



REVIEW ARTICLE

BAYESIAN REGRESSION ALGORITHM AND ITS MODIFICATION WITH APPLICATION TO PUBLIC HEALTH DATA

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ABSTRACT

This paperwork emphasizes an alternative approach of SAS programming language for Linear Bayesian Regression with combination of Fuzzy Regression. The special of this method is, the method itself comprises of modeling, bootstrapping for linear minimization programming through fuzzy regression modeling based on the dependent and independent variables.

Key words:

Bootstrap,
Linear Regression.

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INTRODUCTION

Multiple linear regression (MLR) analyses are commonly employed in science and non-science fields. The multiple linear regression is given as follows

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i3} + \epsilon_i$$

$$i = 1, 2, \dots, n$$

The best-fitting for the regression linear model is by using method of least squares. Least square is the standard approach. The least-squares estimates $\beta_0, \beta_1, \dots, \beta_n$ are usually computed by statistical software. The least square criterion is generalized as follows for general linear regression model

$$Q = \sum_{i=1}^n (Y_i - \beta_0 - \beta_1 x_{i1} - \dots - \beta_{p-1} x_{i,p-1})^2$$

The least square estimator are those values of $\beta_0, \beta_1, \dots, \beta_{p-1}$ that minimize Q . let us denote the vector of the least square estimate regression coefficient $\beta_0, \beta_1, \dots, \beta_{p-1}$ as \mathbf{b} :

$$\mathbf{\beta}_{p \times 1} = \begin{bmatrix} \beta_0 \\ \vdots \\ \beta_{p-1} \end{bmatrix}$$

The least square normal equations for the general linear regression model are given as follow

$$\mathbf{X}'\mathbf{X}\mathbf{\beta} = \mathbf{X}'\mathbf{Y}$$

And the least square estimator are:

$$\mathbf{\beta}_{p \times 1} = (\mathbf{X}'\mathbf{X})^{-1} (\mathbf{X}'\mathbf{Y})_{p \times 1}$$

The method of maximum likelihood leads to the same estimators for normal error regression model $\mathbf{Y} = \mathbf{X}\mathbf{\beta} + \mathbf{\epsilon}$

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as those obtained by the method of least square

$$\beta = (X'X)^{-1} (X'Y)$$

β $p \times 1$ $(X'X)$ $p \times p$ $(X'Y)$ $p \times 1$

The bootstrap method starts with an original sample which is taken from the considered specific population. The next step is to duplicates the original sample in a number of times to create a new population regard to original population. In that case, the bootstrap draws several samples with replacement by random sampling approach, and as a result it provides a different sample from the original sample. This technique stores the new set of data and creating a new distribution for further analysis. (Efron *et al.*, 1993; Higgins, 2005). The advantage of using bootstrap is its ability to develop a sample the same size of the original, which may include an observation several times while omitting other observations.

Fuzzy regression be written as $Y = Z_0 + Z_1x_1 + Z_2x_2 + \dots + Z_kx_k$, with the explanation variables x_i 's are assumed to be precise. Our aim is to estimate these parameters (Amir et. al, 2016). In this case, Z_i 's are assumed as symmetric fuzzy numbers which can be presented by intervals. In fuzzy regression methodology, parameters are estimated by minimising total vagueness in the model. $y_j = Z_0 + Z_1x_{1j} + Z_2x_{2j} + \dots + Z_kx_{kj}$

.Using $Z_i = \langle a_{ic}, a_{iw} \rangle$, it can be written $y_j = \langle a_{0c}, a_{0w} \rangle + \langle a_{1c}, a_{1w} \rangle x_{1j} + \dots + \langle a_{nc}, a_{nw} \rangle x_{nj}$ (Amir et. al, 2016). y_{jw} represents radius and cannot be negative, therefore, on the right-hand side of equation $y_{jw} = a_{0w} + a_{1w}|x_{1j}| + \dots + a_{nw}|x_{nj}|$, absolute values of x_{ij} are taken. Suppose there m data point, each comprising $a(n+1)$ -row vector (Amir et. al, 2016). Then parameters Z_i are estimated by minimising the quantity, which is total vagueness of the model-data set combination, subject to the constraint that each data point must fall within estimated value of response variable. This can be visualized as the following linear programming problem, minimised

$$\sum_{j=1}^m (a_{0w} + a_{1w}|x_{1j}| + \dots + a_{nw}|x_{nj}|)$$

and subject to

$$\left\{ \left(a_{0c} + \sum_{i=1}^n a_{ic}x_{ij} \right) + \left(a_{0w} + \sum_{i=1}^n a_{iw}x_{ij} \right) \right\} \geq Y_j \text{ and}$$

$$\left\{ \left(a_{0c} + \sum_{i=1}^n a_{ic}x_{ij} \right) - \left(a_{0w} + \sum_{i=1}^n a_{iw}x_{ij} \right) \right\} \leq Y_j.$$

and $a_{iw} \geq 0$. Simple procedure is commonly used to solve the linear programming problem. (Kacprzyk and Fedrizzi, 1992). Data for this study is a sample which is composed of four variables (Amir et. al, 2016)

Sample Size Determination

Sample size for multiple regression analysis were calculated by using G*power with effect size = 0.35, 0.05, power of the study = 0.90 and number of predictor were 4. The minimum sample size requires is 50 respondents.

Analysis: A priori: Compute required sample size
Input: Effect size f^2 = 0.35
 α err prob = 0.05

Power (1- β err prob) = 0.90
 Number of predictors = 4

Output: Noncentrality parameter $\lambda=17.5000$
 Critical F = 2.5787
 Numerator, df. = 4
 Denominator, df. = 45
 Total sample size = 50
 Actual power = 0.90

Table 1. Description of Cholesterol Data

Num.	Variables	Explanation of user variables
1.	Choltot	Total Cholesterol
2.	Hdl	HDL Cholesterol
3.	Trig	Triglycerides
4.	Waist	Waist circumferences

Algorithm and Flow Chart for Modified Bayesian Linear Regression Analysis Method

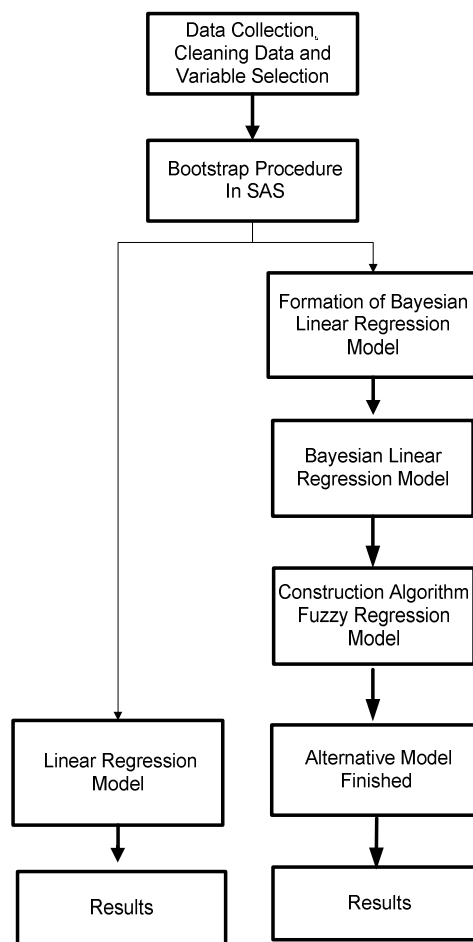


Figure 1. Modified Bayesian Linear Regression Analysis

*/*ADDING BOOTSTRAPPING ALGORITHM TO THE METHOD*/*

%MACRO bootstrap(data=_last_, booted=booted, boots=2, seed=1234);

DATA &booted;

**** randomly picks an integer from 1 to n;**
 pickobs = INT(RANUNI(&seed)*n)+1;

```

** POINT tells SAS to read value pickobs
** NOBS sets n to number of obs in &Data;
** when the point option is used SAS will loop through
the data step forever;
SET &data POINT = pickobs NOBS = n;
** saves number of current bootstrap;
REPLICATE=int(i/n)+1;
i+1;
** stop will leave data set when n*&boots obs have been
created;
IF i > n*&boots THEN STOP;
RUN;
%MEND bootstrap;

```

```

Data Cholesterol;
Input choltot Hdl Trig Waist;
Cards;

```

```

1814676 98.0
22039151 94.0
22039151 94.0
21345123 95.0
17942139 81.0
17942139 81.0
1144262104.0
1144262104.0
26771122 91.5
26771122 91.5
2357391 96.5
2475585 92.0
19957126116.5
19957126116.5
16245100 88.0
23770222 91.5
2076681 85.0
20249118106.5
1844398 90.0
29956207113.0
18447118 95.0
1819271 97.5
22039151 94.0
22039151 94.0
1804758 97.0
17942139 81.0
17942139 81.0
17942139 81.0
17942139 81.0
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1144262104.0
2475585 92.0
19957126116.5
19957126116.5
16245100 88.0
21032193 95.5
23770222 91.5
2076681 85.0
20249118106.5
29956207113.0
18447118 95.0

```

```

;
ods rtf file='abc.rtf' style=journal;

```

```

**generate bootstrap sample;
%bootstrap(data=Cholesterol, boots=2);
run;

```

```

/*PRINT DATA */

```

```

proc print data=booted;
run;
ods rtf close;

```

```

/* LINEAR REGRESSION MODELING AND RESIDUAL
NORMALITY CHECKING*/

```

```

Data Booted;
Input choltotbayes hdl trig waist;
Cards;

```

```

207.5473.0091.00 96.50
190.9445.00123.00 95.00
193.4066.0081.00 85.00
202.9942.00139.00 81.00
207.5473.0091.00 96.50
190.9445.00123.00 95.00
203.4739.00151.00 94.00
202.9942.00139.00 81.00
170.8143.0098.00 90.00
137.8642.0062.00104.00
203.4739.00151.00 94.00
264.4856.00207.00113.00
190.9445.00123.00 95.00
193.4066.0081.00 85.00
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203.4739.00151.00 94.00
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178.0355.0085.00 92.00
203.4739.00151.00 94.00
190.1247.00118.00 95.00
203.4739.00151.00 94.00
189.4149.00118.00106.50
190.1247.00118.00 95.00
189.4149.00118.00106.50
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204.0057.00126.00116.50
303.1270.00222.00 91.50
203.4739.00151.00 94.00
190.1247.00118.00 95.00
run;
Ods rtf file='abc.rtf' style=journal;

ods graphics on;
proc reg data=Booted plots=all;
model choltotbayes = hdl trig waist/p ;
run;
ods graphics off;
ods rtf close;
run;

/* BAYESIAN REGRESSION MODEL*/
Data Booted;
Input choltotbayesian hdl trig waist;
Cards;
207.5473.0091.00 96.50
190.9445.00123.00 95.00
193.4066.0081.00 85.00
202.9942.00139.00 81.00
207.5473.0091.00 96.50
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204.0057.00126.00116.50
303.1270.00222.00 91.50
203.4739.00151.00 94.00
190.1247.00118.00 95.00
;
run;
ods rtf file='abc.rtf' style=journal;

ods graphics on;
proc genmod data=Booted;
model choltotbayesian = hdl trig waist / dist=normal
link=identity;
bayes seed=1 OutPost=Post diagnostics=all summary=all;;
run;
ods graphics off;

ods rtf close;
run;

/* BAYESIAN FUZZY REGRESSION*/

Title 'Linear programming';
data plant;
input choltotbayesian hdl trig waist;
datalines;

```

```

207.5473.0091.00 96.50
190.9445.00123.00 95.00
193.4066.0081.00 85.00
202.9942.00139.00 81.00
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204.0057.00126.00116.50
204.0057.00126.00116.50
303.1270.00222.00 91.50
203.4739.00151.00 94.00
190.1247.00118.00 95.00
;
run;
ods rtf file='result_ex1.rtf' ;

proc optmodel;
  set j= 1..84;
  number choltotbayesian{j}, hdl{j}, trig{j} waist{j};
  read data plant into [_n_]choltotbayesian hdl trig waist;

  /*Print choltotbayesian hdl trig waist*/
  print choltotbayesian hdl trig waist;

  number n init 8;
  /*Total number of Observations*/
  /*Decision Variables*/
  var aw{1..4}>=0;

  /*Theses four variables are bounded*/

  var ac{1..4};
  /* These four variables are not bounded*/

  /* Objective function*/
  min z1= aw[1] * n + sum{i in j} hdl[i] * aw[2] + sum{i in j}
  trig[i] * aw[3]+ sum{i in j} waist[i] * aw[4];

  /*Linear Constraints*/
  con          c{i          in          1..n}:
  ac[1]+hdl[i]*ac[2]+trig[i]*ac[3]+waist[i]*ac[4]-aw[1]-
  hdl[i]*aw[2]-      trig[i]*aw[3]-      waist[i]*aw[4]      <=
  choltotbayesian[i];

  con          c1 {i          in          1..n}:
  ac[1]+hdl[i]*ac[2]+trig[i]*ac[3]+waist[i]*ac[4]      +aw[1]+
  hdl[i]*aw[2]+trig[i]*aw[3]+waist[i]*aw[4]      >=
  choltotbayesian[i];

  expand; /* This provides all equations */

  solve;
  print ac aw;
  quit;
ods rtf close;

```

RESULTS

Part I: Results from Bayesian Multiple linear Regression

Table 3. Results from Bayesian Multiple linear Regression

Analysis of Maximum Likelihood Parameter Estimates				
Parameter	Estimate	Standard Error	Wald Confidence Limits	95%
Intercept	62.5793	0.0028	62.5739	62.5847
Hdl (X_1)	1.4686	0.0000	1.4685	1.4686
Trig (X_2)	0.7511	0.0000	0.7511	0.7511
Waist (X_3)	-0.3170	0.0000	-0.3170	-0.3169

With Choltotbayesian (Y)

Multiple Bayesian Linear Regression (MBLR) is given as follows:

$$(Y) = 62.5793 + 1.4686 (X_1) + 0.7511 (X_2) - 0.3170 (X_3)$$

where

(X₁) is High Density Lipoprotein reading

(X₂) is a Triglycerides reading

(X₃) is Waist reading

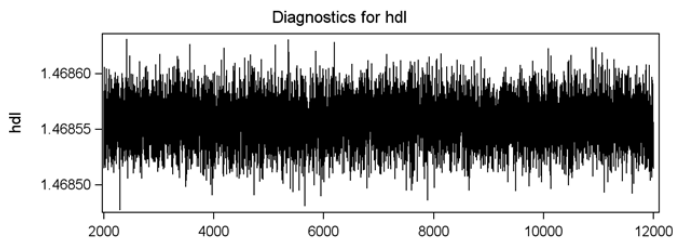


Figure 1. Trace Plots for HDL

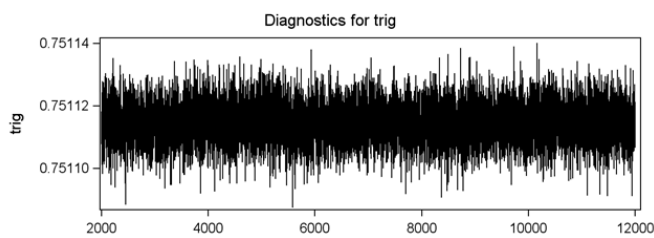


Figure 2. Trace Plots for TRIG

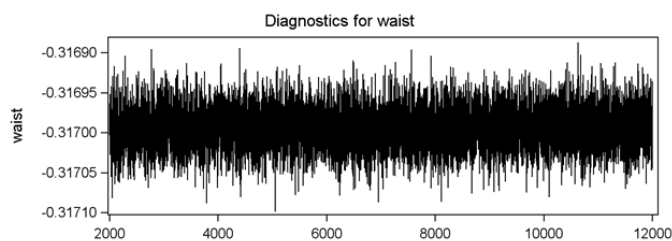


Figure 3. Trace Plots for Intercept

We also can assess convergence by visualization examination through trace plot. Trace plot consist of the plot sampled values of a parameter versus the sample number. Figure 1.1 till Figure 1.3 summarize the result of trace plot of our finding. The Figure 1.1, 1.2 and 1.3 shows the behaviour of the trace plots. From the plot, we can see that all parameters have relatively good mixing properties. Good mixing of the chain indicate that we can get the good results and the samples stay close to the high-density region of the target distribution.

Fitted Bayesian Multiple Linear Regression with standard error is given as follows:

$$(Y) = 62.5793 + 1.4686 (X_1) + 0.7511 (X_2)$$

Std. Error (0.0028) (0.0000) (0.0000)

$$-0.3170 (X_3) \dots\dots\dots (2.1)$$

Std. error (0.0000)

Upper or lower limits of prediction interval are computed from the prediction equation (2.1) by taking the coefficient as their corresponding estimated values plus or minus standard error.

Upper limits

$$(Y) = 62.5821 + 1.4686 (X_1) + 0.7511 (X_2) - 0.3170 (x_3) \dots\dots\dots (2.2)$$

Lowerlimits

$$(Y) = 62.5765 + 1.4686 (x_1) + 0.7511 (x_2) - 0.3170 (x_3) \dots\dots\dots (2.3)$$

Lower limit	Upper limit	Width
207.544	207.550	.0056
190.934	190.939	.0056
193.398	193.404	.0056
202.984	202.989	.0056
207.544	207.550	.0056
190.934	190.939	.0056
203.470	203.476	.0056
⋮	⋮	⋮
303.117	303.123	.0056
203.470	203.476	.0056
190.116	190.121	.0056
Average width		0.0056

Part II: Results From Fitted Model For Fuzzy Regression

Table 4. Value of centre (AC) and radius (AW)

[1]	ac	aw
1	62.65633	0.0015848
2	1.46796	0.0000000
3	0.75085	0.0000000
4	-0.31716	0.0000000

Fitted model for fuzzy regression (FR) for

$$\begin{aligned} \text{Choltotbayesian (Y)} = & <62.65633, 0.0015848> + \\ & <1.46796, 0.0000000> \text{Hdl} + \\ & <0.75085, 0.0000000> \text{Trig} + \\ & <-0.31716, 0.0000000> \text{Waist} \dots\dots\dots (2.4) \end{aligned}$$

Upper or lower limits of prediction intervals are computed from the prediction equation (2.4) by taking the coefficient as their corresponding estimated values plus or minus standard error.

Upper limits

$$Y = <62.6547452> + <1.46796, 0> (X_1) + <0.75085, 0> (X_2) + <-0.31716, 0> (X_3) \dots\dots (2.5)$$

Lowens limits

$$Y = <62.6579148> + <1.46796, 0> (X_1) + <0.75085, 0> (X_2) + <-0.31716, 0> (X_3) \dots\dots (2.6)$$

Lower limit	Upper limit	Width
202.990	202.987	0.0032
207.540	207.537	.0032
190.940	190.937	.0032
203.474	203.470	.0032
202.990	202.987	.0032
170.819	170.816	.0032
137.880	137.877	.0032
⋮	⋮	⋮
303.084	303.081	.0032
203.474	203.470	.0032
190.122	190.119	.0032
Average width 0.003170		

The width of prediction intervals with respect to bayesian multiple linear regression model and bayesian fuzzy regression model corresponding to each set of observed explanatory variables is computed in SPSS and the results are reported in Table 4. From this table, the average width for former was found to be 0.005600, while that of the latter was only 0.003170, thereby indicating the superiority of fuzzy regression methodology.

SUMMARY AND DISCUSSION

This paper presents an algorithm and illustrated the procedure of modeling by using modified Bayesian linear regression through SAS language. Our aim is to share the algorithm and also provide the researcher with an alternative programming that suitable for a small sample size. This proposed method can be applied to small sample size data, especially when limited data is obtained for example in public health.

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