

Contents

Contents	viii
List of Figures	ix
1 Introduction	1
2 K-Nearest Neighbor	4
2.1 Introduction	4
2.2 Genes Selection	4
2.3 Regression And Estimation	5
2.4 Calculation of Pseudoinverse	5
2.5 Jacobi algorithm for calculation of eigen value and eigen matrix	6
3 Singular Value Decomposition	8
3.1 Introduction	8
3.2 SVD Calculation Algorithm	9
3.3 Multiple Linear Regression	9
3.4 Estimating Regression Models Using Least Squares	9
3.5 Row Average	11
4 Results and Discussion	12
4.1 Normalized Root Mean Square Error (NRMSE)	12
4.2 Dataset	13
4.3 Comparison Between The Three Implemented Methods	13
5 Conclusion and Future Work	17
5.1 Conclusion	17
5.2 Future Work	17
Bibliography	18

List of Figures

1.1	Matrix containing 26 microarray DNA data in 13 experiments.	2
4.1	Table of the outcome of the data when the different percentage of data are missing from the data set.	13
4.2	Graph showing the effect of different percentage of missing values with NRMSE. The different curve represents the different method used for missing value calculation.	14
4.3	Table of the outcome of the data when the different percentage of data are missing from the data set.	15
4.4	Graph showing the effect of different percentage of missing values with NRMSE. The different curve represents the different method used for missing value calculation.	15
4.5	Table of the outcome of the data when the different percentage of data are missing from the data set.	16
4.6	Graph showing the effect of different percentage of missing values with NRMSE. The different curve represents the different method used for missing value calculation.	16