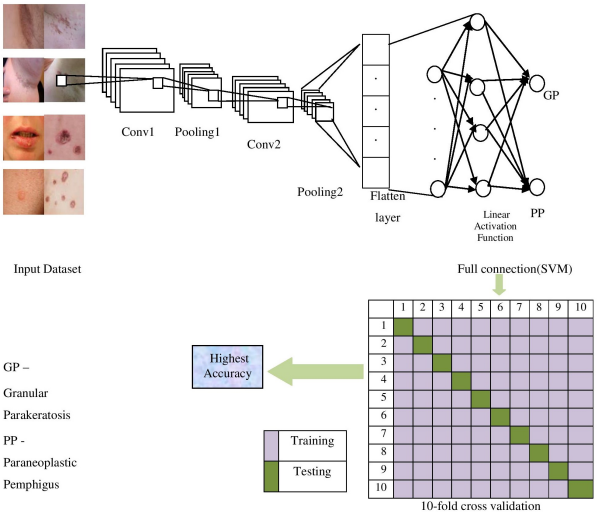

Fig. 1. Proposed system architecture

3.2. System architecture

The architecture of the proposed system is shown in Fig. 1. Granular parakeratosis and paraneoplastic pemphigus lesion images are included in the dataset, and the proposed system is used to classify these lesions. To train and evaluate the algorithms, a dataset of 1505 dermoscopic images was used. Table 2 contains a description of the dataset. To improve the system's accuracy, the input dataset is provided to a linear SVM with hinge loss for identifying the lesion, and the classifier output is then ensembled with 10 fold cross validation. The system is evaluated using test dataset and graphs are generated for the results obtained. The system further classifies the type of skin lesion as Granular Parakeratosis or Paraneoplastic Pemphigus. The proposed model requires lesion color images of size 224×224.

3.3. Svm with hinge loss function

SVM is a supervised learning procedure developed by Vapnik and is mainly used for classification problems [18]. SVM tries to find the best separator in differentiating two different classes [19]. An advantage of SVM is that it provides a framework for classifying the data through a suitable kernel selection [20]. Thus, the support vector machine serves as a binary classifier [21].

A linear kernel SVM is used to classify our dataset. The main purpose for opting the linear kernel is its speed and accuracy in classifying the binary problems. The proposed SVM classifier with hinge loss and linear activation function consists of the following layers in architecture:

1. Convolution

Table 1. Literature Survey

Reference	Method	Dataset	Result
[4]	SVM and Feed forward Neural Network (FNN)	MED-NODE dataset and the Dermofit dataset	Accuracy above 90%
[12]	SVM Classifiers	ISIC 2017	Area under the curve (AUC) - 97.55%
[15]	Deep Neural Network	ISIC 2018 dataset	Balanced multi-class accuracy (BMA) was obtained as 60%
[16]	Super Pixels And Deep Learning Framework	PH2, ISBI 2016, and HAM1000 dataset	Accuracy of 95.40%, 91.1%, and 85.50%
[17]	HSBS structure	PH2 and Ganster datasets	Accuracy PH2 - 98.5%, Ganster - 97.78%

Table 2. A detailed dataset

	Granular Parakeratosis	Paraneoplastic Pemphigus
Training set	1080	71
Test set	425	28
Total	1505	99

The first and foremost layer in a neural network is convolution. It accepts images and filters as inputs and extracts the features from an input image, leading to a feature map.

$$(f * g)(t) \stackrel{\text{def}}{=} \int_{-\infty}^{\infty} f(t-\tau)g(\tau)d\tau \tag{1}$$

The rectifier function, ReLu increases the non-linearity in the network. Because of its computational efficiency, ReLu was chosen over sigmoid.

2. Pooling

   The pooling layer highlights the elements of the feature map that originated from the convolution layer, lowering the number of parameters and improving the model's stability.

   - Second convolutional layer

     Convolutional layers do not work only on the input data, but also on the output of other layers. This stacking of convolutional layers leads to hierarchical decomposition of the input.

3. Flattening

   After a feature map is pooled, it is converted to a 1-D array and fed to the next layer by flattening it into a column. The fully-connected layer is then connected to the final classification model.

4. Full Connection

   This is where the steps discussed earlier are merged, thereby creating a convolutional neural network. The main role of the fully connected layer is to combine the features into a number of attributes that make the CNN more capable of classifying images accurately.

5. Output Layer

   To generate the final output in the form of a class, a fully connected layer is applied to get an output equal to the number of classes required. Convolution layers give rise to 3D activation maps, but what output is needed is to know whether a lesion belongs to a granular parakeratosis or not. The output layer has three parameters:

   - Hinge loss function to compute the error in prediction;
   - L2 regularizer;
   - Linear activation function;

The combination of these parameters leads to a simulation of the SVM classifier. A detailed explanation of these parameters is given below:

Hinge Loss

The hinge loss is a function that trains the classifiers, mostly SVM classifier. The following equation gives the formula for calculating the hinge loss:

$$l = \max\left(0, 1 - y^i\left(x^i - b\right)\right) \tag{2}$$

Where y^i and x^i refer to the i^{th} instance in the training set and **b** refers to the bias term.

This formula can be re-written as:

$$l = \left\{ \begin{array}{cc} 0 & \text{if } y \cdot (w \cdot x) \geq 1 \\ 1 - y \cdot (w \cdot x) & \text{otherwise.} \end{array} \right\} \tag{3}$$

Regularizers

During optimization, regularizers impose penalties on parameters or activity of the layer. These penalties are applied to the network's loss function, which is optimized. On a layer-by-layer basis, regularization penalties are applied. There are three arguments in these layers:

– kernel_regularizer: it applies a penalty to the kernel of the layer.

- bias_regularizer: this applies a penalty to the bias of the layer.
- activity_regularizer: this one applies a penalty to the output of the layer.

Regularization of neural networks is a technique for reducing model overfitting. There are various types of regularization. The tf.keras.regularizers module includes two built-in regularizers: L1 class and L2 class.

The most commonly used form is L2 regularization. It adds a term to the training algorithm's error function and this additional term penalizes large weight values. The two most frequent error functions in neural network training are squared error and cross entropy error. In L2 regularization, a proportion (called as L2 regularization constant, and represented by the lambda) of the sum of the squared weight values is added to the base error.

The penalty for L2 regularization is calculated as follows:

$$loss = l2^{*}reduce\_sum(square(x)) \tag{4}$$

L2 regularization reduces overfitting by keeping the weights and bias values minimal.

$$E = \frac{1}{2} * \sum (t_k - o_k)^2 + \frac{\lambda}{2} * \sum w_i^2 \tag{5}$$

The math equation is given in the Eq. (5). 'It is squared error augmented with the L2 weight: one-half the sum of the squared differences between the target values and the computed output values, plus half a constant lambda times the sum of the squared weight values'.

$$\begin{aligned} \Delta w_{jk} =& \eta * \left[x_j * (o_k - t_k) * o_k * (1 - o_k) \right] \\ &+ \left[\lambda * w_{jk} \right] \end{aligned} \tag{6}$$

The back-propagation algorithm adds a positive or negative weight-delta to each weight iteratively during training. 'The weight-delta is a fraction (called the learning rate and represented by the letter η) of the weight gradient. The weight gradient is the calculus derivative of the error function as given in Eq. (6)'.

Activation functions

These determine the neural network's output. Associated with neurons, this function decides whether a neuron should be activated or not, depending on whether its input is appropriate for predicting the model.

Two types of Activation Functions:-

- Linear Activation Function
- Non-linear Activation Functions

A linear activation function takes the form:

$$A = cx$$

where c is the derivative with respect to x. It accepts inputs, multiplies them by the weights, and creates an output in proportion to the input.

3.4. 10-fold cross-validation

The SVM classifier performance relies on the parameters, C (regularization) and the kernel parameters. These "hyperparameters" can be adapted to select the SVM model. The most basic approach is CROSS-VALIDATION.

Cross-validation (CV) is a well-known method for fine-tuning predictive model hyper-parameters. In 10-fold CV, the input dataset S is partitioned into 10 subsets S1,...,S10. Each point in S is randomly assigned to one of the subsets, so that they are of equal size.

$$(i.e., \lfloor |S|/K \rfloor \leq |S_i| \leq \lceil |S|/K \rceil)$$

'Further, $S_{\setminus i} = U_{j=1,\ldots,K \wedge j \neq i} S_i$ is defined as the union of all data points except those in S_i. For each i=1,...,10, an individual model is built by applying the algorithm to the training data $S_{\setminus i}$. This model is then evaluated by means of a cost function using the test data in S_i. The average of the K outcomes of the model is called *cross-validation performance* and is used as a predictor of the performance of the algorithm when applied to S'.

4. Results and analysis

4.1. Dataset description

The dataset is taken from [22, 23]. Initially, 224x224 pictures are loaded and turned into numpy arrays using their RGB values. To avoid overfitting, data augmentation technique is applied that artificially creates a new training set from an existing training set. Finally, the pictures are appended to a training set and shuffled (a method of elastic transformation).

4.2. Experimental setup

Here, the parameters employed during the calculation of results are discussed. All simulations of the proposed framework are implemented on a Windows 10 OS configured with an Intel Core i5 processor and 8 GB of DDRAM. An Anaconda IDE with spyder editor is utilized to implement a program. The training epoch number is 10, and the batch

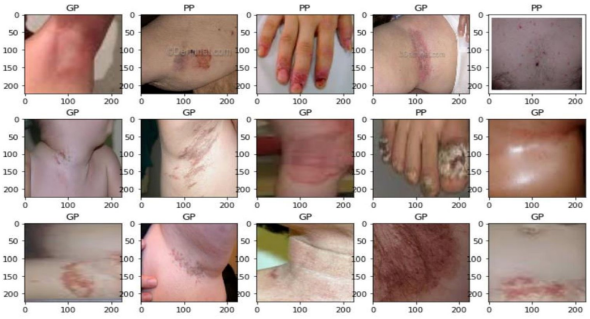

Fig. 2. Training results for the classification of granular parakeratosis and paraneoplastic pemphigus

size is 8. In the classification phase, a ratio of 75/25 training and testing images are employed and 10-fold cross-validation is performed.

4.3. Evaluation metrics

The proposed model is evaluated using the confusion matrix. It is a table that describes the performance of a classifier on the test data in machine learning. The performance of the proposed system is determined using accuracy, sensitivity, and specificity. Sensitivity, specificity and accuracy are described in terms of TP, TN, FN and FP.

$$Sensitivity = TP/(TP + FN)$$

$$Specificity = TN/(TN + FP)$$

$$Accuracy = (TN + TP)/(TN + TP + FN + FP)$$

Where FP → False Positive, FN → False Negative, TP → True Positive, TN → True Negative

4.4. Analysis

The system initializes the SVM architecture and trains the network by setting the epoch manually. This CNN framework includes several convolution layers, filters, maxpool layers, dropout layers, softmax layers, and an activation function.

The dataset, consisting of 224x224 resolution images, is first fed into the training stage. This training set is then split into K (here K is chosen as 10) subsets, thereby training the model on one partition and evaluating it on the other partitions. Here, K represents the number of groups a given dataset is to be split into. The overall performance of the model is then taken as the average of k time's performance. The result of the model is improved with the application of 10-fold cross validation. The proposed model training results are shown in Fig. 2.

Fig. 3-(i) depicts the model's accuracy on training and validation sets. This suggests that our model is an excellent

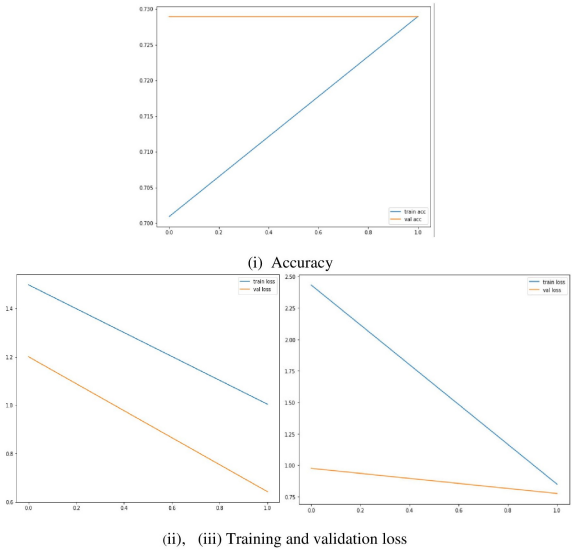

Fig. 3. (i) Accuracy of the model on the training and validation set, (ii) and (iii) Training and validation loss obtained on the given dataset

predictor, considering all types of boundary cases. That is, in training the dataset, the hyperparameters chosen are very good and eventually resulted in a better prediction in the validation dataset.

Fig. 3-(ii) and (iii) show the training and validation losses obtained on the given dataset. Here we find the validation loss is much better than the training one, which indicates that the validation dataset is easier to predict than the training dataset. An explanation could be the validation data is scarce but widely represented by the training dataset, so the model performs extremely well on these few examples.

Graphs in Fig. 3 indicate the performance of the SVM-10 fold model on the given dataset. It clearly shows that accuracy increased gradually and reached around 94%, whereas loss values fell off against the iterations of the network.

The dominance of the proposed SVM with hinge loss function can be validated by conducting a comparative study. A comparison is made with existing techniques such as Joint Reverse Classification, ClsNet, and GoogleNet [31] in terms of accuracy, sensitivity and specificity.

In Table 3, the results obtained by these algorithms are compared with the proposed method. Our network showed better performance compared to the existing techniques. The proposed SVM-10 fold model achieved an accuracy of 94%, a sensitivity of 93%, and a specificity of 91% on the Dermnet dataset.

Table 4 compares the accuracy of the proposed model

Table 3. Comparison of proposed SVM-10 fold model with existing methods

S. No	Ref	Year	Classifier	Accuracy	Sensitivity	Specificity
1.	[24]	2016	Joint Reverse Classification (JRC)	92.00	87.50	93.13
2.	[25]	2014	Bag-of-words (BoW) model and Gray transform Shades	-	93	76.30
3.	Proposed		SVM-10 fold model	94	93	91

Table 4. SVM classification accuracy of the proposed approach in comparison with other approaches from the literature

	ClsNet [26]	SVM classifier [29]	EfficientNet-B0 [27]	CNN SENet [28]	GoogLeNet, AlexNet and VGGNet [30]	Proposed Model
Accuracy	80	83.83	93	91	84	94

with other state-of-the-art techniques, including ClsNet, SENet etc and again it is proved that the proposed model outperforms those techniques.

5. Conclusion

Skin diseases must be diagnosed early and precisely in order to improve treatment outcomes and save recovery time. As a result, an automated skin lesion identification system is proposed as an early caution for skin lesion classification in this study. The proposed system is mainly focused on the classification of Granular Parakeratosis lesions in order to aid in the improvement of recovery rates. The SVM classifiers with hinge loss, linear activation function, and the L2 regularizer, as well as 10-fold cross validation, were primary contributions. This proposed ensemble model achieved superior performance when compared with existing techniques. In addition, lesions classified using the SVM-10 fold model achieved an outstanding performance accuracy of 94%, sensitivity of 93%, and specificity of 91%.

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