The Accuracy of KNN, SVM, neural network, naive Bayes classifier and DBSCAN, kmeans for Determining the Cancer by Gene-expression signatures And the Arrhythmia Types

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Abstract

Nowadays, using machine to give an early diagnosis of a cancer type is widely studied. In this paper, based on the gene-expression dataset on Synapse.org, we compare the performance of machine learning techniques, including data preprocessing, e.g., Principal components analysis (PCA), Autoencoder (AE), classification, e.g., k-nearest neighbors (KNN), support vector machine (SVM), neural network (NN), and clustering for dealing with unknown types, e.g., k-means, density-based spatial clustering of applications with noise (DBSCAN).

The result of gene dataset shows that, with PCA reducing the dimension of the dataset to 32, use KNN for classifying the known types, and finally apply DBSCAN on the remaining data, the accuracy of predicting can reach about 94%, which beats the other methods out. In the other way, the result of arrhythmia dataset shows that, with raw data, use KNN and k-means, the highest accuracy of predicting can reach about 53%.

The source code can be found in here.

1 Introduction

Over the years, machine learning methods for early predict various disease are widely used in medical field. [1] [2] From diabetes [3], heart disease [4], to lung adenocarcinoma [5] etc., machine learning methods is universally studied attributed to the promising perspective. With a well-built database of disease and a well-choose combination of machine learning mathods, within seconds, a machine may determine the type of disease that this person may have by collecting the data from the person, and thereby achieve the goal of personalized medicine. As a result, machine learning methods have become a popular tool for medical researchers.

In real application, besides from the konwn diseases in the train data, there're numerous unkown types of diseases. When a new type of disease appears, how shall the machine results? In ideal situation, this new type of disease should be reported as an unkonwn type, which can be done by the combination of classification and clustering. However, how to choose the proper machine learning methods is a hot potato, since the different combinations of machine learning methods have different performance.

In this work, the dataset on Synapse.org is used, which contains 20531 RNA sequences and 3 types of cancer in the train data, i.e., kidney renal clear cell carcinoma (KIRC), breast invasive carcinoma (BRCA), lung adenocarcinoma (LUAD), and 2 new types in test data, i.e., colon adenocarcinoma (COAD), prostate adenocarcinoma (PRAD). And also, the dataset of arrhythmia is included, which caintains 8 types in train data, and 5 new types in test data. To find out which techniques is more suitable to fit these two datasets, this work examines the the accuracy of the combinations of some major machine learning techniques, including PCA, AE, KNN, SVM, NN, k-means, DBSCAN.

2 Related works

Data preprocess

Autoencoder (AE): An AE is a type of neural network used for unsupervised learning and dimensionality reduction. It is designed to learn efficient representations or encodings of input data by training the network to reconstruct its own inputs. The AE consists of an encoder and a decoder. The encoder compresses the input data into a lower-dimensional representation, often called the latent space or code. The decoder then aims to reconstruct the original input data from this compressed representation. By learning a compact representation of the input data, AEs can capture important features and discard noise or irrelevant information [6]. This makes them effective in tasks such as image [7] [8] [9] or text classification [10] [11], where reducing the dimensionality of the data can improve performance.

Principal components analysis (PCA): PCA is a statistical technique used for dimensionality reduction and data exploration. It aims to transform a dataset with a large number of variables into a lower-dimensional space while preserving the most important information. PCA accomplishes this by identifying the principal components, which are linear combinations of the original variables. Applications of PCA span various fields, including image [12] [13] and signal processing [14] [15], genetics [16] [17]. It is particularly useful in scenarios where the dataset is high-dimensional and the interpretation and visualization of the data are challenging.

Classification algorithm

k-nearest neighbors (KNN) classification algorithm: The KNN classification algorithm is a supervised learning method which is first developed by Fix and Hodges [18]. The idea of KNN is based on the idiom, "birds of a feather flock together". By picking the k-nearest neighbors of a data point, the unkonwn class label can be determined. Lots of works [19] [20] [21] show the fact that KNN performs well for prediction of diabetes disease.

support vector machine (SVM): Given a set of training datas, where each data is labeled as a binary class, such as 0 and 1, SVM training algorithm creates a model that assigns new examples to the binay labels by making it a non-probabilistic binary linear classifier. In addition, accroding to [22] [23], SVM can also use a method called kernel trick to effectively perform non-linear classification by implicitly mapping its inputs into a high-dimensional feature space.

neural network (NN): Neural network have been used in many fields to deal with intricate datas. With input layer, hidden layer and output layer constructed by neurons, each data in dataset is processed while passing through neurons, layer by layer. After the processing, the outcome can be used to predict. Using back propogation, the accuracy of predictions increase in each training. In order to construct the hidden layer more efficient, NAS(Neural Arcitecture Searching) is used to search suitable structure for hidden layer, increasing the accuracy. According to [24][25], many neural network have been constructed and trained already, with high efficiency and accuracy in prediction of diabetes.

Clustering algorithm

k-means: K-means is a popular and easily implemented clustering method in machine learning and data analysis. With n data points in a dataset, k-means algorithm partition them into k distinct clusters. The algorithm works iteratively and converges to a solution by minimizing the sum of squared distance between the data points and the center of their cluster. K-means is a useful algorithm for clustering data, which is widely applied on many researches, e.g. [26], [27], [28].

Density-based spatial clustering of applications with noise (DBSCAN): DBSCAN is a data clustering algorithm proposed by Ester et al. [29] DBSCAN is particularly effective in discovering clusters of arbitrary shapes and handling noise in the data. Unlike k-means need user specify how many clusters, DBSCAN determine the clusters and noise automatically by the density of data points. This characteristic makes it particularly useful when addressing the datasets where the number of cluster is unkonwn. DBSCAN is the major clustering algorithm in machine learning field, since the ability to discover the number of clusters automatically. And the variants of DBSCAN [30] is also developed widely.

3 Main Process

The main algorithm to process the dataset is shown as below:

Algorithm 1 The Main Algorithm

Require: Dataset
1 Data, Labels ← Dataset
2 Data′ ← preprocess(Data)
3 Konwns, Unkonwns ← classify(Data′)
4 Clusters ← clustering(Unkonwns)
5 Accuracy ← calacc((Konwns, Clusters), Labels)

First, preprocess the dataset, e.g. normalize, apply PCA, apply AE. Second, classify the data after preprocessing. With this step the konwn types and the unknown types will be separated by a certain criterion. This criterions will be varied depending on the classification algorithm. For KNN, the criterion is distance and probability. More specifically, assume a data point x, and the k-nearest data points are $p_1, ..., p_k$. Only those points whose distance between x smaller than L will be marked valid. Denote the valid data points as $p'_1, ...p'_n$, and the corresponding labels are $l_1, ..., l_n$. If this data point satisifies Eq 1, mark it as unkown type.

$$\frac{\arg\max_{t \in \text{types}\{N(t)\}}}{n} < P \tag{1}$$

where P is a manunally set probability and $N(t)$ is the number of type t in those n valid data points.

As for SVM, the criterion born in the designed. Since SVM is meant to be a binary classifier, the SVM classification algorithm must be redesigned. As shown in Algo 2.

After classifying, the konwn types and unkonwn types are separated. The data marked as unkonwn types will be thrown into clustering algorithm, e.g., DBSCAN, k-means. Subsequently, the process is completed.

Algorithm 2 The SVM Multi-classification Algorithm

Require: Train Data, Labels, Test Data
Assumption: Length(Train Data) = Length(Labels) = N, Length(Test Data) = M
for t in Known Types **do**
  for i in $[1, N]$ **do**
    if Labels$[i] \neq t$ **then**
      Labels$'[i] = +1$
    else
      Labels$'[i] = -1$
    end if
  end for
  SVM$[t]$.fit(Train Data, Labels$'$)
end for
for t in Known Types **do**
  for i in $[1, M]$ **do**
    if SVM$[t]$.predict() $= +1$ **then**
      Test Labels$[i] = t$
    else
      Test Labels$[i]$ = UNKNOWN
    end if
  end for
end for

4 Experiment result

The experiment result of arrhythmia dataset is shown in Table 1. And the result of gene expression cancer RNA-Seq data set is in Table 2.

From the result, the fact that SVM performs worse than KNN can be seen. The main reason is because the multiple classification SVMs method designed here can't separate well in most of types. Fig 1 illurates the situation. For type 1 SVM, the negative/positive classification makes the data hard to separate, and also for type 2, 3, etc. This happens even when the kernel trick is applied, though the kernel trick sometimes ease the pain. In the other hand, KNN performs extraordinarily. In arrhythmia dataset, KNN with k-means in raw data gets 53.1646% accuracy, which is the highest accuracy comparing to others methods. And in gene expression cancer RNA-Seq dataset, KNN with k-means in PCA data gets 94.8795%. And KNN with DBSCAN performs well too. This method shows similar performance in these two datasets, which also gets 94.5783% in gene expression cancer RNA-Seq dataset PCA data.

Table 1: COMPARISON OF CLASSIFICATION TECHNIQUES. (ARRHYTHMIA DATASET)

Method	Raw		Normalized		PCA-32		PCA-32 Normalized		AE-32		AE-32 Normalized	
	Search (s)	acc	Search (s)	acc	Search (s)	acc	Search (s)	acc	Search (s)	acc	Search (s)	acc
KNN-Brute-Force + DBSCAN	0.0285	47.4684 ± 0	0.0254	46.8354 ± 0	0.0070	38.6076 ± 0	0.0071	42.4051 ± 0	0.0071	**37.9747 ± 0**	0.0071	**44.3038 ± 0**
SVM (linear) + DBSCAN	1.7269	25.9494 ± 0	8.9285	35.4430 ± 0	0.2186	32.2785 ± 0	0.8162	29.7468 ± 0	0.2169	31.6456 ± 0	0.1552	27.8481 ± 0
SVM (polynomial) + DBSCAN	0.9993	25.9494 ± 0	1.6100	25.3165 ± 0	0.1997	1.2658 ± 0	0.4577	33.5443 ± 0	0.2402	30.3797 ± 0	0.4924	30.2785 ± 0
SVM (RBF) + DBSCAN	0.9915	25.9494 ± 0	1.4681	22.7848 ± 0	1.4328	0.6329 ± 0	11.9417	30.3797 ± 0	13.5147	22.1519 ± 0	24.7346	34.1772 ± 0
SVM (sigmoid) + DBSCAN	3.5272	28.4810 ± 0	6.4731	20.2532 ± 0	1.5779	30.3797 ± 0	0.9797	36.0759 ± 0	0.5284	22.1519 ± 0	0.8430	24.6835 ± 0
KNN-Brute-Force + kmeans	0.0236	**53.1646 ± 0**	0.0343	**50.6329 ± 0**	0.0068	**43.0380 ± 0**	0.0069	**43.0380 ± 0**	0.0069	36.0759 ± 0	0.0080	41.7722 ± 0
SVM (linear) + kmeans	1.7719	25.3165 ± 0	37.9747	37.9747 ± 0	0.2317	25.3165 ± 0	0.8932	27.8481 ± 0	0.2331	24.0506 ± 0	0.1596	20.2532 ± 0
SVM (polynomial) + kmeans	1.0456	25.3165 ± 0	1.4942	26.5823 ± 0	0.2326	14.5570 ± 0	0.4094	28.4810 ± 0	0.2033	24.0506 ± 0	0.4884	25.3165 ± 0
SVM (RBF) + kmeans	34.5382	8.8608 ± 0	43.0936	29.7468 ± 0	110.589	0.6329 ± 0	112.945	1.2658 ± 0	38.7497	22.7848 ± 0	14.1561	27.2152 ± 0
SVM (sigmoid) + kmeans	4.0277	22.6582 ± 0	8.0918	17.7848 ± 0	0.7529	25.3165 ± 0	0.7967	12.0253 ± 0	0.6921	17.7215 ± 0	0.4013	28.4810 ± 0

Table 2: COMPARISON OF CLASSIFICATION TECHNIQUES. (GENE EXPRESSION CANCER RNA-SEQ DATASET)

Method	Raw		Normalized		PCA-30		PCA-30 Normalized		AE-30		AE-30 Normalized	
	Search (s)	acc	Search (s)	acc	Search (s)	acc	Search (s)	acc	Search (s)	acc	Search (s)	acc
KNN-Brute-Force + DBSCAN	14.5101	59.0361 ± 0	10.3013	**66.5663 ± 0**	0.0224	94.5783 ± 0	0.0237	78.3133 ± 0	0.0258	**64.4578 ± 0**	0.0235	59.3373 ± 0
SVM (linear) + DBSCAN	124.593	61.7470 ± 0	610.6730	9.9398 ± 0	0.6466	9.9398 ± 0	0.1193	10.5422 ± 0	0.1407	63.2530 ± 0	0.1122	13.5542 ± 0
SVM (polynomial) + DBSCAN	81.6495	61.7470 ± 0	86.6406	1.2048 ± 0	0.2585	64.4578 ± 0	0.3012	61.1446 ± 0	0.2013	63.2530 ± 0	0.2056	50.3012 ± 0
SVM (RBF) + DBSCAN	X	X	X	X	12.5077	9.9398 ± 0	3.8838	63.2530 ± 0	5.0461	40.3614 ± 0	11.4194	49.6988 ± 0
SVM (sigmoid) + DBSCAN	X	X	X	X	0.6372	71.6867 ± 0	0.8222	65.9639 ± 0	0.6236	44.2771 ± 0	0.2273	38.2530 ± 0
KNN-Brute-Force + kmeans	22.754	**74.0964 ± 0**	6.36577	53.6145 ± 0	0.0212	**94.8795 ± 0**	0.0214	**84.9398 ± 0**	0.0214	42.1687 ± 0	0.0220	**65.9639 ± 0**
SVM (linear) + kmeans	136.408	61.7470 ± 0	664.2860	9.9398 ± 0	0.5914	9.9398 ± 0	0.1077	10.5422 ± 0	0.1274	63.2530 ± 0	0.1084	13.2530 ± 0
SVM (polynomial) + kmeans	81.4276	61.7470 ± 0	81.1669	63.8554 ± 0	0.2003	64.4578 ± 0	0.2167	25.3012 ± 0	0.1780	63.2530 ± 0	0.1930	50.3012 ± 0
SVM (RBF) + kmeans	1772.32	9.9398 ± 0	1800.6	9.9398 ± 0	1.3625	9.9398 ± 0	1.3848	9.9398 ± 0	11.1729	39.7590 ± 0	4.7882	28.6145 ± 0
SVM (sigmoid) + kmeans	190.866	26.5060 ± 0	81.7487	63.8554 ± 0	0.8287	65.9639 ± 0	0.4269	65.9639 ± 0	0.9908	28.9157 ± 0	0.2360	39.4578 ± 0

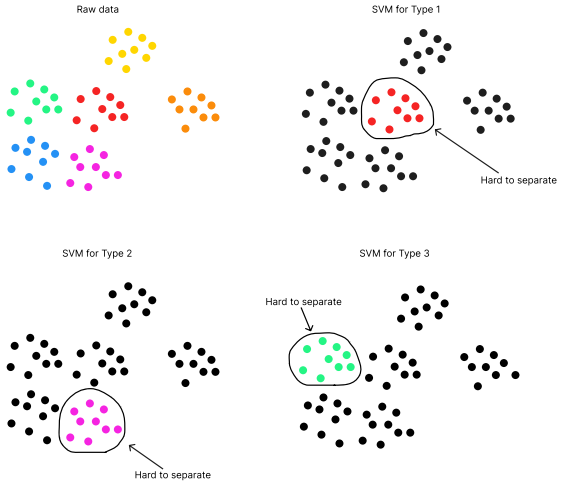

Figure 1: An example that multiple SVMs fail

5 Conclusion

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