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K-Means Based Regression Model for Gene Function

P.Hema,
Assistant Professor,
Department of Mathematics,
*R.M.K. College of Engineering and Technology, RSM Nagar,*GummidipoondiTaluk, Puduvoyal, Thiruvallur, Tamil Nadu, 601206, India,
hemaraghav74@gmail.com

ShwetambariPandurangWaghmare,
Assistant Professor,
Department of Mathematics,
Bharati Vidyapeeth College Of Engineering
Belpada, Navi Mumbai.
shwetambari.deore@bvcoenm.edu.in

J.SujiPriya,
Assistant Professor,
Department of Master of Computer Applications, Sona College of Technology,
Salem-636 005, Tamil.Nadu.
sujipriya@sonatech.ac.in

RamakrishnanRamanathan, *Associate professor, Department of Information Technology, Vignan's Foundation for Science, Technology and Research,*
Guntur,Andhra Pradesh,India,
ramki21in@gmail.com

V.V.SatyanarayanaTallapragada,
Professor, Mohan Babu University,
Tirupati, Andhra Pradesh India ,
satya.tvv@gmail.com

Dhiraj Kapila,
Associate Professor,
Department of Computer Science & Engineering, Lovely Professional University,
Phagwara, Punjab, India,
dhiraj.23509@lpu.co.in

Abstract—This challenge has been overcome by developing a broad platform based on the K-Nearest-Neighbour (KNN) methodology for functional genomic estimation. KNN was chosen because of its usability or adaptability by incorporating distinct information formats, but also by adapting to unusually extracted features. Conventional KNN algorithms have a flaw in that their efficiency often depends on the random selection of a statistical method, particularly when combined with enormous data sets. We employ estimation techniques to deduce a measure of similarity as a weighted summation of every series various foundation clustering algorithm, which aids in locating the neighbors who are most probably in the same category also as gene product. In addition, they propose a new community consensus to generate insurance ratings to assess projected performance. An approach could be used to resolve difficult interclassification situations. By considering data generated through transcripts or sequence information, they apply this concept to molecular biological estimation based on three well-known categories of Salmonella typhimurium. By extending heterogeneous data sets, they show that our technique outperforms conventional KNN techniques, but is also equivalent to support vector machine (SVM) technologies. We also show if merging separate information providers could significantly improve prediction performance.

Keywords—Support vector machine; K-Means; heterogeneous data; multi-way categorization

I. INTRODUCTION

The rapid advancement of genomic sequence information over the last generation, understanding the biological processes of genes involved substances have become an important approach in article era. On the basis of appropriate biomedical information, computational strategies have been introduced to predict expression profiles [1]. For decades, approaches based on pattern resemblance, like as bloated, were used to annotate determine the sequence chromosomes performance [2]. Since subsequently, a range of new biological financial information, such as gene co-evolution patterns, nutrient fusion processes, transcriptomics information, enzyme production, and nutrient associated issues, were used for operational forecasting [3]. Despite the abundance of whole sequences across hundreds different organisms, either of these methodologies used in combination still creates a bigger number of genes annotated [4].

Combining various data sources for operational forecasting would be a crucial next stage. Various prediction analyses for integrating heterogeneous information have been presented [5]. A supervised classification methodology based on the Markov random field (MRF) concept is employed to describe the enzyme effect in relation of physical processes, biological conversations, and cell proliferation.. When contrasted with using a single quantity of analysis, they determined that using many information sources boosted predictive performance. Investigators attained 87 % affectability or 57 % validity when applying the MIPS classification technique to yeast posttranslational modifications forecasting [6]. Another drawback of their methodology is that it is entirely based on binary coupled linkages. Due to quantization, there could be a loss of data for observed variables such as transcriptomic observations. SVMs have also been improved to handle diverse large datasets [7]. Commonly diagnosed concatenates the relevant features of each data frame, moderate computation provide the associated kernel vectors, while final assimilation includes the different variables from each data document's SVM [8]. More new studies [9] suggest a method for successfully combining numerous units. The challenge of aggregating harmonizing was formulated as a combinatorial optimization problem that may be addressed with moderate computation. Component (nine) departs evidence [9] proposes a way for optimally combining numerous cones.

In this paper, they propose K-nearest-neighbor (KNN) methodologies as a possible solution to this issue. KNN techniques, despite their complexity, are some of the highest performance in a wide range of classification tasks [10].Because KNN configuration contains no assumptions about nature information, they are particularly effective when the classification algorithm was asymmetric or a class included several implementations [11].For biomedical research classification methods, where substantial academic are intrinsically ambiguous and several categories cannot be classed by a simplified example, KNN's adaptability is extremely useful.

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This same original KNN's primary concept is as follows: Create a set of quantitative attributes to characterize each piece of information, and then choose a measure to quantify the similarity of pieces of information predicated on all characteristics, such as Euclidean distance [12]. Furthermore, balanced measure, selects the KNN elements in training instances for a destination address, or allocated to the democratic congress of its peers in a group. This technique's performance is impeded by the arbitrary adoption of a statistical technique, especially for large datasets with related created attributes of various kinds and scales [13]. Moreover, the computational burden issue afflicts conventional KNN methods. In a high-dimensional structure, the neighborhood of a fixed location becomes pretty limited, resulting in massive variability. Our methodology alters a usual structure. They develop numerous "foundation" statistical features, among couples of sample points, one estimate from each data provider, rather than creating a separate "universal" matching score among the new providers [14]. Then, based on the fundamental characteristics, they try to maximize the probability of a couple belonging to the different category. The probability calculation could be handled as a typical prediction model in this style.

As previously, the predicted conditional probability should be used as a universal statistical method to select the KNN neighbors. Another of the framework's significant benefits is that even the standardized data system was normalized and their connection is managed instantly through stalling, enabling one to design one clustering algorithm at a moment from a particular dataset while disregarding related link [15-16]. In some ways, our method is analogous to the fractionation process kernels. Each KNN statistical method is equivalent to an SVM kernel, with the exception that the earlier does not have to be moderated, allowing for more formability. Lanckriet's technique incorporates kernel grading with the objectives of increasing SVM classification accuracy. The base similarity metrics are evaluated in our methodology to find the "greatest" k nearest neighbors', who is most inclined to share the different category of the target destination, and so provide the most accurate forecast [17-18]. By decreasing the uninteresting dimensionality of the input space and pushing more essential neighbors' closer to the target location, this method also helps to ease the computational burden.

II. Materials and Methods

The summary is a short summary of our methodology: During the training stage, they estimate the foundation statistical features for all genes in the training dataset and use a regression technique to integrate them into a universal mutual information. In the classification process, they identify k nearest neighbors in the training dataset based on the learned mutual information for a gene with uncertain operational categories, and then apply a customized election system to provide a list of recommendations using posterior probability. Two important aspects are the intricacies of its calculations.

In other aspects, they try to calculate the probability of a set of genes belonging to the same category as a consequence of a set of structural clustering algorithm, which operate as the universal statistical method for determining the closest neighbors. This measurement, in a perfect world, would award a value of 1 to all pairings in the same category and a value of 0 to couples in other categories. Depending on this assessment, the nearest neighbors are in the same class as the template strand, resulting in a prediction. Furthermore, due to the limitations of both collecting data and knowledge on correlating the parameter h, the learning, inference likelihood is only an estimate in practice. Nonetheless, it is an inexpensive KNN framework that incorporates the essential, necessary insights. The matching constant h belongs to the category of traditional regression and classification. (1) To counter this issue, we used two prediction techniques: linear regression or regional prediction.

Let $T_x = \langle l_x^1, l_x^2, \ldots . l_p^n \rangle$ be the feature vector

$$log \left[\frac{xr\{D_x = 1 | Z_x\}}{xr\{D_x = 0 | Z_x\}} \right] = \int \partial^v Z_x + \rho \quad (1)$$

This varies and is the scale parameter. Because the log posterior probability is asymmetric, supervised classification predictions and could be determined quickly. The probability method is utilized as the statistical method, and the acquired training algorithm reflects the perceived importance of each characteristic. To capture the connections between features, the statistical method might be expanded to complex numbers, presumably including interaction components.

Another way for resolving this issue is to use native instability. In essence, this method calculates the correction factor to matching a different, yet basic predictor (such as a quadratic equation) to each target position simultaneously. Only measurements that are close to the desired location should be used to validate the data, and their ranges for the target position are evaluated accordingly. The local extrapolation model provides more versatility than regression analysis since the prediction curve could mimic any smooth variable. By comparing each simulation in a limited region determined collectively by all the features, this technique could easily incorporate the connection between the characteristics. Regional extrapolation, on either extreme, is more computationally intensive but less extensible. At each random value, a somewhat compact neighborhood is designed to satisfy local algorithms. With discrete features and perimeter data sets, local extrapolation could have problems.

III. Proposed Work

We constructed a basic KNN technique using Euclidean distance, adjusted so that separation relating to an individual source data has a maximum value of 1, assess the performance to the logistic regression both component weighting and the polling mechanism. The basic KNN approach finds this same operational category that receives to most votes from the KNN neighbors provided the k similarity measure. To share power across sections having fair elections, the one of the quickest distance across all sympathetic friends is chosen. We also evaluated the RB-

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KNN approaches against the naive Knn algorithm, which is based on all permutations of datasets.

On the different database, we evaluated the SVM algorithm to evaluate RB-KNN to other approaches for merging massive datasets. They found that combining the kernels delivered the best results out of three ways of combining several data sources: concatenate relevant features, integrate the kernels, and combined the differentiator scores. This approach is an unadjusted variation of the methodology, which determines the strengths of each kernel using a moderately computing technique. Even though the latter option appears to be superior, the necessary technology is temporarily unavailable. Interestingly, in many circumstances, the approximate methodology is almost as good as the weighted method, particularly when all picked kernels have similar estimates of future (William Stafford Noble, personal communication), which seems to be the case in our scenario.

The prologue parameter is a kernel, just as the block signal, because it could be expressed to the embedding of the prologue metricizing bring the three particles together, divide the expressive kernel by 8 and put them together so that all three kernels have comparable proportions. For a variety of purposes, we did not employ the chromosomal separation in SVM. First, because the proximity has been calculated on a single chromosome, an acceptable kernel is not immediately evident. They used the partial derivative of either the Euclidean distance row columns as a kernel in the experimental kernel map approach. This same generated SVM, unfortunately, performs poorly (ROC score =. 581). Furthermore, provided another three datasets, the experimental findings for such RBKNN techniques in Table I show suggesting chromosomal separation are repetitive. As a consequence, the SVM is not penalized over neglecting this data.

TABLE I. VALIDITY OF PERFORMANCE

Combination	Navie km	Glm	loss
1111	0.48	0.59	0.65
1011	0.56	0.52	0.65
1010	0.48	0.49	0.51
1000	0.41	0.42	0.48
0100	0.45	0.47	0.54
0010	0.39	0.65	NA
0001	0.39	0.65	NA

IV. RESULTS AND DISCUSSION

To highlight the capability of proposed strategies regarding component grading and casting, they will first evaluate the results of RB-KNN and that of conventional KNN techniques in this chapter. Furthermore, we'll contrast our methodologies with an SVM-based strategy for combining large datasets. Eventually, we'll look at effectiveness based on the structural categories. A short description of the relationship among posterior probability and forecasting models has been included, as well as aggregate information based on all three classification systems. Furthermore, the chapter discusses the findings of erroneous assumptions, they would examine several of the difficulties with this issue. All of KNN techniques they examined were titled that after techniques, which could be keen (deluded KNN methodology), glm (logistics extrapolation predicated KNN), or less (regional stagnation predicated KNN), but then the information sources. In the sequence of interpretation association, chromosomal separation, block signal, and paralog signifier, this requirement usually expressed in sequence in that each value denotes whether a collected information was included. For instance, Laos. 0001 denotes a KNN approach depending on local extrapolation that only uses the prologue signal, while knn. 1111 denotes a naive KNN method that uses two, four data collections. They used "svm. Comb" to test SVMs on a group of statistics that included the statement, restrict, and paralog statistics. They also tried SVMs in this scenario, termed "svm. Exp," because expression data independently is often employed during operational categorization. They did the 5-fold classification algorithm across each experiment or presented overall results.

4.1 Comparative approach

We evaluated various RB-KNN approaches toward the naive KNN methodology in order to see how effective they are in integrating different data sources using appropriate feature grading and casting algorithms. We investigated the predictive ability of each additional source of information or whether integrating more data sources significantly improve by testing each approach with varying configurations of different databases. By standard, the KEGG classification methodology has been used except otherwise stated. They only looked at the 1603 genes that were allocated to operational classifications. Each gene could be classified into numerous functional categories, with a maximum of 2144 operational categories. Because the naive KNN strategy allows only one forecast for each transcript, they choose the greatest single estimate for each genotype for RB-KNN methodologies the ensure an equal assessment. We discovered also that naive KNN's effectiveness appears highly dependent to k, this same neighborhood radius, but that lower k is typically preferred.

They also discovered that throughout the RB-KNN techniques, using more sources of information seems usually invariably advantageous. Considering some other three data sources, the dataset includes "1011" delivering exceptional results throughout our studies, implying that chromosomal separation is really a superfluous source of data for operational forecasting. The effectiveness of RB-KNN algorithms for information source "1111" is nearly always different downweighting unnecessary features. In glm. 1111, Table 2 provides algorithm values to every source data. Introducing chromosomal proximity to some other three sources of data, on either extreme, leads of considerable fall in effectiveness using naive KNN. Even though only one or two information systems are utilized, loss performed better than film, fore more the variation in performance in different approaches approaches trivial when more information sources were employed. Weights to every data provider are listed in Table II.

TABLE II. DATA WEIGHTS

Sources of Data	Expr Correlation	Chromosomal distance	Block indicator	Paralog indicator

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Weights(w)	1.96 ± 0.15	0	71 ± 0.06	4.61 ± 0.10

The reliability of the RB-KNN and Svm classifiers was evaluated. We employed transmitter operational conditions (ROC). A ROC curve shows the relationship between the likelihood of detection and responsiveness as a function of a weighting factor. Because this is an inter classification task, the overall amount of forecasts typically computed as the sum of the group of genes or the number of subjects, although in the case of KEGG is 1603 * 18 = 28854. Each forecast has a grade assigned to it, such as RBKNN probability value or the SVM differentiate quality. The positive result frequency and sensitivity for one spot also on ROC curve have been computed using forecasts beyond a specified tolerance, which are sorted depending the overall ratings. (One downside of using differentiator ratings to grade forecasts is that they're not equivalent across categories because each group has its own SVM.). Fitting a deterministic sigmoid activation function depending on characteristic ratings for each class separately would be a reasonable solution. They anticipated the instrument for assessing to become more consistent across categories therefore generate higher standing, although the associated ROC rating seems to be definitely lower, just 0.81 as opposed that 0.91 throughout the existing approaches, therefore they didn't use it.

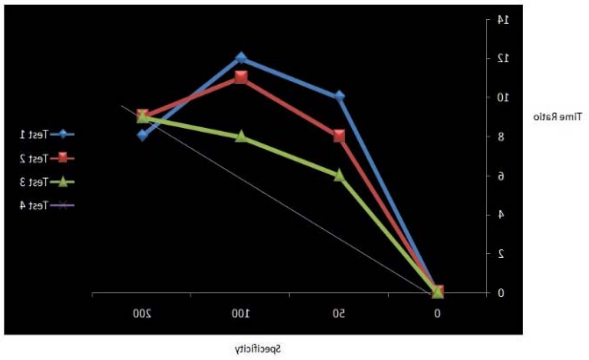

Fig.1. ROC curve assessment

In Fig.1. represents the ROC curves of a few of the techniques they investigated are shown in Table 1. It's worth noting that the overall amount of erroneous categories in this challenge is approximately an astronomical amount more than the proportion of actual categories. Although the techniques' ROC scores seem to be relatively similar, they are only concerned inside this portion of ROC curves where the prediction error relatively minimal in practice. The techniques perform very differently in this area. The ROC curves reveal that the predictive capacities of all the information sources are relatively close, including prologue signal, chromosomal separation, block signifier, and transcriptional relationship listed from greatest to worst. Glm.1000 is a swimmer. The efficiency of methods depends on differential expression is fairly similar, maybe less so. 1000 is a significant improvement. Furthermore, due to increased model adaptability, Laos. 0100 outperforms glum. 0100 (data not shown).

4.2 Performance measurement

Fig.2 demonstrates the vulnerability of four strategies (Exp, Laos 1000, SVM, glum 1111, classifier. Comb) at 50% right for all functional domains. They categorized all estimates based on the genuine operational multiple genes for each technique. Then, to every class, we chose the estimates that were above a 50% confidence criterion and determined the proportion of genes that were successfully predicted. Except for class 15, we found that loss. 1000 significantly beats SVM, Explain in class. This is particularly true in class 17, where swim. Explain has a susceptibility of 8.7% and less. 1000 has a sensitivity of 71.7 percent so at boundary limit. SVMs employing quadratic or circular kernels also perform badly (0 percent, 10.9 percent conversely, susceptibility). That demonstrates that classification methods for class 17 has a unique feature that cannot be captured using SVM modules, but could be detected using RB-KNN techniques in Fig.2.

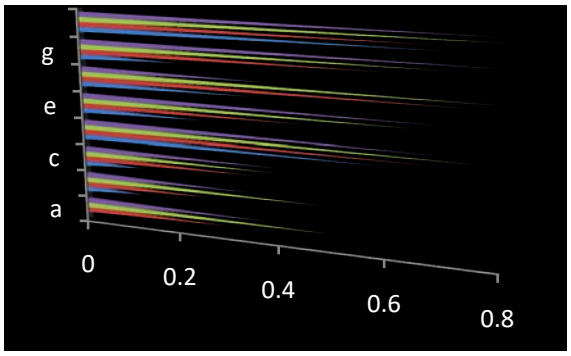

Fig.2. Sensitivity, accuracy in organizational procedures

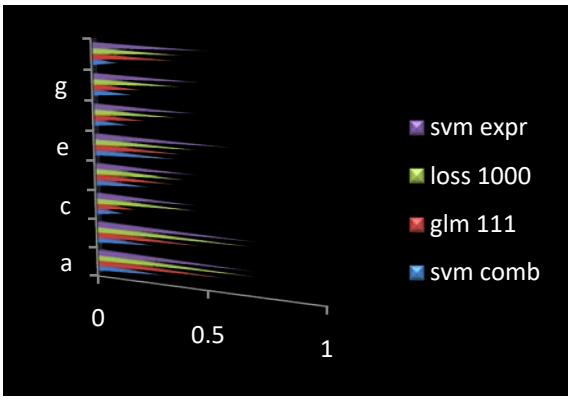

Fig.3. Proposed with existing algorithm comparison

Through all operational categories, glum, 1111 and swam. Comb has reasonably similar effects; both are preferable to technologies based solely on microarray datasets in Fig.3.. Both classes 20 (Cell Digestibility) and category 13 (Interpretation) have excellent prediction performance when all four techniques are used. In darkness, the ROC values for such 2 categories, 1111 are 0.97 and 0.96, correspondingly. Most genes in these 2 categories are recognized to be co-regulated, and most are expressed in integrons, which explains the excellent categorization findings for such 2 categories. Because many representatives of Class 17 (Signal Effector) and Class 16 (Membrane Mobility) have comparing specific protein structures, the prologue signal is useful in both categories .It

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seemed gloomy. 0001 has a responsiveness of 80 percent for another 2 categories, but 76 percent in the other.

They looked at a set of erroneous forecasts with a great deal of confidence. Many of them would be caused by the fact that genes can correspond to different functional groups. Various classification approaches for such genes could focus on the importance of their functional activities, and comments may be lacking. Furthermore, because all genes connect with one another in some way, the beforehand such are hazy. It's hard to see the difference across class 1 "Complex Carbohydrate Respiration"Glucose Metabolism" are two categories. Several genes engaged in signalling pathways (class 17) processes, for instance, are also participating in membrane integrity (class 16). False negatives, or correct forecasts with low levels of confidence, were also examined.

Heterogeneous or small method categories cause a lot of false negatives. Class 10 (Metabolites of Bioactive Molecules), in an instance, has just 24 genes in their database but can be divided into nine classifications. Such classes are notoriously hard to characterize. False negatives are further exacerbated by deserting neighborhoods caused by the lack of knowledge. Approximately 20% of genes in KEGG have no operationally evaluated paralogs, co-expressed genes, or chromosome neighbors with identified measures larger than 5, implying they had professionally foundered genes, evaluated paralegals, or chromosome relations. The only way to overcome this problem is to provide additional training examples.

This research makes a major addition by proposing a new methodology to merging heterogeneous data in the KNN paradigm, which comprises two essential elements: a regression-based grading methodology and a deterministic election process. The prediction model, which takes into account their exceptional acceleration factor affecting, encompassing their interconnections, affects the intensity of each data provider. An election technique made inferential analysis easier by combining component category suggestions from the KNN neighbors, but also producing a sorted list of recommendations having posterior probability. This method also permits a gene to be classified into numerous performance categories. The local estimation technique performs better via one of two information sources, likely to increase model variability, while linear model is more resilient or adaptable, according to our findings. We've shown that merging four datasets produces good outcomes. We produced incredibly competitive performances in comparison towards the Neural Network Based technique, which mixes large datasets. Their ROC curves are extremely similar in accuracy was obtained larger than 50%. SVM performs better for genes located near to class boundary, but at the expense of a significant false alarm rate. RB-KNN algorithms have the excellent potential at same degrees of effectiveness: SVM requires tractor trailer support vectors, whereas RBKNN supports unlimited interpersonal correlations. Furthermore, RBKNN generates supplemental data (e.g., nearest neighbors along corresponding resemblance ratings) to aid throughout the discussion of the data during post-processing.

V. Conclusions

There are several ways in which we might enhance our techniques. We created a single prediction model for all data in the testing phase in this investigation. The prediction accuracy of each source of data, on either extreme, may range from grade to grade, and they may be evaluated accordingly. An amount of training data is such benefit of our current strategy; one disadvantage is the clear lack of performing this task. A one-class-one-model strategy, on either extreme, is the absolute antithesis. For categories with massive populations, an alternative approach is to construct class-specific models. The regression analysis can be very problematic when parameters are highly correlated. To construct more predictive results, you can use principal deconstruction or controlled extrapolation approaches like regression. Another possibility is to employ improvement complex predictive model. For example, from 106 types of experiments, we only derived one fundamental similarity measures, transcriptional association. Nonetheless, some palettes are more useful than some others, or the relationship between them might vary greatly depending on the number of studies used. By employing Correlation analysis depending on all 106 trials, such evidence is omitted. One method would be to divide the operations across different subgroups and calculate a baseline semantic similarity for each group. They could be immediately combined with other sources of data, such as chromosomal similarity, or they can be blended using regression techniques, which could then be correlated with other information. A pyramidal techniques have advantages to use only a few terms for each extrapolation, making it more durable than a conventional framework that incorporates all characteristics. They found overall optimism ratings are directly correlated with forecast performance, however, the association is not continuous, and the values expand as the size of such neighborhood grows. We would want a scoring system which is the more regular overall reliability of standardized methods.

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