

Support Vector Machine Parameter Optimization to Improve Liver Disease Estimation with Genetic Algorithm

Hani Harafani
STMIK Nusa Mandiri
Jakarta

hani.hhf@nusamandiri.ac.id

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Abstract— Liver disease is an important public health problem. Over the past few decades, machine learning has developed rapidly and it has been introduced for application in medical-related. In this study we propose Support Vector Machine optimization parameter with genetic algorithm to get a higher performance of Root Mean Square Error value of SVM in order to estimate the liver disorder. The experiment was carried out in three stages, the first step was to try the three SVM kernels with different combination of parameters manually, The second step was to try some combination of range parameters in the genetic algorithm to find the optimal value in the SVM kernel. The third step is comparing the results of the GA-SVM experiment with other regression methods. The results prove that GA has an influence on improving the performance of GA-SVM which has the lowest RMSE value compared to another regression models.

Keywords—Support Vector Machine;Genetic Algorithm;Liver;Parameter;Estimation

I. INTRODUCTION

Liver disease is an important public health problem that mostly manifested as abnormal Liver Function Test (Yao, Li, Guan, Ye, & Chen, 2020). Patient with liver disease have been continuously increasing because of many causes such as excessive alcohol consumption (McDermott & Forsyth, 2016), inhale of harmful gases, intake of contaminated food, pickles, drugs (Venkata Ramana, Babu, & Venkateswarlu, 2011), inherited metabolic liver disease (Kelly, 2019), epidemic, and endemic outbreaks by geographical settings (Beeching & Dassanayake, 2019).

The way to diagnose liver disease is by undergoing liver function test (Yao et al., 2020), and liver disease screening by LFT data is helpful for computer aided diagnosis. Over the past few decades, machine learning has developed rapidly and it has been introduced for application in medical-related fields (Yao et al., 2020), like fertility prediction

(Harafani & Maulana, 2019), breast cancer prediction (Purwaningsih, 2019), Liver disease screening (Yao et al., 2020), liver disease diagnosis (Venkata Ramana et al., 2011) and so on. Therefore, in the regression tasks several Machine learning methods are widely applied such as K-NN (Goyal, Chandra, & Singh, 2014),

Linear Regression (Lira, Da Silva, Alves, & Veras, 2014), and Support Vector Machine (Harafani & Wahono, 2015).

Support Vector Machine has advantages in overcoming classification (Support Vector Classifier Machine) and regression (Support Vector Regression Machine) tasks both with linear kernel or nonlinear kernel (Maimon & Rokach, 2010), besides SVM can provide alternative to computational cost (Zaghloul, Hamza, Iorhemen, & Tay, 2020), and good for overcoming the curse of dimensionality (Wang, Wen, Zhang, & Wang, 2014).

However the forecast accuracy is highly affected by three parameter of SVR (Kavousi-Fard, Samet, & Marzbani, 2014) containing C (a parameter to tradeoff between training error and regression function flatness), kernel function parameter, and ϵ (constant value to determine the width of the loss function in SVR), so that there are so many research studies to solve that major issues by suggesting different approaches (Kavousi-Fard et al., 2014) such as Particle Swarm Optimization (Liang, Zou, Li, Junaid, & Lu, 2019), and Genetic Algorithm (Chen, Liang, Hong, & Gu, 2015). In this study genetic algorithm proposed to optimize support vector machine parameters. The objective of this research is to get a higher estimation performance of the liver disease estimation.

II. LITERATURE REVIEW

Support Vector Machine can be imagined as a surface that creates a boundary between points of data plotted in multidimensional that represent examples and their feature value (Lantz, 2015). The goal is to create a flat boundary called a hyperplane which divides the space to create fairly homogenous partition on either side. Support Vector Regression (SVR) is gaining popularity in regression and classification due to its excellent generalization performance (Liang et al., 2019). In regression applications, to extend to nonlinear regression, the SVR kernel function has been used to project the input space into the feature space producing the linear or nearly linear regression hyper surface in the feature space, therefore, the selection of the SVR penalty parameter C , and the kernel function parameter γ has an important influence on the SVR regression performance.

The basic idea of SVR is to map data from the input space into high dimensional feature with non-linear mapping and to do linear regression into that space. $x_{i+1} = f(x_t, x_{t-1}, x_{t-2}, \dots, x_{t-(m-1)})$ where x_{i+1} is the predicted value and x_t is the predicted value. A set of training data for SVM Regression represented as the function below

$$D = \{(x_1, y_1), (x_2, y_2), \dots, (x_m, y_m)\} \quad (1)$$

Where x_i is the n-dimensional vector, and y is the real amount for each x_i .

The standard of Support vector regression is to use the loss function $L_\epsilon(y, f(x))$ that describes the deviation of estimation function from the original data. Some type of the loss function that can be extracted from the literature are: linear, quadratic, exponential, loss function Huber, etc (Raghavendra. N & Deka, 2014). In this context the loss function ϵ insensitive can define as:

$$L_\epsilon(y, f(x)) = \begin{cases} 0 & \text{for } |y - f(x)| \leq \epsilon \\ |y - f(x)| - \epsilon & \text{and vice versa} \end{cases} \quad (2.2)$$

By using loss function ϵ insensitive, first of all we can found $F(x_i)$ function that can approximate y vector as actual output and it has the superior error tolerance from y_i target to all data training, SVR makes the mapping of the x_i input vector to y_i target with this regression function:

$$F(x) = w * \phi(x) + b \quad (2.3)$$

Where w is weighting vector and b is a bias. The goal is to estimate w and b parameter from the function to give the best result according to the data. Based on the lowest value of w , with minimizing $\|w\|^2$ it can maximize the margin, so that the flatness of the curve along with the complexity of the model can be ascertained. So the regression problem can be stated like the following convex optimization problem:

Minimum function:

$$L(w, \xi) = \frac{1}{2} \|w\|^2 + c \sum_i (\xi_{2i}, \xi'_{2i}), c > 0$$

(2.4)

Subject to:

$$\begin{aligned} y_i - w * \phi(x_i) - b &\leq \epsilon + \xi_i \\ w * \phi(x_i) + b - y_i &\leq \epsilon + \xi'_i \end{aligned}$$

(2.5)

$$\xi_i, \xi'_i \geq 0 \quad (3)$$

(2.7)

Where ξ_i , dan ξ'_i are the slack variable introduced to evaluate the deviation of the training samples outside the ϵ insensitive zone or the distance of the training dataset point from the area where the error value is less than ϵ value will be ignored.

Trade-off between the flatness $F(x)$ with the quantity of deviation value until greater than ϵ value can be tolerated by $C > 0$. C is a positive constant that influences sanction for losses when training errors occurs.

To solve optimization problem ini minimum function we can use the Lagrange function of the objective function with introduce one double set of the α_i , dan α'_i variable for appropriate constraints. The optimal condition are exploited at the saddle point of Lagrange function leading to the formulation:

$$\begin{aligned} & \max_{\alpha_i \alpha'_i} -\frac{1}{2} \sum_{i,j=1}^n \alpha_i - \alpha'_i (\alpha_j - \alpha'_j) (\phi(x_i) \cdot \phi(x_j)) \\ & - \varepsilon \sum_{i=1}^n (\alpha_i + \alpha'_i) + \sum_{i=1}^n y_i (\alpha_i - \alpha'_i) \quad (2.8) \\ & \text{subject to : } \sum_{i=1}^n (\alpha_i - \alpha'_i) = 0 \\ & \quad 0 \leq \alpha \leq C, i = 1 \dots n \\ & \quad 0 \leq \alpha'_i \leq C, i = 1 \dots n \quad (4) \end{aligned}$$

Some popular kernel function (Liu, Tian, Chen, & Li, 2013) are used to solve nonlinear mapping problem in SVR namely :

1. Polynomial : $K(x_i, x_j) = (x \cdot y + 1)^d$ (2.10)
2. Linear : $K(x_i, x_j) = x_i^T \cdot x_j$ (2.11)
3. Sigmoid : $K(x_i, x_j) = \tanh(\beta x^T x_i + \beta_1)$ (2.12)
4. Radial Basis Function (RBF) : $K(x_i, x_j) = \exp(-\gamma \|x_i - x_j\|^2)$ (2.13)

In this study RBF kernel is used as the most widely used kernel by the world researcher, thus $F(x)$ function of SVR becomes into the following function:

$$F(x) = \sum_i (\alpha_i - \alpha'_i) K(x_i x_j) + b \quad (5)$$

Genetic algorithm according to Holland in (Zhang & Wang, 2018) is a global heuristic search technique that attempts to emulate the mechanic of natural evolution and the principles of survival of the fittest, and also, according to Goldberg in (Bhuvanewari & Therese, 2015), Genetic algorithm belong to the larger class of evolutionary algorithm, which generate solutions to optimization problems using techniques inspiring by natural evolution, such as inheritance, mutation, selection, and crossover. GA contains a population of individuals, each of which has a known level of fitness (Raikar, Wang, Shih, & Hong, 2016). The population is evolved through successive generations; the individuals in each new generations are bred from the fitter individuals of the previous generation. The process continues through successive generations until the satisfactory conditions.

III. PROPOSED METHOD

In this study, we use secondary data from UCI Machine Learning Repository namely Liver Disorders Dataset from BUPA medical research. The dataset consists of 345 rows and 7 columns. Each row corresponds to one human male subject (McDermott & Forsyth, 2016). The first 5 columns are integer-valued and represent the results of various blood test which may be of use in diagnosing alcohol related

liver disorders. The 6th columns is a real-valued and represents the number of alcoholic drinks taken per day by the subject, by self reported. The last column is the “selectors” that split the dataset into training and testing subsets. It was created by the BMRDL researchers. The attributes of the dataset namely MCV (Mean Corpuscular Volume), ALKPHOSE (Alkaline Phosphotase), SGPT (Alanine Aminotransferase), SGOT (Aspartate Aminotransferase), GAMMAGT (Gamma Glutamyl Tranpepsidase), drinks number of half-pint equivalent of alcoholic beverages drunk per day, and the selector to split the dataset into training and testing subsets. However, liver disorders datasets has been misinterpreted by many studies for classification tasks for which the classification target is the last attribute of the datasets. Therefore (McDermott & Forsyth, 2016) suggested to use the 6th attribute as a target of regression tasks.

In the first step we delete the last attribute of the dataset since we use 10-fold cross validation method to split the dataset into 90% of training and 10% of testing. Then the data is trained and tested 10 times by the SVM with manually optimize parameter of the SVM kernels.

The Second step, the parameters of SVM kernel will optimized directly with genetic algorithm 10 times. So the SVM RMSE value can be compared and the means of all iteration between SVM and SVM-GA can be compared with t-test. After that the last step is to compare the lowest value of RMSE SVM with another regression method.

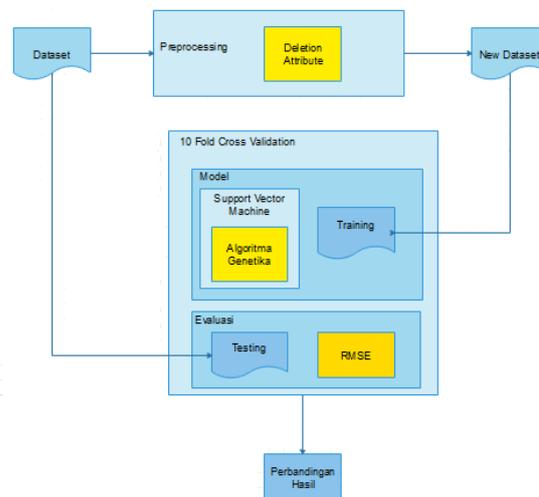


Fig1. Proposed Method

IV. RESULT AND DISCUSSION

In the first experiment the parameters of the SVM kernels were optimized manually. The kernel consist

of (dot, polynomial, and RBF). In the dot kernel C and ϵ parameter are tried 10 times manually, and then we assign 10 minimum and maximum range value to the genetic algorithm to find the optimum parameters values to get the lowest RMSE. In the manual experiment, we got the lowest RMSE value of 3.16 which was obtained from a combination of C (0.05) and ϵ (1) that represented in TableI. In the experiment using GA, we got the lowest RMSE value of 3.09 which was obtained from a combination of optimum C (0.11544) and ϵ (0,518398) as shown as TableII.

The comparison graph of RMSE values in the SVM(dot) can be seen in the Fig2.

TABLE I. EXPERIMENT RESULT OF SVM(DOT)

C	ϵ	RMSE
0	0	3,307
0,1	0	3,149
0,01	0	3,12
0,001	0	3,263
0,01	0,1	3,121
-0,5	0,1	3,302
-0,5	0	3,307
-1	0	3,307
0,01	1	3,307
0,05	1	3,106
Mean		3,229

TABLE II. EXPERIMENT RESULT OF GA-SVM(DOT)

Range Parameters		Optimum Parameters		RMSE
C	ϵ	C	ϵ	
-1 - 1	0 - 1	0,11601	0,07952	3,126
-1 - 1	0,1 - 1	0,11544	0,1459	3,118
-1 - 1	0,5 - 1	0,11544	0,518398	3,09
-1 - 1	0,8 - 1	0,11544	0,8	3,215
-0,5 - 1	0,5 - 1	0,18386	0,72496	3,362
0,1 - 1	0,5 - 1	0,2495	0,9668	3,362
0-1	0,5-1	0,2495	0,9668	3,195
-1 - 1	0,3-1	0,11544	0,33215	3,113
-1 - 0,5	0,5 - 1	-0,15224	0,53575	3,203
-1 - 0,5	1-10	-0,15224	1,62024	3,258
Mean				3,2042

Based on the experiment of SVM(dot), a statistical analysis of the different paired sample t-test was performed. The results obtained are listed in TabelIII. Based on the different paired sample t-test, value of table t-stat is more than t critical two tail which means H1 is accepted, and the alpha value is less then 0,05 which means there is significant difference between SVM(dot) RMSE and GA-SVM(dot) RMSE.

TABLE III. STATISTIC DIFFERENT TEST RESULT BETWEEN SVM(DOT) AND GA-SVM(DOT)

t-Test: Paired Two Sample for Means

	Variable 1	Variable 2
Mean	3,2289	3,2042
Variance	0,008433	0,009756
Observations	10	10
Pearson Correlation	-0,07906	
Hypothesized Mean Difference	0	
df	9	
t Stat	0,55759	
P(T<=t) one-tail	0,29536	
t Critical one-tail	1,833113	
P(T<=t) two-tail	0,590721	
t Critical two-tail	2,262157	

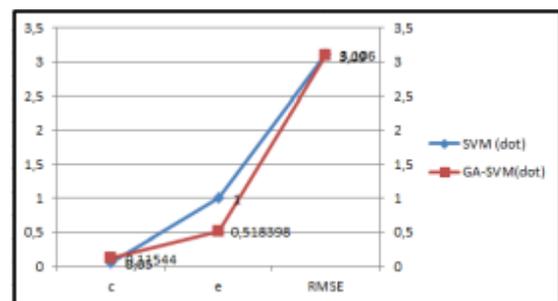


Fig2. RMSE Comparison of SVM(dot) and GA-SVM(dot)

In the polynomial kernel C and ϵ parameter are tried 10 times manually, and then we assign 10 minimum and maximum range value to the genetic algorithm to find the optimum parameters values to get the lowest RMSE. In the manual experiment, we got the lowest RMSE value of 3.085 which was obtained from a combination of C (0.1) , ϵ (0) , and kernel degree (0,9) ,that represented in TableIV. In the experiment using GA, we got the lowest RMSE

value of 3.06 which was obtained from a combination of optimum C (0.0659), ϵ (0,6828), and kernel degree (0,9345) as shown as TableV.

Based on the experiment of SVM(polynomial), a statistical analysis of the different paired sample t-test was performed. The results obtained are listed in TabelVI. Based on the different paired sample t-test, value of table t-stat is more than t critical two tail which means H1 is accepted, and the alpha value is less then 0,05 which means there is significant difference between SVM(polynomial) RMSE and GA-SVM(polynomial) RMSE.

TABLE IV. EXPERIMENT RESULT OF SVM(POLYNOMIAL)

C	ϵ	Kernel Degree	RMSE
0	0	2	3,437
0,05	0	2	3,496
0,01	0	2	3,453
0	0,01	2	3,453
0	0,1	2	3,453
0	0	1	3,095
0	0	0,5	3,095
0	0	0,1	3,095
0,1	0	0,1	3,088
0,1	0	0,9	3,085
Mean			3,275

TABLE V. EXPERIMENT RESULT OF GA-SVM(POLYNOMIAL)

Range Parameter			Optimum Parameter			RMSE
C	ϵ	Kernel Degree	C	ϵ	Kernel Degree	
-1 - 1	0 - 1	0 - 1	-0,5493	0,51331	0,2378	3,043
-0,5 - 1	0,5 - 1	0 - 1	-0,4265	0,8567	0,9366	3,063
-1 - 1	0,5 - 1	0,5 - 1	-0,5493	0,5133	0,61754	3,043
-1 - 1	0 - 1	0 - 1	-	0,6883	0,9482	3,042
-1 - 1	0,01 - 1	0,01 - 1	-	0,688	0,94272	3,042
0 - 1	0,01 - 1	0 - 1	0,8633	0,6956	0,936637	3,049
0,01 - 1	0,01 - 1	0 - 1	0,0723	0,7136	0,9462	3,036

0,01 - 1	0,01 - 1	0 - 1	0,0874	0,6956	0,9366	3,060
0,01 - 1	0,01 - 1	0 - 1	0,0659	0,6828	0,9345	3,060
-0,1 - 1	0,01 - 1	0 - 1	0,7625	0,5633	0,63	3,068
Mean						3,0506

TABLE VI. STATISTIC DIFFERENT TEST RESULT BETWEEN SVM(POLYNOMIAL) AND GA-SVM(POLYNOMIAL)

t-Test: Paired Two Sample for Means

	Variable 1	Variable 2
Mean	3,275	3,0506
Variance	0,037601	0,000124
Observations	10	10
Pearson Correlation	-0,34764	
Hypothesized Mean Difference	0	
df	9	
t Stat	3,583039	
P(T<=t) one-tail	0,002951	
t Critical one-tail	1,833113	
P(T<=t) two-tail	0,005903	
t Critical two-tail	2,262157	

The comparison graph of RMSE values in the SVM(polynomial) can be seen in the Fig3.

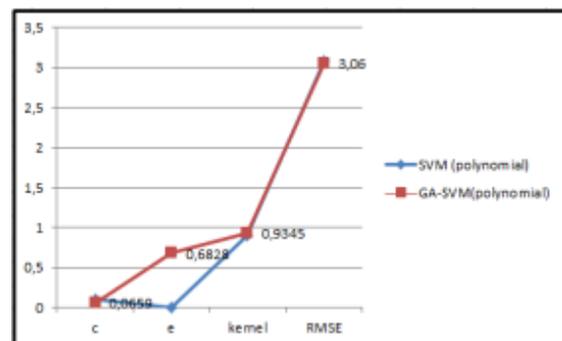


Fig3. RMSE Comparison of SVM(Polynomial) and GA-SVM(Polynomial)

In the Radial Basis Function kernel C and ϵ parameter are tried 10 times manually, and then we assign 10 minimum and maximum range value to the genetic algorithm to find the optimum parameters values to get the lowest RMSE. In the manual experiment, we got the lowest RMSE value of 2.957 which was obtained from a combination of C (0) , ϵ (0.1) , and γ (0,1012) ,that represented in TableVII. In the experiment using GA, we got the lowest RMSE value of 2,92 which was obtained from a combination of optimum C (0.646), ϵ (0,8736), and γ (0,2634) as shown as TableVIII.

Experiment Result of SVM(RBF)

C	ϵ	γ	RMSE
0	0	1	3,131
0,1	0	1	3,27
0	0,1	1	3,13
0	0,5	1	3,134
0	0,1	0,5	3,065
0	0,1	0,25	2,985
0	0,1	0,125	2,968
0	0,1	0,115	2,964
0	0,1	0,105	2,961
0	0,1	0,1012	2,957
Mean			3,057

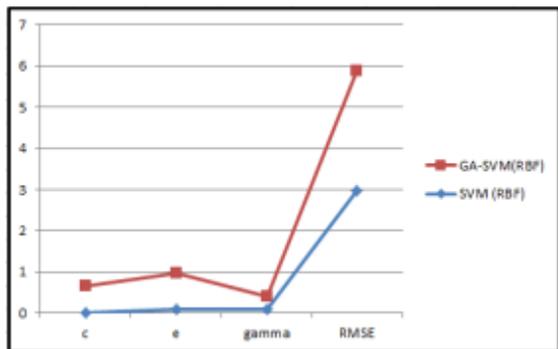


Fig4. RMSE Comparison of SVM(RBF) and GA-SVM(RBF)

Based on the experiment of SVM(polynomial), a statistical analysis of the different paired sample t-test was performed. The results obtained are listed in TabelIX. Based on the different paired sample t-test, value of table t-stat is more than t critical two tail which means H1 is accepted, and the alpha value is

less than 0,05 which means there is significant difference between SVM(RBF) RMSE and GA-SVM(RBF) RMSE. The comparison graph of RMSE values in the SVM(RBF) can be seen in the Fig4.

Based on the experiment of three kernel of SVM we can see that genetic algorithm absolutely can improve the RMSE performacne of SVM. The comparison between SVM and GA-SVM represented in Fig5.

TABLE VII. EXPERIMENT RESULT OF GA-SVM(RBF)

Range Parameter			Optimum Parameter			RMSE
C	ϵ	γ	C	ϵ	γ	
-1 - 1	0 - 1	0 - 1	- 0,5148	0,3984	0,193	2,957
-1 - 1	0,1- 1	0,1- 1	- 0,5224	0,4668	0,2766	2,972
-1 - 1	0 - 1	0,1- 1	- 0,5224	0,38014	0,2654	2,956
-1 - 1	0 - 1	0,01 - 1	- 0,5431	0,4164	0,1973	2,963
-1 - 1	0,01 - 1	0,1- 1	- 0,5501	0,3861	0,2654	2,965
0 - 1	0 - 1	0,1- 1	0,646	0,8736	0,2634	2,92
0 - 1	0,1- 1	0,1- 1	0,6034	0,893	0,28677	2,953
0 - 1	0 - 1	0,01 - 1	0,238	0,41146	0,18446	3,012
0 - 1	0 - 1	0 - 1	0,2654	0,9875	0,1885	2,97
0,1 - 1	0 - 1	0,1- 1	0,3095	0,4078	0,26197	2,999
Mean						2,9667

TABLE VIII. STATISTIC DIFFERENT TEST RESULT BETWEEN SVM(RBF) AND GA-SVM(RBF)

t-Test: Paired Two Sample for Means

	Variable 1	Variable 2
Mean	3,0565	2,9667
Variance	0,011459	0,000636
Observations	10	10
Pearson Correlation	-0,15826	
Hypothesized Mean Difference	0	

df	9
t Stat	2,495347
P(T<=t) one-tail	0,017061
t Critical one-tail	1,833113
P(T<=t) two-tail	0,034121
t Critical two-tail	2,262157

The last step of experiment is comparing GA-SVM performance with another regression model, in this case we use K-NN and Linear Regression. K-NN and Linear Regression have been trained 10 times to with each optimized parameter manually. K-NN trained with differences of K value, hence Linear Regression trained with differences of forward alpha and backward alpha combination. The comparison of the mean of RMSE value can be seen in Fig6.

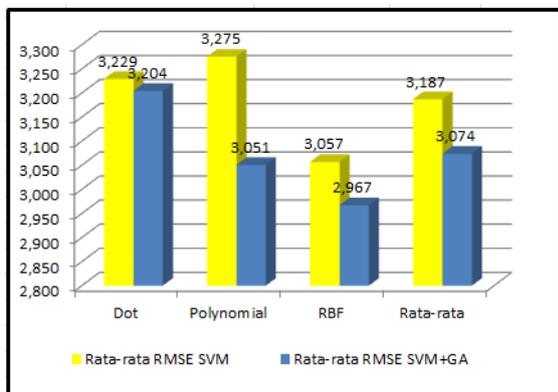


Fig4. Mean of RMSE Comparison of SVM) and GA-SVM

As we can see Fig4 shows that RBF kernel of SVM has lowest value event when SVM doesn't improve by GA optimization.

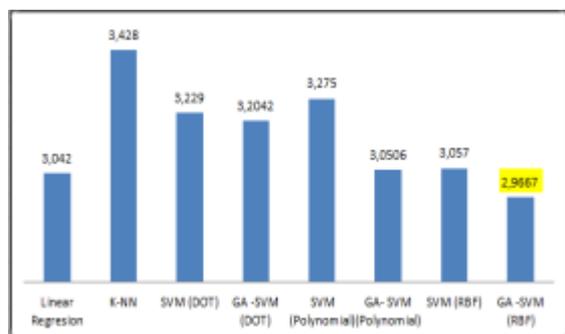


Fig5. Mean of RMSE Comparison of SVM) and GA-SVM

Based on Fig5. We can see that GA-SVM with RBF kernel has the lowest value of all regression models, the second rank is occupied by linear regression, and the third rank is GA-SVM with a polynomial kernel. All models show a slight difference in RMSE values. However, RMSE value of the GA-SVM not at all close to zero, we suspect that the feature of this dataset must be selected first (Suryadi, 2019) like what another researcher do.

V. CONCLUSION AND SUGGESTION

Based on the entire experiment of the GA-SVM, we found that RBF kernel has a high performance of all regression model, however the RMSE generated in the GA-SVM experiment is still around number 2 and not at all close to zero which is a condition for a good RMSE value. In the case of the Liver Disorder dataset from BUPA, we suspect that the features of this dataset must be selected or weighed first, therefore for future work, we recommend selecting features or ranking features first in the BUPA dataset.

VI. ACKNOWLEDGMENT

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