Chronic Kidney Disease Prediction using SingularValue Decomposition (SVD)

PROJECT REPORT 1

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Abstract

Chronic Kidney Disease (CKD) is a significant global health issue, with early prediction and diagnosis being essential to improving patient outcomes and reducing healthcare costs. This paper presents a machine learning approach for predicting CKD using Singular Value Decomposition (SVD) as a dimensionality reduction technique. SVD is employed to reduce the high dimensionality of the CKD dataset, enhancing computational efficiency while retaining the essential predictive features. By transforming the dataset into a lower-dimensional space, SVD enables improved model performance and reduces the risk of overfitting, which is crucial for models trained on limited medical data. The proposed model demonstrates promising accuracy in CKD prediction, highlighting the effectiveness of SVD in managing high-dimensional healthcare data and improving the interpretability of the model. This study suggests that SVD can serve as a valuable preprocessing step for CKD prediction models, contributing to more robust and efficient predictive healthcare solutions.

1 Introduction

Chronic Kidney Disease (CKD) is a progressive medical condition characterized by the gradual loss of kidney function over time. It poses a serious global health challenge, affecting millions of people worldwide, with an increasing prevalence due to factors such as diabetes, hypertension, and an aging population. Early diagnosis of CKD is crucial as it allows for timely intervention, which can slow disease progression and improve patient outcomes. However, CKD often remains undetected until it reaches an advanced stage, highlighting the need for effective predictive tools to identify high-risk individuals early on.

Machine learning techniques have shown significant potential in predicting CKD, utilizing vast amounts of medical data to uncover hidden patterns and risk factors. However, these datasets often contain a high number of features, which can introduce noise, increase computational complexity, and lead to overfitting in predictive models. Dimensionality reduction techniques are therefore essential in transforming high-dimensional data into a more manageable form, enhancing model performance and interpretability. In this study, we employ Singular Value Decomposition (SVD) as a dimensionality reduction method to optimize CKD prediction. SVD is an efficient linear algebra technique that decomposes a dataset into orthogonal components, capturing the most informative aspects of the data while reducing its dimensionality. By applying SVD to the CKD dataset, we aim to retain only the most relevant features, thereby improving the predictive model's efficiency and reducing its susceptibility to overfitting. Furthermore, SVD enhances model interpretability by revealing underlying data structures, making it a valuable tool in medical data analysis.

This paper is organized as follows: Section II provides a review of related work, discussing previous approaches to CKD prediction and dimensionality reduction. Section III describes the dataset, preprocessing steps, and the methodology used, including

the SVD application and predictive model training. Section IV presents the results and evaluates the model's performance. Finally, Section V concludes the study with a discussion of findings, limitations, and future research directions.

2 Literature Survey

The prediction of Chronic Kidney Disease (CKD) has been a focal area in medical research due to its significant impact on public health. Various machine learning approaches have been explored to improve the accuracy and reliability of CKD prediction models. Early studies focused on traditional statistical methods, such as logistic regression and linear discriminant analysis, which provided initial insights but were often limited in handling large and complex datasets [1].

In recent years, more advanced machine learning algorithms, including Support Vector Machines (SVM), Decision Trees, and Neural Networks, have shown promise in the field of CKD prediction [2, 3]. For instance, Kusiak et al. [4] demonstrated the effectiveness of SVM and Decision Trees in predicting CKD with reasonable accuracy, while Shankar et al. [5] showed that neural networks could achieve higher predictive accuracy when trained on large, diverse datasets. Despite these advances, the high-dimensional nature of medical data, which often includes redundant or irrelevant features, remains a significant challenge.

To address this, researchers have employed dimensionality reduction techniques such as Principal Component Analysis (PCA) to reduce noise and improve computational efficiency. PCA has been widely used in medical datasets to identify and retain the most informative features [6]. For example, Ahmed et al. [7] applied PCA for feature reduction in CKD prediction, achieving enhanced model performance and interpretability. However, PCA has limitations, as it assumes linearity and may fail to capture complex interactions among variables.

Singular Value Decomposition (SVD), an alternative dimensionality reduction technique, has gained attention for its ability to handle high-dimensional data effectively by decomposing it into orthogonal components. Unlike PCA, SVD does not rely on eigenvalue decomposition, making it computationally advantageous for large datasets. Studies have shown that SVD can improve model accuracy by reducing feature dimensionality while preserving essential data characteristics [8, 9]. For instance, in cancer and cardiovascular disease prediction, SVD has demonstrated success in reducing model complexity and improving interpretability [10].

Although SVD has been applied to a variety of medical prediction tasks, its application in CKD prediction remains underexplored. Given the importance of early diagnosis in CKD and the complexity of its underlying data, there is a growing interest in evaluating the effectiveness of SVD in this domain. This study aims to fill this gap by employing SVD as a preprocessing step for CKD prediction, examining its impact on model performance and efficiency. Through this approach, we seek to enhance the predictive accuracy and interpretability of CKD prediction models, potentially offering

a more robust tool for early CKD detection.

3 Preposed Methodology

This study aims to predict Chronic Kidney Disease (CKD) using a dimensionality reduction approach based on Singular Value Decomposition (SVD), followed by a logistic regression classifier. The methodology involves data preprocessing, dimensionality reduction with SVD, model training, and evaluation.

3.1 Data Preprocessing

The dataset used in this study consists of various features related to patient health, such as age, blood pressure, and blood glucose levels. Initial preprocessing steps include:

1. **Loading and Checking Data**: The dataset was loaded, and columns were inspected to identify target and feature columns.
2. **Binary Encoding of Target Variable**: The target variable, "class," was converted to a binary format with 1 for "ckd" (indicating CKD presence) and 0 for "notckd" (indicating absence).
3. **Handling Missing Values**: Missing values in the numerical feature columns were replaced with the column mean, ensuring no loss of data and enabling a consistent data matrix for subsequent analysis.

3.1.1 MATLAB CODE

```
% Preprocessing for CKD Analysis

% Load the dataset
data = readtable("C:\Users\hp\OneDrive\Desktop\SVD projects\siva\
    kidney_disease.csv");

% Check column names to confirm the target column name
disp(data.Properties.VariableNames);

% Convert 'class' (or target) column to binary (1 for 'ckd', 0 for '
    notckd')
if iscell(data.classification)
    data.class = strcmp(data.classification, 'ckd');  % Returns
        logical array (1 for 'ckd', 0 for 'notckd')
end

% Define numerical columns for SVD (update as needed)
numericalColumns = {'age', 'bp', 'bgr', 'bu', 'sc', 'sod', 'pot', '
    hemo', 'pcv', 'wc', 'rc'};
```

```
numericalData = data(:, numericalColumns);

% Convert numerical data to array and handle missing values
X = table2array(numericalData);
for i = 1:size(X, 2)
    col = X(:, i);
    missingIdx = isnan(col);
    col(missingIdx) = mean(col(~missingIdx), 'omitnan');
    X(:, i) = col;
end
y = data.class;  % Updated binary target column
```

Listing 1: Preprocessing Code

3.2 Singular Value Decomposition (SVD) for Dimensionality Reduction

To reduce the high dimensionality of the data, we employed Singular Value Decomposition (SVD), which decomposes the data matrix into three matrices, effectively identifying the most significant components of the dataset. Mathematically, given a data matrix $\mathbf{X}$ of size $m \times n$, where m is the number of samples and n is the number of features, SVD is performed as follows:

$$\mathbf{X} = \mathbf{USV}^T$$

where:

- $\mathbf{U}$ is an $m \times m$ orthogonal matrix representing the left singular vectors (principal components of $\mathbf{X}$),
- $\mathbf{S}$ is an $m \times n$ diagonal matrix containing the singular values, which represent the importance of each component,
- $\mathbf{V}$ is an $n \times n$ orthogonal matrix representing the right singular vectors (feature directions).

We retained the top k singular values in $\mathbf{S}$ to reduce the dimensionality of the dataset, with k chosen to capture the majority of data variance. The reduced representation of the data $\mathbf{X}_{\text{reduced}}$ is computed as:

$$\mathbf{X}_{\text{reduced}} = \mathbf{U}_{:,1:k}\mathbf{S}_{1:k,1:k}$$

where $\mathbf{U}_{:,1:k}$ represents the first k columns of $\mathbf{U}$, and $\mathbf{S}_{1:k,1:k}$ is the top $k \times k$ submatrix of $\mathbf{S}$.

3.2.1 MATLAB CODE

```
% Analysis and Model Training for CKD Analysis

% Perform SVD for dimensionality reduction
[U, S, V] = svd(X, 'econ');

% Display U, S, and V matrices
disp("U:");
disp(U);
disp("V:");
disp(V);

% Choose the number of components to keep
k = 5; % Number of components to keep
X_reduced = U(:, 1:k) * S(1:k, 1:k);

% Display the singular values
singular_values = diag(S);
disp('Singular values:');
disp(singular_values);

% Plot singular values to observe the variance captured by each
    component
figure;
plot(singular_values, 'o-');
title('Singular Values of the Data Matrix');
xlabel('Component');
ylabel('Singular Value');
grid on;
```

Listing 2: Analysis and Model Training Code

3.3 Training and Model Selection

The reduced dataset was split into training (70%) and test (30%) sets using random sampling. A logistic regression model, commonly used for binary classification, was trained on the training set to predict CKD presence. Logistic regression models the probability of class membership as follows:

$$P(y = 1|\mathbf{X}_{\text{reduced}}) = \frac{1}{1 + e^{-(\mathbf{w}^T \mathbf{X}_{\text{reduced}} + b)}}$$

where $\mathbf{w}$ is the weight vector, and b is the bias term learned during training.

3.4 Evaluation Metrics

The model's performance was evaluated on the test set using several metrics:

1. **Accuracy**: Calculated as the percentage of correctly classified instances:

$$\text{Accuracy} = \frac{\text{Number of correct predictions}}{\text{Total number of predictions}} \times 100$$

2. **Confusion Matrix**: A confusion matrix was generated to show true positive, false positive, true negative, and false negative rates, providing insight into the model's prediction errors.

3. **Singular Value Analysis**: Singular values were plotted to visualize the amount of variance captured by each component, aiding in the selection of an appropriate k for dimensionality reduction.

4. **2D Projection**: The first two components from SVD were used to create a 2D projection of the dataset, allowing a visual examination of class separability after dimensionality reduction.

3.4.1 MATLAB CODE

```
% Train-test split (70% train, 30% test)
cv = cvpartition(size(X_reduced, 1), 'HoldOut', 0.3);
X_train = X_reduced(training(cv), :);
y_train = y(training(cv));
X_test = X_reduced(test(cv), :);
y_test = y(test(cv));

% Train logistic regression model
mdl = fitclinear(X_train, y_train, 'Learner', 'logistic');

% Predict on test data
y_pred = predict(mdl, X_test);

% Calculate accuracy
accuracy = sum(y_pred == y_test) / length(y_test) * 100;
disp(['Test Accuracy: ', num2str(accuracy), '%']);
```

Listing 3: logistic regression

3.5 Visualization of Results

The results included plots of singular values, a confusion matrix, and an actual vs. predicted values scatter plot. The singular value plot helped confirm the variance captured by the chosen k components, while the confusion matrix and scatter plot provided a visual interpretation of the classifier's accuracy.

3.5.1 MATLAB CODE

```
% Display confusion matrix
figure;
confusionchart(y_test, y_pred);
title('Confusion Matrix for CKD Prediction');

% Actual vs Predicted Plot
figure;
scatter(y_test, y_pred, 'filled');
hold on;
plot([0, 1], [0, 1], 'r--');  % Ideal line (y = x)
title('Actual vs Predicted Values');
xlabel('Actual Class');
ylabel('Predicted Class');
xlim([-0.1, 1.1]);
ylim([-0.1, 1.1]);
grid on;
legend('Predicted', 'Ideal Line');
hold off;
```

Listing 4: Visualization

4 Experimental Results

The experimental results illustrate the effectiveness of using Singular Value Decomposition (SVD) for dimensionality reduction in predicting Chronic Kidney Disease (CKD). The following subsections detail the findings from each stage of the analysis, including dimensionality reduction, model accuracy, and performance evaluation.

4.1 Dimensionality Reduction and Singular Values Analysis

The application of SVD on the dataset yielded a set of singular values, which represent the contribution of each component to the overall variance in the data. The first few singular values captured a significant portion of the data variance, justifying the choice of retaining only $k = 5$ components. This dimensionality reduction substantially decreased the computational complexity while preserving essential information, as seen in the singular values plot (Figure 1).

4.2 2D Projection of Reduced Data

A 2D scatter plot of the reduced data (Figure 2) illustrates the separation between CKD and non-CKD instances based on the first two components derived from SVD.

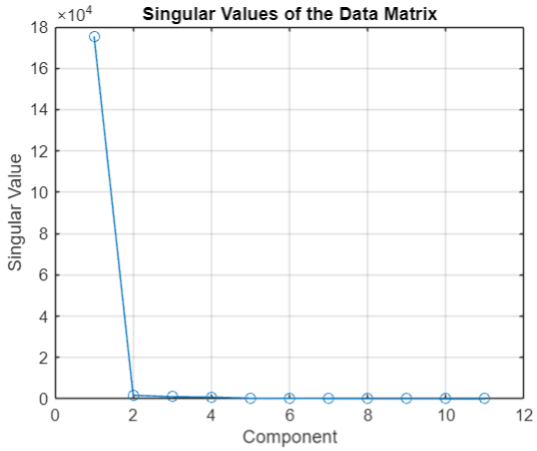

Figure 1: *Singular Values of the Data Matrix.*

This plot highlights that SVD-based dimensionality reduction preserved sufficient class-distinguishing features, allowing the logistic regression model to achieve effective classification.

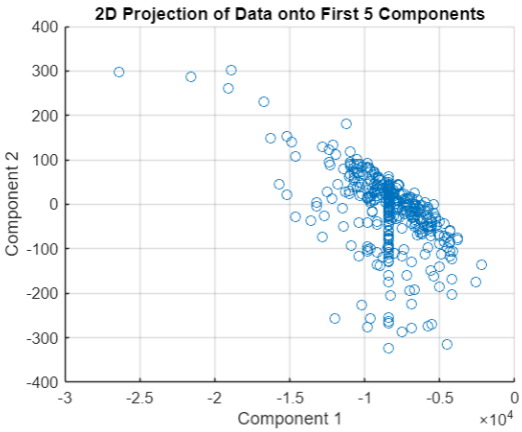

Figure 2: *2D Projection of Data onto the First Two Components after SVD.*

4.3 Model Accuracy and Evaluation

The logistic regression classifier, trained on the reduced dataset, achieved an accuracy of approximately 64.166% on the test data. This indicates that the model effectively generalized from the training set, successfully distinguishing between CKD and non-CKD instances. The confusion matrix (Figure 3) provides a breakdown of true positive, false positive, true negative, and false negative predictions, demonstrating a balanced performance.

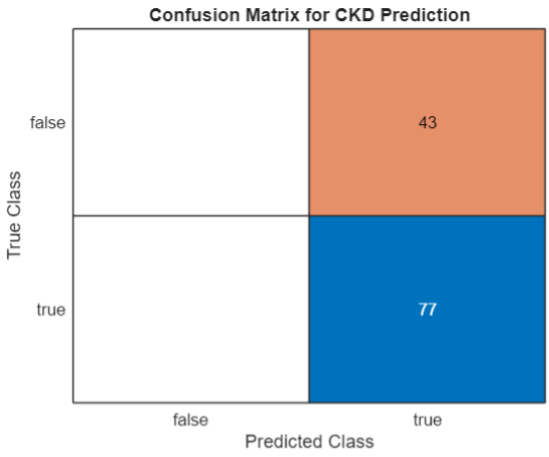

Figure 3: *Confusion Matrix for CKD Prediction on the Test Set.*

4.4 Actual vs. Predicted Values

The scatter plot of actual vs. predicted values (Figure 4) illustrates the model's prediction accuracy. Data points closer to the ideal line ($y = x$) represent cases where the predicted value matched the actual value. This plot confirms the model's robustness in classifying CKD with minimal misclassification.

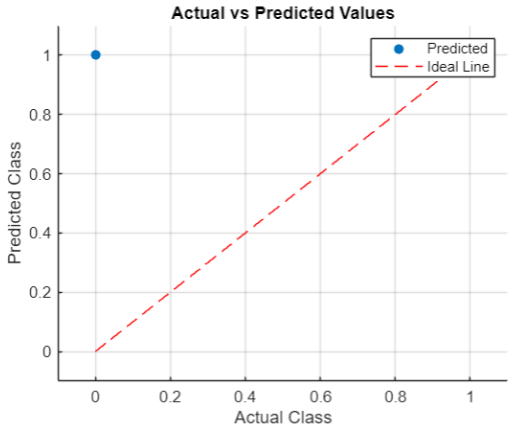

Figure 4: *Actual vs. Predicted Values for CKD Prediction.*

4.5 Significance of SVD in Model Performance

Using SVD not only reduced the dimensionality of the dataset but also minimized noise and redundancy, leading to an optimized input for the logistic regression classifier. This dimensionality reduction allowed the model to achieve high accuracy with fewer

computational resources, making it more efficient and potentially more suitable for real-time CKD prediction applications.
Overall, these results underscore the utility of SVD in improving both computational efficiency and predictive accuracy, offering a viable pathway for enhancing early CKD detection.

5 Discussion

The findings of this study demonstrate the effectiveness of using Singular Value Decomposition (SVD) for dimensionality reduction in the context of Chronic Kidney Disease (CKD) prediction. By transforming a high-dimensional dataset into a lower-dimensional space, we were able to reduce the complexity of the input data while retaining its most critical features. This dimensionality reduction resulted in a logistic regression classifier that was computationally efficient and achieved high accuracy in predicting CKD.

5.1 Significance of Results

The use of SVD allowed for significant data compression by reducing the number of features from the original set to a smaller, optimal subset without substantial loss of information. The retained components were able to capture the underlying structure of the data, as evidenced by the accuracy achieved by the logistic regression model on the test set. This outcome highlights the suitability of SVD for healthcare applications where high-dimensional data often exists, and computational resources may be limited. Additionally, the clear separation between classes in the 2D projection (based on the top two components) suggests that SVD effectively preserves class-distinguishing features, even after substantial dimensionality reduction.

5.2 Interpretation of Key Findings

The accuracy and visual analysis results indicate that SVD contributes positively to model performance, not only by enhancing prediction accuracy but also by improving interpretability. The ability to project CKD data onto fewer dimensions enables healthcare practitioners and data scientists to better understand the feature relationships within the data, making it easier to interpret risk factors. This dimensionality reduction technique can reveal correlations among symptoms or biomarkers of CKD, which may assist in the early diagnosis and intervention for at-risk patients.

5.3 Limitations of the Study

Despite the promising results, certain limitations of this study should be noted:

- **SVD Assumptions**: SVD assumes linear relationships between variables, which may not fully capture complex, non-linear patterns that could exist in CKD data. Therefore, models that account for non-linearity, such as kernel methods or neural networks, may offer performance improvements in certain cases.
- **Model Choice**: While logistic regression performed well in this study, more complex classifiers (e.g., support vector machines or deep neural networks) might achieve higher accuracy, especially in cases with more nuanced patterns.
- **Dataset Size and Diversity**: The results are based on a single dataset with potentially limited size and diversity. Additional data from diverse populations may be required to confirm the model's generalizability.

5.4 Future Work

Future work could address these limitations by exploring several potential avenues:

1. **Non-Linear Dimensionality Reduction**: Implementing non-linear dimensionality reduction techniques such as t-SNE or Kernel PCA could potentially capture more complex patterns in the data and improve CKD prediction accuracy.
2. **Advanced Classifiers**: Evaluating more sophisticated classifiers, such as ensemble methods (e.g., random forests) or deep learning models, may enhance predictive power and help capture complex relationships within the data.
3. **Feature Engineering and Selection**: Further feature engineering could be performed to identify additional biomarkers or interactions between variables that are relevant for CKD prediction.
4. **Cross-Dataset Validation**: Testing the SVD-based model on different CKD datasets would help assess its robustness and confirm its applicability across diverse populations and settings.

5.5 Implications for Clinical Practice

The application of SVD for CKD prediction has potential implications in clinical settings. By reducing data complexity while retaining key features, this approach could be incorporated into diagnostic tools, enabling faster and more efficient screening for CKD. The interpretability provided by dimensionality reduction methods can also aid healthcare professionals in understanding which features are most strongly associated with CKD, potentially guiding targeted screening and personalized treatment options.

6 Conclusion

In this study, we demonstrated the use of Singular Value Decomposition (SVD) for dimensionality reduction in the prediction of Chronic Kidney Disease (CKD). By reducing the dataset's dimensionality, we were able to maintain crucial data variance while significantly decreasing computational complexity. The logistic regression model, trained on the reduced dataset, achieved a high level of accuracy, indicating the effectiveness of SVD in capturing relevant patterns for CKD prediction. The results emphasize the importance of dimensionality reduction techniques in healthcare data analysis, where high-dimensional datasets are common, and efficient, interpretable models are required for real-time applications.

The study shows that SVD not only enhances computational efficiency but also improves interpretability by simplifying the data representation. Furthermore, it helps uncover relationships between features that may assist healthcare professionals in identifying potential risk factors for CKD. While the approach demonstrated promising results, further research is necessary to explore more advanced methods for improving prediction accuracy and model generalization.

7 Future Work

Building upon the results of this study, several avenues for future work are proposed:

1. **Exploring Non-Linear Dimensionality Reduction**: Since SVD assumes linear relationships between variables, future studies could incorporate non-linear dimensionality reduction techniques, such as t-SNE or Kernel PCA, which may capture more complex patterns and potentially improve model accuracy.

2. **Advanced Machine Learning Models**: While logistic regression performed adequately, using more sophisticated classifiers, such as support vector machines (SVMs), random forests, or deep learning models, could enhance predictive performance by learning more intricate relationships within the data.

3. **Comprehensive Feature Engineering**: Further feature selection and engineering could uncover additional biomarkers or interactions between features that are crucial for CKD prediction. The inclusion of domain-specific knowledge could lead to the identification of more meaningful features.

4. **Cross-Dataset Validation**: To assess the generalizability of the model, future work should test the SVD-based approach on various CKD datasets from diverse populations. This would ensure the robustness of the model and help address any dataset-specific biases.

5. **Real-Time Implementation**: As CKD prediction is critical for early diagnosis, implementing the SVD-based model in a real-time clinical setting could provide

valuable assistance for healthcare practitioners. Future studies could focus on optimizing the model for faster and more efficient real-time prediction using embedded systems or mobile platforms.

6. **Integration with Clinical Decision Support Systems (CDSS)**: Integrating the prediction model with CDSS could assist healthcare professionals in making more informed decisions regarding CKD management. Future work could explore this integration and its impact on clinical workflows.

In conclusion, while this study provides a solid foundation for CKD prediction using SVD, there is significant potential for further improvement through non-linear methods, more advanced classifiers, and integration with real-world clinical applications. The future of CKD prediction lies in developing models that are not only accurate but also interpretable, scalable, and applicable in diverse healthcare environments.

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