

Heart Disease Prediction and Detection Using Association Rule Mining Techniques

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Abstract

Data science mining methods are utilized in the field of medication for different purposes. Mining affiliation rule is one of the intriguing points in information mining which is utilized to produce continuous itemsets. It was first proposed for market bushel examination. Analysts proposed varieties in methods to create incessant itemsets. Creating huge number of incessant itemsets is a tedious cycle. In this paper, the creators contrived a strategy to anticipate the danger level of the patients having coronary illness through incessant itemsets. The dataset of different coronary illness patients is utilized for this exploration work. The information mining strategies-based frameworks could vitally affect the workers' way of life to anticipate heart sicknesses. There are numerous logical papers, which utilize the strategies of information mining to anticipate heart infections. Nonetheless, restricted logical papers have tended to the four cross-approval methods of dividing the informational index that assumes a significant part in choosing the best procedure for foreseeing coronary illness. Pick the ideal blend between the cross-approval methods and the information mining, order strategies that can upgrade the exhibition of the forecast models. This paper means to apply the four-cross-approval methods (holdout, k-overlay cross approval, separated k overlap cross-approval, and rehashed irregular) with the proposed techniques Extended Support Vector Machine and Extended KNN to work on the precision of coronary illness expectation and select the best forecast models. It investigates these procedures on a little and huge dataset gathered from various information sources like Kaggle and the UCI AI archive. The assessment measurements like exactness, accuracy, review, and F-measure were utilized to quantify the presentation of forecast models. Experimentation is performed on two datasets, and the outcomes show that when the dataset is epic (50000 records), the ideal mix that accomplishes the most noteworthy precision is holdout cross-approval with the neural organization with an exactness of 71.82%. Simultaneously, Repeated Random with Random Forest considers the ideal blend in a little dataset (303 records) with a precision of 89.01%. The best models will be prescribed to the doctors in business associations to help them anticipating coronary illness in workers into one of two classifications, cardiovascular and non-heart, at a beginning phase. Successive itemsets are produced dependent on the picked indications and least help esteem. The separated successive itemsets assist the clinical professional with settling on indicative choices and decide the danger level of patients at a beginning phase. The proposed strategy can be applied to any clinical dataset to anticipate the danger factors with hazard level of the patients dependent on picked factors. An exploratory outcome shows that the created technique distinguishes the danger level of patients effectively from continuous itemsets. The early recognition of heart illnesses in representatives will further develop efficiency in the business association.

Keywords: Data Mining; Heart Disease; Feature Selection; Cross-Validation Methods; Data Preprocessing; Classification Algorithms; Productivity; Business Organizations; Frequent Itemsets; Heart Disease Prediction; Association Rule Mining; Data Mining; Medical Data Mining; SVM; ESVM; ANN and EKNN

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Introduction

Data mining is currently broadly utilized in numerous spaces. It assumes a significant part in the clinical field. Step by step, enormous quantities of patients are visiting emergency clinics with the end goal of different medicines. Number of patients' records are expanding in each division in the emergency clinic. In the clinical field, information mining calculations are utilized to mine the secret information in the dataset of the clinical area [1]. The found examples may help navigation and saving of lives. Different information mining approaches like grouping, bunching, affiliation rule mining, factual learning, and connection mining, all have their importance in information innovative work [2]. Affiliation rule mining is the most proficient calculation for removing regular itemsets from enormous information. To discover the successive itemsets, help esteem has been utilized. Support worth of the itemset more noteworthy than or equivalent to help esteem is called regular itemset. On the chance that an itemset is successive, all of its subsets additionally should be regular [3]. Coronary illness is one of the main human executioner sicknesses. In the United States, the reason for death for all kinds of people is essentially by coronary illness. It is an equivalent chance executioner which guarantees roughly 1 million lives yearly. The infection had killed almost 787,000 individuals alone in 2011 and 380,000 individuals every year by coronary illness. At regular intervals somebody has a cardiovascular failure and somebody passes on from a heart-related infection like clockwork [4]. In this paper, the creators proposed another mining strategy to foresee the danger level of coronary illness dependent on picked side effects by breaking down the coronary illness dataset. The expectations of this technique will help the clinical experts in settling on indicative choices to save the lives of patients in danger. Constant infection finding is significant in the business area as these sicknesses persevere over an extensive stretch. The major persistent infections contain joint inflammation, coronary illness, diabetes, hepatitis C, and disease. Internationally, the main source of death is coronary illness due to various reasons like actual inertia, uneven eating routine, evolving way of life, elevated cholesterol, ill-advised nourishment, hypertension, and stress [1]. Accordingly, the early analysis of coronary illness is of vital significance. The World Health Organization assesses that almost 23.6 million individuals will have coronary illness in 2030 [2]. In the globe, a large extent of more established and more youthful individuals is impacted by heart infections. Distinguishing coronary illness at the beginning phase saves people groups' lives and empowers them to make successful treatment and preventive moves at an underlying stage [3].

Literature Survey

Heart illnesses are considered the most significant explanations behind death across the globe. The need to amplify the indicative exactness of coronary illness becomes significant. There is a lot of information put away inside medical service framework; while separating concealed information from the information is fairly poor. Subsequently, we really want to utilize the large size of the clinical dataset and break down information to remove significant information. Information mining is the main innovation that works on coronary illness' quality or nonattendance. This part endeavors to study some new methods applied to information revelation for coronary illness. Many examinations are analyzing coronary illness expectations utilizing information mining methods, as displayed in Table 1. These investigations focus on utilizing just a single strategy of cross-approval with a portion of the information mining arrangement strategies overlooking different methods of cross-approval as displayed in Table 1. Choosing the right cross-approval procedure with information mining, the arrangement strategy will boost and further develop the coronary illness forecast precision. Besides, help doctors in business associations to have a canny framework that assists them with finding heart infections in representatives at the beginning phase. It additionally diminishes the number of times the information base is examined. Incessant itemset mining without the age of restrictive successive example braid was communicated by Meera Narvekar et al. [6]. The ideal affiliation rules are additionally found in the continuous itemset. Alagugowri et al. fostered an anticipated framework to foresee coronary illness [7]. K Means the grouping method is utilized to recognize the dangerous and nonunsafe variables to sort. Tzung-Pei Hong et al. created MFFP-Tree Fuzzy Mining Algorithm to discover the semantic continuous Itemsets [8]. Marghny et al. have fostered another technique to mine successive itemsets by staying away from the expensive up-and-comer age and test handling. It likewise packs fundamental data pretty much, all itemsets, insignificant and maximal length of regular itemsets and data set outputs over and again [9]. Jahangir Kabir et al. proposed an original technique to decide maximal successive itemsets with hereditary calculation [10]. The weighted help measure is presented by Subrata Bose et al. that embraced a reasonable way to deal with mine continuous examples [11]. To mine the incessant

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shut successive examples of worldly exchange information, Antonio Gomariz et al. proposed a ClaSP calculation [12]. To mine incessant itemsets dependent on nodesets, a proficient FIN calculation was created by Zhi-Hong Deng et al. [13]. Hai Duong et al. fostered another calculation with twofold requirements to discover all regular itemsets [14]. Mengchi Liu et al. proposed a HUI Miner (High Utility Itemset Miner) calculation to mine high utility itemset [15]. Umair Shafique et al. executed three different calculations (Neural Network, Decision Tree, and Naïve Bayes) to find fascinating examples from heart patients' information. The outcomes uncover that the Naïve Bayes calculation has the most noteworthy exactness among them [16]. Darshan M. Tank has proposed a calculation to lessen pruning tasks. It utilizes apriori-gen activity to produce the competitor itemsets-2 and furthermore it ascertains support esteem rapidly by embracing the tag-counting technique [3].

System Methodology

Existing System

There are two existing methods that are accessible in profound learning strategies, for example, convolution neural organization and intermittent neural organization. KNN calculation Drawbacks: The disservices are as per the following:

- ✓ Less precision
- ✓ High Time Complexity
- ✓ High Execution Time
- ✓ High Error Rate
- ✓ Less Data Size

SVM calculation downside: The inconveniences are as per the following:

- ✓ Less precision
- ✓ High Time Complexity
- ✓ High Execution Time
- ✓ High Error Rate
- ✓ Less Data Size

Proposed System

There are two proposed techniques that are available in deep learning techniques such as Extended K-Nearest Neighbor (EKNN) and Extended Support Vector Machine (ESVM).

EKNN algorithm Advantages: The advantages are as follows:

- ✓ High accuracy
- ✓ Less Time Complexity
- ✓ Less Execution Time
- ✓ Less Error Rate
- ✓ Large Data Size

ESVM algorithm advantages: The advantages are as follows:

- ✓ High accuracy
- ✓ Less Time Complexity
- ✓ Less Execution Time
- ✓ Less Error Rate
- ✓ Large Data Size

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Experimental Results

The fundamental thought of our framework plan and execution, is to guarantee that the heart disease infection patient's data worked in a manner that can oblige arrangement, sections from their initial expectations. This framework configuration is hence a technique or strong point of depicting the arrangement, parts, modules, interfaces, and information for an appropriate construction to fulfill the fundamentals. There are some spread and joint exertions in the informational collections as far as their construction's evaluation, framework strategy and framework's structure. Implementation or capability is assessed dependent on their yield predictable by the application. Essential specifics have found to consume a large impact in the examination of their system. Given the fitting patients' essential subtleties it brings about a possible construction of a prevalent structure; that in the end fits into our necessary condition. It additionally hopes to lay to an extraordinary degree on the current customers of the current system, through the need specifics.

ESVM Algorithm

Two trials of one or the other CC or MLO seen should be adjusted utilizing the picture enlistment method. At that point, a distinction picture is got by deducting the earlier test from the current test and afterward scaled to the full-range force. The territorial pictures from the refined district proposition are trimmed from the three pictures and scaled to 224×224×3 for each picture, which are utilized for EKNN and ESVM highlight extraction. The three channels are rehashed from one-channel grayscale pictures (e.g., current sweep of 224×224×1) since the pretrained EKNN and ESVM models expect 3-channel pictures. Multi-measurements of three-state highlights (from earlier sweep, current output, and contrast pictures) are made to prepare a LSTM model. For instance, The EKNN and ESVM highlights utilizing ResNet-60V3 of 2048×3 measurements for each view (CC or MLO) of a subject's side (left or right bosom). Remember that earlier sweep consistently relates to the ordinary (sound) status in any event, for a destructive subject. Assume we code sound and carcinogenic as 0 and 1 individually, at that point the ground realities (yields) compared to the three states (earlier, current, distinction) of a destructive view are [0 1 1]. This coding instrument can be handily stretched out to at least two earlier sweeps.

Stage 1: Checks the measure of put-away information from experience. Stage 2: Checks the measure of information being added in the current execution. Stage 3: Checks measure of the yield information is being exact.

In light of the heart disease infection informational index, for example, a complete 198 pictures, our experimentation contained the accompanying thirteen stages:

Stage 1: Introduce the necessary libraries.

Stage 2: Introduce the preparation dataset.

Stage 3: Perform include scaling to change the information.

Stage 4: Producean associateinfo structure with 60-time steps and one yield.

Stage 5: Introduce Keras library with its required bundle of libraries.

Stage 6: Initialization of the ESVM.

Stage 7: Plugin the LSTM algorithm layer and loss regularization technique.

Stage 8: Attaching yield layer in the system.

Stage 9: Accumulate the ESVM.

Stage 10: Start Work with ESVM to prepare the model.

Stage 11: Load the heart disease infection test picture information for 2020.

Stage 12: Anticipated heart disease infection for Dec 2019.

Stage13: Visualize the aftereffects of anticipated and genuine heart disease infection.

In this manner, the perforce of our calculation is discovered to be of more precision, devouring little executing instance of time; specifying the heart disease infection cases in the initial expectation.

EKNN Algorithm

Considering accomplishing more exactness, execution and time intricacy, we are compelled to expand CNN to an all-inclusive CNN (EKNN). Eknn [12] is a class of NN. Arrangement Labeling-Part of discourse labeling and named element acknowledgment. To infer the above benefits, we rolled out certain improvements to CNN (traditional) and get EKNN; by making a group [13, 14] of changes :

Stage 1: Checks the measure of put-away information from experience.

Stage 2: Checks the measure of information being added in the current execution.

Stage 3: Checks measure of the yield information is being exact.

In light of the heart disease infection informational index, for example, an absolute 198 picture, our experimentation involved the accompanying thirteen stages:

Stage 1: Introduce the necessary libraries.

Stage 2: Introduce the preparation dataset.

Stage 3: Execute highlight ordering to change of information.

Stage 4: Make an information composition with 70-time phases and 2 yield.

Stage 5: Introduce Keras deep learning library with all supporting bundles of the library.

Stage 6: Initialize the EKNN.

Stage 7: Enhance the LSTM part and some regularization of loss calculation function.

Stage 8: Enhancement of yield part.

Stage 9: Accumulate the EKNN.

Stage 10: Fitting the EKNN in the preparation dataset.

Stage 11: Load the heart disease infection test picture information for 2020.

Stage 12: Become an anticipated heart disease infection in Dec 2019.

Stage 13: Imagine aftereffects with anticipated or genuine heart disease infection.

Hence, the outcome of calculations they are discovered to be of more precision, devouring little executing time; specifying the heart disease infections in the initial expectation.

Input Datset

Here the input dataset is having 14 columns with target class, i.e., severity level of the heart disease.

4	A	8	C	D	E	F	G	н	1	1	K	L	M	N
1	Age	Sex	CP	Trestbps	Chol	FBS	Restecg	Thalach	Exang	Oldpeak	Slope	CA	Thal	Target
2	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
3	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
5	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
5	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1
7	57	1	0	140	192	0	1	148	0	0.4	1	0	1	1
3	56	0	1	140	294	0	0	153	0	1.3	1	0	2	1
3	44	1	1	120	263	0	1	173	0	0	2	0	3	1
0	52	1	2	172	199	1	1	162	0	0.5	2	0	3	1
1	57	1	2	150	168	0	1	174	0	1.6	2	0	2	1
2	54	1	0	140	239	0	1	160	0	1.2	2	0	2	1
3	48	0	2	130	275	0	1	139	0	0.2	2	0	2	1
4	49	1	1	130	266	0	1	171	0	0.6	2	0	2	1
5	64	1	3	110	211	0	0	144	1	1.8	1	0	2	1
6	58	0	3	150	283	1	0	162	0	1	2	0	2	1
7	50	0	2	120	219	0	1	158	0	1.6	1	0	2	1
8	58	0	2	120	340	0	1	172	0	0	2	0	2	1
9	66	0	3	150	226	0	1	114	0	2.6	0	0	2	1
0	43	1	0	150	247	0	1	171	0	1.5	2	0	2	1
1	69	0	3	140	239	0	1	151	0	1.8	2	2	2	1

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Results

The following are the results for heart disease detection by integrating EKNN and ESVM.

t File Edit View Search Terminul Help rror: Libcuda.so.1: cannot open shared object 2021-03-31 31:33:50.5690792: W tensorflow/strea	barvat@controller:-/Downloads/free-spoken-digit-dataset-maxter file: No such file or directory	
File Edit View Search Terminal Help rror: libcuda.so.1: cannot open shared object 2021-03-31 13:33:50.500792: W tensorflow/strea	file: No such file or directory	
<pre>rror: libcuda.so.1: cannot open shared object 2021-03-31 13:33:50.500792: W tensorflow/strea</pre>	file: No such file or directory	
302-80-31 1333359.368669:1 1 consort/ov/stree c (controller) jnsc/stree/two/rotta/work/motta/w	m_executor/cods/cods_friver-cc:326] failed call to cint: UMXAMM_ERROW [28, m_executor/cods_ded_sciencestics(c:iii) knewni fiver dees not appear to be pressure to the second s) moning on this mos newPT Deep Neural N 1ces not set asses are emabled (uracy: 0.823 uracy: 0.823 uracy: 0.823 uracy: 0.823 uracy: 0.823 uracy: 0.823 uracy: 0.823 uracy: 0.823 uracy: 0.823

4.2 illustrate the execution flow through Epoches on Heart disease dataset from Google database, UCI, and Kaggle dataset.



Fig 4.3 illustrates the execution flow through Epoches on Heart disease dataset from Google database, UCI, and Kaggle dataset.

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Fig 4.4 illustrates the CPU utilization according to the number of Epoches on heart disease dataset from Google database, Microsoft DB, Amazon, and UCI.



Fig 4.5 illustrates the CPU utilization according to the number of Epoches on Heart disease dataset from Google database, Microsoft DB, Amazon, and UCI.

Evaluation Methods

We used the following methodologies to demonstrate and assess the effects of our suggested technique on EKNN and ESVM. Actual positive (AP), Untrue Positive (UP), Untrue negative (UN), and Actual Negative (AN) are initially defined on an individual basis to investigate the confusion matrix. Due to OP, the number of cases was effectively predicted as required. At the same time, the number of examples required was incorrectly estimated due to B measures.

Quality = AP + UN/AP + UP + AN + UN Preciseness = AP/AP + UP

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Callback = AP/AP + UN F-measure = 2 x Preciseness x Callback/Preciseness + Callback

Fig 4.5 illustrates the execution flow through epoches between data loss vs accuracy, on heart disease dataset from Microsoft, Amazon, and UCI datasets. For exhibiting the likelihood of illness, every data set and all parameters are taken into account, and the preciseness of jeopardy prediction are supposed to rely on diverse assortment highlights of clinical information. Which is, the higher in the exactness, the better the element presentation of the disease becomes. The precision rate in our study was 81.22 percent and 85.93 percent.

Execution Time / Time Complexity

It has been discovered that our methodology takes 50% less time than other existing techniques. The use of a graphic processing unit (GPU) and a tensor processing unit (TPU) can reduce this time even more (TPU). The time it takes to complete this task is also dependent on the system's performance. Finally, the system performance is determined by the system software and system hardware.

Data Input

As previously said, our experiment will take into account 198 images. As a result, the chart looks like this:



Figure 4.6: Heart disease dataset number of processors vs. execution time.

Fig 4.6 illustrates the execution epoches between accuracy and number of iterations of the given dataset, that is, heart disease dataset from Microsoft and Amazon dataset.



Figure 4.7: Execution time between heart disease dataset vs. Number of Processors.

Fig 4.7 illustrates the execution epoches between Accuracy and number of iterations of the given dataset, that is, heart disease dataset from Microsoft and Amazon dataset.

A 1	1	1 1	1	0	1	0	1	a	a	1	6	a	a	0	0	1	a	1	0		0	a			0	0	0	0					0		
1 1	a	1 1	1	1	a	1	a	a	1	1	a	1	a	1	a	1	a	a	a	a	a	a	a	a	a	1	1	a	a	1	a	a	1	a	
0 0	1	A 1	a	â	0	0	a	a	a	1	1	9	1	a	a	a	1	1	a	1	a	1	ñ	1	a	1	1	a	1	1	å	1	6	1	
0 1	0	0 0	0	0	1	0	0	0	1	1	0	0	1	0	1	0	1	1	0	1	0	1	1	1	1	1	0	0	0	1	0	0	ø	0	
0 0	1	1 0	1	0	1	0	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	1	1	0	1	1	0	0	1	0	0	0	1	
10	0	0 1	0	0		0	0	0	0		0	0	0	0	0		0			0	0	0			0	0		0						0	
0 1	0	0 0	0																0																
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ma	cr	o a	vg				0	.99	9			0	.99	9			0.	.99	,				279												
eigh	te	d a	vg				0	.99	9				.99					99)				275												
ccur	ac	y:	0.	99:	27	27	272	27	272	27	27																								

Fig 4.8 illustrates the execution time between loss and accuracy of the given dataset, that is, heart disease dataset from Microsoft and Amazon dataset.

Parameter	EKNN	ESVM
Accuracy	83.12	99.27
Loss	46.88	49.08
Precision	79.55	98.23
Epoches	10	10
Time Complexity	0(n ³)	0(n ²)
Data Size	275	275

Table 1: Heart disease dataset with EKNN vs ESVM.

Table 1. illustrates the comparison of heart disease detection using EKNN vs ESVM with parameters loss, accuracy, time complexity, data size, and epoches of the given dataset, that is, heart disease dataset from Microsoft and Amazon dataset.

Conclusions

In the proposed strategy, manifestation addressing sections and patient record addressing columns are eliminated from the additional examination with the chance that they do not fulfill the picked rules. The proposed technique is applied over a coronary illness dataset of 1000 records of patients experiencing different heart-related infections. The forecast results are empowering and the effectiveness of the strategy in successive itemset ages is better compared to existing strategies. This paper is novel since it looks to add to the flow writing discussion and the feature the effect of applying the four cross-approval methods to information mining calculations to find heart sicknesses early. The logical oddity of the paper additionally comprises of a leading large scope correlation between the four-cross approval with the most famous and significant information mining arrangement procedures (Linear Discriminant Analysis, Logistic relapse, Support Vector Model, KNN, Decision Tree, Naïve Bayes, Random Forest, and Neural Network). The expectation models endorse the significance of parting datasets utilizing the four procedures to choose the best forecast model with the most elevated precision. The test was led on two datasets, Kaggle and UCI Cleveland, to observe the best forecast models, which accomplished the most noteworthy precision. We decide the best forecast models and afterward suggest these models for doctors in business associations to save the existence of representatives. The outcomes showed that the best two information mining grouping strategies, which acquainted the most elevated precision to foreseen coronary illness, are holdout cross-approval with a neural organization and calculated relapse in a large dataset. Rehashed Random with Random Forest and holdout with KNN they have the most noteworthy exactness in the little dataset.

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