Multiple Linear Regression Assumption Test: Detecting Outlier and Influential Point on Laboratory Measurement Data Using Diagnostic Methods

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Abstract.
This study aims to test the assumptions of multiple linear regression by detecting the presence of outlier, high leverage point, and influential point in laboratory measurement data using diagnostic methods. The study was conducted using 321 samples of lady finger bananas, including acidity (pH), total dissolved solids (ºBrix), and peel color components (Red, Green, Blue/RGB). The analysis stages include building an initial regression model using the R Studio application, applying diagnostic methods consisting of: R-student for outliers, hat matrix for high leverage point, and DFFITS for influential point, and performing automatic iterations by removing data detected as influential point until a convergent data condition (free from influential point) is obtained. The data iteration process stops at the 17th iteration, with the final result being 178 data sets free from influential point. The final iteration results for the pH prediction model obtained a regression equation $\hat{y}_i = 5{,}8096 + 0{,}0143R - 0{,}0263G + 0{,}0138B$ *with a coefficient of determination* (R^2) *of 82,25% and a residual variance (s2) of 0,0138. The final iteration results for the Brix prediction model obtained a regression equation* $\hat{y}_i = 22{,}3332 - 0{,}0936R + 0{,}1175G - 0{,}0521B$ *with a coefficient of determination* (R^2) *of 47.57% and a residual variance* (s^2) *of 0.5424. The presence of outlier and influential point data can damage the assumption of normality and affect the results of regression parameter estimation. The use of repeated diagnostic methods (iterations) is very necessary to clean the model from the influence of unusual data so that a more accurate and reliable regression model is produced.*

Keywords*: Multiple linear regression, diagnostics, outliers, high leverage points, DFFITS, lady finger bananas.*

I. INTRODUCTION

Regression analysis is a type of statistical analysis that investigates how one or more independent variables interact with a dependent variable. The Least Squares Method (LSM) is commonly used to estimate regression parameters (Zulkarnain et al., 2020). The LSM is one method that can be used to calculate regression coefficients. A regression model is reliable if it meets the classical assumptions, namely, that the error is normally distributed, the error variance is homogeneous, the error does not experience autocorrelation, and there is no multicollinearity between the independent variables (Destiyani et al., 2019). If the regression model does not meet any of the classical assumptions, the resulting regression model does not fit the modeled data (Hoerl and Kennard, 1970). If there are outliers in the analyzed data set, the use of the LSM becomes less appropriate, because it can affect the results of the regression parameter estimation and can also damage the assumption of data normality (Zulkarnain et al., 2020). Outliers, or data items that differ significantly from the general pattern, are a common problem in regression analysis. Outliers are typically caused by errors in the data measurement system, errors in the data input or writing process, or by unusual occurrences. The presence of outliers in a data set can disrupt the data analysis process, primarily because the assumption of normality of error is no longer met (Indra et al., 2013). In addition to causing data to be non-normally distributed, outliers can also impact research conclusions or decisions (Sihombing et al., 2022). Outliers can be identified as outliers, high leverage points, or influential point, requiring diagnostic methods to identify them (Seber and Lee, 2003).

It is known that the linear regression model is:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon} \tag{1}$$

where **y** is a response variable vector of size n x 1, **X** is a matrix of independent variables of size *n* x *p* where *n* represents the number of observations and *p* represents the number of parameters, **β** is a parameter vector of size *p* x 1, and **ε** is an error vector of size *n* x 1 with a mean of zero and a variance of σ^2.

Using the least squares method, the parameter estimates for **β** are:

$$\mathbf{b} = (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y} \tag{2}$$

Suppose the estimator of **y** is **ŷ**, then:

$$\hat{\mathbf{y}} = \mathbf{Xb} \tag{3}$$

If equation (2) is substituted into equation (3), then:

$$\hat{\mathbf{y}} = \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}$$

$$\hat{\mathbf{y}} = \mathbf{Hy} \tag{4}$$

where **H** = $\mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'$. **H** is called a hat matrix which has a size of *n* x *n*. **H** is used to detect the presence of a high leverage point where an observation *i* can be suspected as a high leverage point if $h_{ii} > 2p/n$ where *p* represents the number of parameters and *n* represents the number of observations (Myers, 1990)

The value of h_{ii} is:

$$h_{ii} = \mathbf{x}'_{\boldsymbol{i}}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{x}_{\boldsymbol{i}} \tag{5}$$

for $\mathbf{x}'_i$ denotes every *i*-th row of **X**.

The residual in a linear regression model is defined as:

$$e_i = y_i - \hat{y}_i \tag{6}$$

The residual used to detect the presence of outliers is the externally studentized residual or also known as R-student, which is defined as:

$$t_i = \frac{e_i}{s_{-i}\sqrt{1-h_{ii}}} \tag{7}$$

where s_{-i} is the standard deviation calculated without including the i-th observation, with the value:

$$s_{-i} = \sqrt{\frac{(n-p)s^2 - e_i^2/(1-h_{ii})}{n-p-1}}$$

for the value of $s^2 = \sum_{i=1}^{n} \frac{(y_i-\hat{y}_i)^2}{n-p}$.

An observation is suspected to be an outlier if the observation has a value of $|t_i| > t_{\alpha/2;n-p-1}$ at the significance level α (Indra et al., 2013).

Influential point is determined by the DFFITS value. DFFITS is used to determine the influence of the *i*-th observation on the regression model as seen from its fit value. The value of DFFITS is:

$$DFFITS_i = t_i\sqrt{\frac{h_{ii}}{1-h_{ii}}} \tag{8}$$

An observation *i* is said to have an influence on the fit value if the observation has a value of $|DFFITS_i| > 2\sqrt{p/n}$ (Belsley et al., 2005).

II. METHOD

Material

The data used in this study were laboratory measurements used as data in the study (Simanungkalit and Manurung, 2024). The total data consisted of 321 measurements of acidity (pH) levels, total dissolved solids (°Brix) and value of peel color component Red, Green, and Blue (RGB) of lady finger bananas. These data were obtained from daily measurements of lady finger bananas, from day 0 to day 7.

Tools

The tools used in this research consist of: a laptop and the R Studio application.

Procedures and Data Analysi

The research was conducted by analyzing research data using the R Studio application. The stages of research data analysis consist of:

1. Building a multiple linear regression model using daily measurement data (day 0 to day 7), where the peel color component measurement data for the Red (R), Green (G) and Blue (B) are independent variables and the data for the acidity level (pH) and total dissolved solids (^{o}Brix) are each dependent variable;
2. Using diagnostic methods to detect the presence of outliers, high leverage points and influential point on the multiple linear regression model obtained from stage (1);
3. Re-form the multiple linear regression model by excluding observations detected as influential point data obtained from stage (2);
4. Calculate the changes that occur between the multiple linear regression model at stage (2) and the multiple linear regression model at stage (3), then determine the influence of influential point data that were not included at stage (3) on the parameter estimates in the multiple linear regression model.

The four stages of data analysis above are carried out repeatedly (automatic iteration) using the R Studio application until a convergent data condition is found (a data condition that is free from influential point data).

III. RESULT AND DISCUSSION

pH Prediction Model of Lady Finger Banana

A multiple linear regression model with the acidity level (pH) as the dependent variable and the peel color component values of Red (R), Green (G) and Blue (B) as independent variables from 321 lady finger banana samples data were formed using the R Studio application. The multiple linear regression model at the initial stage (first iteration) is $\hat{y}_i$ = 5,3908 + 0,0130R – 0,0224G + 0,0157B, with R^2 = 70,93% and s^2 = 0,0304. The results of the first iteration of the diagnostic parameter calculation are presented in Table 1.

With the number of parameters (p) = 4 and the number of observations (n) = 321, if the value of $|t_i| > t_{\alpha/2;n-p-1}$ then the i-th sample data is an outlier. By taking the real level of α α = 0,05 then the value limit for $t_{0,025;316}$ based on the t-table is ±1,967. The t_i value of the sample data must be in the range of -1,967 > t_i < 1,967 to not be detected as an outlier. If the value of $h_{ii} > 2p/n$ = 0,0249 then the i-th sample data is detected as a high leverage point. If the value of $DFFITS_i > 2\sqrt{p/n}$ = ±0,2233 then the i-th sample data is detected as an observation that influences the regression model.

Table 1. Results of the calculation of the diagnostic parameters of the first stage iteration of the regression model for predicting the pH of lady finger banana.

No	Sample Code	Regression Variable				Diagnostic Parameters			No	Sample Code	Regression Variable				Diagnostic Parameters		
		pH (x)	R (y_1)	G (y_2)	B (y_3)	t_i	h_{ii}	DFFITS			pH (x)	R (y_1)	G (y_2)	B (y_3)	t_i	h_{ii}	DFFITS
1	H0S1	4.7	134.6	119.3	35.9	-1.966	0.008	-0.172	162	H4S3	5.6	162.5	140.8	67.1	1.268	0.027	0.211
2	H0S2	4.8	136.4	122.9	39.6	-1.559	0.007	-0.126	163	H4S4	5.4	138.7	118.9	50.9	0.360	0.004	0.023
3	H0S3	5.3	97.9	112.6	42.2	2.878	0.031	0.514	164	H4S5	5.5	131.2	108.3	48.2	0.543	0.004	0.035
4	H0S4	5.3	110.2	126.8	47.5	3.159	0.034	0.591	165	H4S6	5.6	136.5	117.6	49.2	1.658	0.003	0.098
5	H0S5	4.6	112.8	123.6	46.9	-1.343	0.025	-0.213	166	H4S7	5.5	133.2	114.1	49.9	0.821	0.004	0.049
6	H0S6	4.6	95.7	108.9	34.1	-0.801	0.031	-0.144	167	H4S8	5.4	127.7	97.9	49.2	-1.193	0.010	-0.120
7	H0S7	4.7	118.8	119.6	39.9	-1.089	0.013	-0.125	168	H4S9	5.5	142.2	122.7	65.4	-0.152	0.015	-0.019
8	H0S8	5.2	99.2	112.9	41.2	2.139	0.029	0.372	169	H4S10	5.5	145.7	121.7	65.3	-0.363	0.015	-0.045
9	H0S9	5.3	97.3	109.7	40.7	2.677	0.029	0.460	170	H4S11	5.5	148.9	124.2	64.8	-0.574	0.015	-0.071
10	H0S10	4.6	100.8	112.6	38.9	-1.141	0.027	-0.189	171	H4S12	5.5	152.0	130.2	71.3	-0.460	0.026	-0.075
11	H0S11	4.7	123.0	123.1	42.2	-1.166	0.012	-0.130	172	H4S13	5.4	152.1	130.1	66.6	-0.454	0.019	-0.063
12	H0S12	5.2	73.5	71.1	52.2	-2.072	0.061	-0.530	173	H4S14	5.4	147.9	113.8	57.6	-1.426	0.010	-0.144
13	H0S13	5.4	106.8	123.8	44.7	4.283	0.033	0.794	174	H4S15	5.5	149.4	127.3	64.3	0.008	0.015	0.001
14	H0S14	4.6	104.8	114.5	40.6	-1.168	0.023	-0.180	175	H4S16	5.5	153.0	128.1	58.4	0.374	0.011	0.039
15	H0S15	4.7	113.1	121.5	46.5	-1.196	0.021	-0.176	176	H4S17	5.5	140.9	121.0	52.7	0.706	0.005	0.049
16	H0S16	4.6	99.7	113.3	37.4	-0.648	0.029	-0.113	177	H4S18	5.4	157.0	133.2	68.2	-0.737	0.023	-0.113
17	H0S17	4.7	107.3	120.5	43.0	-0.404	0.027	-0.067	178	H4S19	5.5	144.9	111.4	56.2	-0.972	0.009	-0.093
18	H0S18	5.6	98.7	114.1	40.6	5.060	0.032	0.913	179	H4S20	5.5	141.9	121.5	51.1	1.012	0.004	0.068
19	H0S19	4.7	132.5	139.7	54.5	-0.862	0.030	-0.151	180	H4S21	5.5	136.3	113.6	51.9	0.515	0.004	0.033
20	H0S20	4.9	148.9	138.1	42.9	0.089	0.015	0.011	181	H4S22	5.5	141.8	118.6	50.5	0.537	0.004	0.034
21	H0S21	4.7	101.8	114.9	39.7	-0.401	0.028	-0.068	182	H4S23	5.4	153.4	124.5	61.3	-0.969	0.012	-0.109
22	H0S22	5.5	106.7	121.0	47.3	3.887	0.030	0.682	183	H4S24	5.5	149.1	116.0	56.3	-0.883	0.009	-0.084
23	H0S23	4.7	107.6	118.7	41.1	-0.479	0.024	-0.075	184	H4S25	5.4	156.1	131.5	65.0	-0.768	0.018	-0.104
24	H0S24	4.9	131.0	118.6	34.6	-0.502	0.009	-0.047	185	H4S26	5.3	137.6	107.6	53.8	-1.853	0.007	-0.158
25	H0S25	5.1	136.6	119.0	37.6	-0.159	0.006	-0.013	186	H4S27	5.4	146.1	122.3	57.3	-0.510	0.008	-0.045
26	H0S26	4.9	133.4	120.4	38.5	-0.627	0.006	-0.051	187	H4S28	5.4	136.2	115.6	52.8	0.119	0.004	0.008
27	H0S27	4.9	122.8	111.9	36.4	-0.920	0.008	-0.081	188	H4S29	5.4	140.3	119.5	50.2	0.372	0.004	0.023
28	H0S28	4.8	105.8	116.6	43.2	-0.405	0.024	-0.064	189	H4S30	5.5	140.5	120.5	53.1	0.804	0.005	0.057
29	H0S29	5.0	153.1	140.3	45.0	0.279	0.016	0.036	190	H4S31	5.3	138.5	110.4	60.2	-1.979	0.010	-0.203
30	H0S30	4.8	98.2	113.9	42.9	0.022	0.032	0.004	191	H4S32	5.3	152.7	129.0	62.9	-0.882	0.015	-0.107
31	H1S1	5.0	118.5	109.0	31.1	-0.075	0.013	-0.008	192	H4S33	5.4	151.6	125.3	55.8	-0.394	0.008	-0.036
32	H1S2	4.7	116.8	121.5	41.5	-0.664	0.017	-0.086	193	H4S34	5.4	144.4	118.1	62.0	-1.177	0.011	-0.125
33	H1S3	5.1	153.0	134.3	43.4	0.219	0.011	0.023	194	H4S35	5.4	134.6	111.5	51.9	-0.370	0.004	-0.025
34	H1S4	5.0	137.0	123.9	42.7	-0.433	0.006	-0.033	195	H4S36	5.4	135.7	108.5	47.7	-0.636	0.005	-0.044
35	H1S5	4.6	104.8	111.7	38.9	-1.738	0.021	-0.252	196	H4S37	5.4	154.4	131.8	68.3	-0.729	0.022	-0.110
36	H1S6	5.1	136.1	116.5	37.2	-0.073	0.006	-0.006	197	H4S38	5.5	148.3	124.9	63.7	-0.341	0.014	-0.040
37	H1S7	5.0	122.2	113.9	31.6	0.567	0.012	0.063	198	H4S39	5.4	141.8	120.0	55.4	-0.139	0.006	-0.011

38	H1S8	5.1	140.1	128.7	36.4	0.936	0.011	0.100
39	H1S9	5.1	123.5	110.1	29.7	0.556	0.013	0.063
40	H1S10	5.3	142.4	117.2	38.2	0.430	0.007	0.036
41	H1S11	4.9	128.8	135.6	53.3	-0.012	0.026	-0.002
42	H1S12	5.1	139.0	128.1	41.2	0.498	0.008	0.046
43	H1S13	5.2	126.3	106.9	33.7	-0.028	0.009	-0.003
44	H1S14	4.8	107.3	115.5	42.5	-0.239	0.021	-0.035
45	H1S15	4.8	103.2	111.4	39.7	-0.215	0.022	-0.032
46	H1S16	5.1	141.8	124.9	42.1	-0.199	0.006	-0.015
47	H1S17	5.1	120.8	117.6	34.9	1.094	0.012	0.121
48	H1S18	5.2	127.3	116.8	34.9	1.067	0.009	0.100
49	H1S19	4.7	139.5	127.1	38.1	-1.526	0.009	-0.147
50	H1S20	4.8	128.8	119.0	36.8	-1.069	0.008	-0.096
51	H1S21	4.7	138.8	133.4	48.1	-1.567	0.013	-0.177
52	H1S22	4.5	99.6	115.2	40.4	-1.615	0.032	-0.291
53	H1S23	4.8	141.9	127.0	38.6	-1.002	0.009	-0.094
54	H1S24	4.8	141.9	123.9	42.7	-1.956	0.005	-0.144
55	H1S25	4.6	98.3	110.6	39.0	-1.399	0.028	-0.238
56	H1S26	4.8	136.5	123.6	37.9	-1.145	0.008	-0.101
57	H1S27	5.1	134.9	116.5	34.8	0.070	0.008	0.006
58	H1S28	4.8	149.0	128.8	41.6	-1.940	0.009	-0.180
59	H1S29	4.8	145.8	129.9	41.9	-1.575	0.009	-0.147
60	H1S30	4.8	144.1	138.8	39.6	-0.087	0.018	-0.012
61	H1S31	4.5	94.1	106.8	38.0	-1.728	0.031	-0.307
62	H1S32	4.8	135.6	124.8	38.1	-1.111	0.009	-0.103
63	H1S33	4.8	153.1	138.9	52.8	-1.952	0.015	-0.240
64	H1S34	4.7	128.9	120.7	39.0	-1.451	0.008	-0.128
65	H1S35	5.0	148.8	126.7	43.9	-1.063	0.007	-0.089
66	H1S36	4.9	141.6	125.8	43.0	-1.308	0.006	-0.102
67	H1S37	4.5	104.8	113.0	37.7	-2.038	0.022	-0.306
68	H1S38	4.8	145.6	134.5	43.4	-0.917	0.012	-0.100
69	H1S39	4.8	134.2	118.6	40.5	-2.041	0.005	-0.142
70	H1S40	4.5	103.9	113.2	39.5	-1.930	0.023	-0.297
71	H1S41	4.8	129.0	116.7	36.0	-1.304	0.008	-0.113
72	H1S42	4.8	116.6	111.5	32.5	-0.719	0.013	-0.083
73	H1S43	4.5	123.2	129.1	48.5	-1.968	0.020	-0.281
74	H2S1	5.2	145.0	116.7	38.6	-0.605	0.008	-0.055
75	H2S2	5.1	146.2	121.6	44.3	-0.807	0.005	-0.059
76	H2S3	5.3	152.9	123.3	38.5	0.411	0.011	0.044
77	H2S4	5.3	137.8	115.0	34.3	0.857	0.009	0.081
78	H2S5	5.1	134.0	120.5	40.3	-0.020	0.006	-0.002
79	H2S6	5.0	134.4	119.5	37.5	-0.325	0.007	-0.027
80	H2S7	5.0	140.4	134.1	43.3	0.577	0.013	0.066
81	H2S8	5.4	129.2	100.8	40.5	-0.483	0.009	-0.046
82	H2S9	5.1	133.2	115.9	37.8	-0.155	0.006	-0.012
83	H2S10	5.3	140.4	114.5	44.1	-0.291	0.004	-0.019
84	H2S11	5.2	135.7	116.7	36.3	0.463	0.007	0.038
85	H2S12	5.0	133.7	121.6	36.7	-0.109	0.008	-0.010
86	H2S13	5.1	130.3	117.5	34.4	0.574	0.009	0.054
87	H2S14	5.3	153.1	130.3	42.5	0.932	0.010	0.092
88	H2S15	5.2	133.1	110.7	32.7	0.221	0.010	0.022
89	H2S16	5.0	160.2	143.9	54.7	-0.679	0.020	-0.098
90	H2S17	5.0	133.5	118.4	41.6	-0.591	0.005	-0.040
91	H2S18	5.1	155.9	139.8	52.3	-0.258	0.015	-0.032
92	H2S19	5.0	150.6	137.9	46.3	0.206	0.014	0.024
93	H2S20	5.1	138.7	121.3	38.1	0.273	0.007	0.022
94	H2S21	5.2	148.1	119.3	42.3	-0.654	0.007	-0.055
95	H2S22	5.2	145.4	124.2	40.1	0.546	0.007	0.046
96	H2S23	5.3	136.1	110.4	32.6	0.547	0.011	0.058
97	H2S24	5.2	133.7	110.0	34.4	-0.065	0.009	-0.006
98	H2S25	5.3	138.0	113.0	33.3	0.676	0.010	0.069
99	H2S26	5.3	135.4	110.9	34.8	0.283	0.009	0.027
100	H2S27	5.2	150.5	108.6	24.5	-0.453	0.035	-0.087
101	H2S28	5.3	155.3	123.9	32.0	0.900	0.019	0.126
102	H2S29	5.1	152.3	130.3	43.5	-0.425	0.009	-0.041
103	H2S30	5.1	161.3	137.1	44.1	-0.105	0.015	-0.013
104	H2S31	5.1	138.9	113.1	33.1	-0.344	0.011	-0.036
105	H2S32	5.1	142.0	115.8	31.2	-0.051	0.014	-0.006
106	H2S33	5.2	131.6	109.9	35.3	-0.176	0.008	-0.016
107	H2S34	5.2	156.9	130.6	41.2	0.070	0.012	0.008
108	H2S35	5.2	135.9	111.9	27.9	0.437	0.016	0.056
109	H2S36	4.9	132.5	124.4	42.8	-0.609	0.007	-0.053
110	H2S37	5.0	134.0	121.6	38.6	-0.290	0.007	-0.024
111	H2S38	5.1	123.2	96.5	27.0	-0.934	0.022	-0.139
112	H2S39	5.1	141.9	113.6	35.0	-0.677	0.010	-0.069
113	H2S40	5.1	138.3	116.5	33.9	-0.105	0.009	-0.010
114	H2S41	5.2	146.8	119.5	33.9	0.050	0.012	0.006
115	H2S42	5.1	140.3	106.0	32.3	-1.465	0.017	-0.191
116	H2S43	5.1	149.0	121.3	40.6	-0.724	0.008	-0.065
117	H3S1	5.0	157.9	135.4	50.6	-1.052	0.012	-0.116
118	H3S2	5.3	138.4	116.7	36.8	0.621	0.007	0.052
119	H3S3	5.2	130.3	104.1	33.8	-0.347	0.011	-0.037
120	H3S4	5.2	153.9	125.1	45.2	-0.441	0.008	-0.040
121	H3S5	5.3	131.6	108.1	31.5	0.691	0.012	0.076
122	H3S6	5.2	127.8	105.8	29.8	0.423	0.014	0.050
123	H3S7	5.3	134.7	113.0	29.1	1.129	0.014	0.134
124	H3S8	5.4	131.1	99.5	31.6	0.002	0.017	0.000
125	H3S9	5.4	150.9	117.6	33.5	0.859	0.016	0.110
126	H3S10	5.1	144.4	121.4	35.3	-0.057	0.010	-0.006
127	H3S11	5.2	131.0	109.6	36.4	0.070	0.007	0.006
128	H3S12	5.4	159.4	133.7	50.3	0.767	0.012	0.084
129	H3S13	5.3	151.0	117.0	34.5	0.101	0.015	0.013
130	H3S14	5.2	129.5	98.4	29.7	-0.648	0.020	-0.092
131	H3S15	5.3	163.6	137.2	42.5	1.214	0.017	0.161
132	H3S16	5.0	132.8	101.7	27.5	-1.443	0.021	-0.213
133	H3S17	5.0	154.8	117.7	30.2	-1.438	0.024	-0.224
134	H3S18	5.1	159.0	131.5	44.6	-0.692	0.012	-0.076
135	H3S19	5.0	163.7	139.4	46.8	-0.800	0.017	-0.104
136	H3S20	5.0	146.7	108.2	33.3	-2.174	0.019	-0.303
137	H3S21	5.2	108.6	82.2	35.6	-1.717	0.026	-0.280
138	H3S22	5.4	142.0	111.2	31.4	1.071	0.015	0.133
139	H3S23	5.3	142.4	117.2	36.2	0.626	0.009	0.058
140	H3S24	5.3	140.4	116.5	33.6	0.914	0.010	0.093
141	H3S25	5.3	151.0	120.9	36.9	0.388	0.012	0.042
142	H3S26	5.3	156.8	122.5	38.1	0.052	0.015	0.006
143	H3S27	5.1	138.8	117.4	36.9	-0.126	0.007	-0.011
144	H3S28	5.4	157.9	130.7	48.2	0.506	0.010	0.051
145	H3S29	5.3	149.9	110.6	32.1	-0.427	0.022	-0.063
146	H3S30	5.2	135.1	100.3	26.2	-0.683	0.026	-0.112
199	H4S40	5.4	136.7	115.6	55.3	-0.311	0.006	-0.023
200	H4S41	5.4	158.0	135.9	70.9	-0.716	0.028	-0.122
201	H4S42	5.3	159.2	135.8	65.9	-0.757	0.022	-0.113
202	H4S43	5.4	147.6	123.2	58.1	-0.405	0.009	-0.038
203	H5S1	5.5	122.9	99.6	45.6	-0.059	0.008	-0.005
204	H5S2	5.5	120.4	96.6	43.9	0.248	0.010	0.024
205	H5S3	5.5	135.7	107.6	54.7	-0.805	0.007	-0.068
206	H5S4	5.5	144.2	117.6	55.0	-0.189	0.006	-0.015
207	H5S5	5.5	130.2	108.3	48.2	0.624	0.004	0.040
208	H5S6	5.5	126.7	106.3	49.3	0.346	0.005	0.025
209	H5S7	5.6	144.5	116.9	52.6	0.492	0.005	0.036
210	H5S8	5.6	133.7	107.9	54.9	0.104	0.007	0.009
211	H5S9	5.5	149.5	125.5	62.1	-0.036	0.012	-0.004
212	H5S10	5.5	145.1	121.6	60.7	-0.086	0.010	-0.009
213	H5S11	5.5	145.3	120.5	58.6	-0.050	0.008	-0.005
214	H5S12	5.6	130.5	107.8	45.3	1.208	0.004	0.078
215	H5S13	5.6	127.1	101.5	51.7	0.073	0.008	0.007
216	H5S14	5.5	134.8	112.0	47.8	0.453	0.003	0.027
217	H5S15	5.5	139.5	117.6	50.4	0.925	0.004	0.057
218	H5S16	5.6	140.9	117.3	53.3	0.912	0.005	0.063
219	H5S17	5.4	146.2	122.2	62.9	-0.698	0.012	-0.078
220	H5S18	5.5	154.3	130.0	59.2	0.619	0.012	0.068
221	H5S19	5.6	129.8	105.0	42.7	1.296	0.006	0.098
222	H5S20	5.6	147.9	123.5	61.6	0.445	0.011	0.048
223	H5S21	5.6	151.6	125.6	58.2	0.740	0.010	0.073
224	H5S22	5.7	134.4	109.2	56.4	0.666	0.007	0.057
225	H5S23	5.6	135.9	100.2	50.9	-0.857	0.012	-0.092
226	H5S24	5.6	134.3	109.4	50.7	0.636	0.005	0.043
227	H5S25	5.5	140.3	110.3	56.9	-0.836	0.008	-0.077
228	H5S26	5.7	136.3	112.8	56.9	0.928	0.007	0.077
229	H5S27	5.6	150.7	125.4	60.8	0.549	0.011	0.059
230	H5S28	5.6	119.9	92.4	55.4	-1.073	0.017	-0.140
231	H5S29	5.6	151.9	123.6	53.5	0.888	0.007	0.077
232	H5S30	5.7	133.1	107.5	58.4	0.363	0.009	0.035
233	H5S31	5.6	131.3	104.8	42.9	0.794	0.006	0.062
234	H5S32	5.6	129.9	105.0	43.4	1.053	0.006	0.078
235	H5S33	5.6	132.0	107.1	40.9	1.406	0.006	0.106
236	H5S34	5.5	141.1	109.6	52.1	-0.541	0.007	-0.045
237	H5S35	5.6	130.1	108.3	48.0	1.052	0.004	0.067
238	H5S36	5.6	147.1	120.7	58.7	0.410	0.009	0.038
239	H5S37	5.6	125.1	100.0	43.5	0.757	0.008	0.067
240	H5S38	5.7	139.9	114.7	55.8	1.192	0.006	0.093
241	H5S39	5.6	137.3	116.0	49.9	1.331	0.003	0.079
242	H5S40	5.7	130.4	104.9	53.2	0.528	0.007	0.044
243	H5S41	5.6	136.6	114.3	47.9	1.534	0.003	0.088
244	H5S42	5.6	148.9	124.0	57.3	0.643	0.008	0.059
245	H5S43	5.6	146.9	123.2	61.6	0.480	0.011	0.051
246	H6S1	5.5	130.8	106.9	44.1	0.426	0.005	0.029
247	H6S2	5.6	140.5	114.7	56.8	0.480	0.007	0.040
248	H6S3	5.7	143.0	116.3	54.5	0.932	0.006	0.071
249	H6S4	5.6	135.4	111.1	52.4	0.614	0.005	0.043
250	H6S5	5.5	133.8	107.9	43.8	0.705	0.005	0.049
251	H6S6	5.7	143.0	118.4	57.4	0.940	0.007	0.080
252	H6S7	5.7	139.1	114.2	56.2	0.798	0.006	0.064
253	H6S8	5.6	136.6	108.1	50.0	0.356	0.005	0.026
254	H6S9	5.8	66.3	54.1	48.2	-0.017	0.086	-0.005
255	H6S10	5.9	130.6	104.6	42.5	2.618	0.006	0.204
256	H6S11	5.4	148.7	121.2	53.7	-0.521	0.006	-0.042
257	H6S12	5.5	130.2	107.7	45.3	0.467	0.004	0.030
258	H6S13	5.5	146.8	120.1	52.8	0.141	0.006	0.011
259	H6S14	5.4	127.3	102.5	56.3	-1.387	0.010	-0.139
260	H6S15	5.5	138.9	114.2	51.1	0.294	0.004	0.019
261	H6S16	5.5	143.3	118.9	56.8	0.053	0.007	0.004
262	H6S17	5.7	120.7	94.1	50.9	0.421	0.013	0.048
263	H6S18	5.5	120.0	91.3	53.7	-1.484	0.017	-0.194
264	H6S19	5.6	143.2	116.7	57.0	0.339	0.007	0.029
265	H6S20	5.4	143.2	118.3	54.0	-0.156	0.005	-0.011
266	H6S21	5.5	111.6	81.5	50.7	-2.025	0.026	-0.333
267	H6S22	5.6	134.1	106.7	55.0	-0.082	0.007	-0.007
268	H6S23	5.5	118.4	92.9	51.9	-0.984	0.014	-0.118
269	H6S24	5.5	126.7	102.8	54.6	-0.578	0.009	-0.054
270	H6S25	5.5	126.5	101.4	48.4	0.000	0.007	0.000
271	H6S26	5.5	142.3	118.6	58.1	-0.198	0.008	-0.017
272	H6S27	5.5	142.1	117.1	56.8	0.081	0.007	0.007
273	H6S28	5.5	134.8	108.6	57.7	-0.717	0.009	-0.067
274	H6S29	5.6	142.0	115.1	54.0	0.319	0.006	0.024
275	H6S30	5.4	133.1	112.8	51.0	-0.019	0.004	-0.001
276	H6S31	5.6	153.1	128.5	58.7	0.786	0.011	0.083
277	H6S32	5.5	147.4	122.4	55.3	0.507	0.007	0.042
278	H6S33	5.7	137.9	114.3	62.8	0.480	0.012	0.053
279	H6S34	5.6	134.8	108.6	53.1	0.274	0.006	0.021
280	H6S35	5.5	144.1	118.7	57.1	0.108	0.007	0.009
281	H6S36	5.6	133.0	106.3	54.2	0.028	0.007	0.002
282	H6S37	5.5	133.3	106.2	51.9	-0.383	0.006	-0.030
283	H6S38	5.5	137.3	110.0	55.9	-0.561	0.007	-0.048
284	H6S39	5.6	137.5	111.7	55.8	0.397	0.007	0.032
285	H6S40	5.5	134.6	109.7	47.3	0.207	0.004	0.013
286	H6S41	5.5	144.2	119.8	58.4	-0.207	0.008	-0.019
287	H7S1	5.5	138.6	112.9	55.5	-0.065	0.006	-0.005
288	H7S2	5.7	136.1	110.3	50.5	1.378	0.005	0.093
289	H7S3	5.8	129.9	102.8	50.3	1.134	0.007	0.095
290	H7S4	5.9	136.0	109.1	51.1	1.994	0.005	0.143
291	H7S5	5.8	121.1	93.2	47.9	0.773	0.013	0.088
292	H7S6	5.7	150.6	122.3	51.8	1.734	0.007	0.140
293	H7S7	5.8	125.0	97.9	49.3	1.300	0.010	0.127
294	H7S8	6.0	125.2	98.4	50.8	2.031	0.010	0.200
295	H7S9	5.8	113.2	89.0	51.4	0.502	0.018	0.068
296	H7S10	5.8	126.9	98.2	45.6	1.189	0.009	0.115
297	H7S11	5.7	126.8	99.3	50.3	0.504	0.009	0.048
298	H7S12	5.6	133.6	108.4	54.2	0.074	0.006	0.006
299	H7S13	5.8	127.0	99.3	48.6	1.220	0.009	0.114
300	H7S14	5.6	117.1	92.3	48.2	-0.051	0.013	-0.006
301	H7S15	5.7	131.6	104.4	50.9	0.763	0.007	0.062
302	H7S16	5.6	125.6	100.1	49.5	0.368	0.008	0.033
303	H7S17	5.6	127.9	102.9	51.5	0.208	0.007	0.018
304	H7S18	5.6	136.5	106.8	48.5	0.149	0.006	0.012
305	H7S19	5.7	100.4	85.8	69.3	-0.990	0.048	-0.221
306	H7S20	5.6	106.2	84.5	52.2	-0.607	0.024	-0.095
307	H7S21	5.6	128.0	101.7	52.6	-0.223	0.008	-0.020

147	H3S31	5.3	138.0	108.8	30.3	0.396	0.015	0.050
148	H3S32	5.4	159.7	135.5	54.5	0.595	0.013	0.069
149	H3S33	5.3	142.7	121.7	38.8	0.769	0.007	0.063
150	H3S34	5.2	150.8	126.4	42.3	0.051	0.008	0.005
151	H3S35	5.3	159.3	136.1	49.5	0.587	0.013	0.067
152	H3S36	5.4	138.6	117.5	30.7	1.855	0.013	0.210
153	H3S37	5.2	155.2	133.5	46.7	0.228	0.011	0.024
154	H3S38	5.4	157.6	129.2	39.5	1.309	0.013	0.153
155	H3S39	5.4	142.7	113.9	39.6	0.441	0.007	0.038
156	H3S40	5.4	144.9	116.5	42.6	0.159	0.006	0.012
157	H3S41	5.4	148.8	115.0	33.7	0.488	0.015	0.061
158	H3S42	5.3	152.5	106.0	32.2	-1.068	0.030	-0.187
159	H3S43	5.4	139.4	111.1	38.0	0.470	0.008	0.042
160	H4S1	5.5	138.1	119.6	47.4	1.217	0.004	0.073
161	H4S2	5.4	161.6	138.0	66.1	-0.099	0.024	-0.015
308	H7S22	5.7	110.7	85.7	50.7	-0.062	0.021	-0.009
309	H7S23	5.7	117.7	91.8	49.8	0.272	0.014	0.033
310	H7S24	5.7	122.5	95.8	48.6	0.531	0.011	0.055
311	H7S25	5.6	131.8	105.2	51.7	0.200	0.006	0.016
312	H7S26	5.8	127.5	102.2	51.2	1.330	0.007	0.115
313	H7S27	5.6	115.3	89.4	50.1	-0.469	0.017	-0.061
314	H7S28	5.7	103.5	76.0	45.9	-0.351	0.032	-0.064
315	H7S29	5.7	105.3	80.1	52.7	-0.580	0.030	-0.101
316	H7S30	5.7	113.0	84.2	44.1	0.334	0.021	0.049
317	H7S31	5.6	131.9	105.8	50.7	0.350	0.006	0.027
318	H7S32	5.6	106.9	83.3	50.9	-0.693	0.024	-0.110
319	H7S33	5.8	151.2	116.0	73.4	-0.870	0.029	-0.149
320	H7S34	5.7	128.4	100.4	46.7	0.867	0.008	0.077
321	H7S35	5.8	120.1	92.0	47.4	0.749	0.014	0.088

Note: Table rows with different colors represent data samples identified as influential point.

Based on the results of the first iteration of the calculation of diagnostic parameters from the multiple linear regression model for predicting the pH of lady finger banana as presented in Table 1. It can be confirmed that in the 321 samples data from the measurement of acidity levels (pH) and peel color components (R, G and B) of lady finger banana, there are outliers, high leverage points and influential points, the details of which are presented in Table 2.

Table 2. Details of data detected as outlier datas, high leverage points and influential points from the results of the first stage iteration of the pH prediction regression model of lady finger banana.

No	Data Categories Based on Diagnostic Parameter Results	Sample Code of Data	Total
1	Outlier (-1,967 < t_i > 1,967)	H0S3, H0S4, H0S8, H0S9, H0S12, H0S13, H0S18, H0S22, H1S37, H1S39, H1S43, H3S20, H4S31, H6S10, H6S21, H7S4, H7S8	17
2	High Leverage Point (h_{ii} > 0,0249)	H0S3, H0S4, H0S6, H0S8, H0S9, H0S10, H0S12, H0S13, H0S16, H0S17, H0S18, H0S19, H0S21, H0S22, H0S30, H1S11, H1S22, H1S25, H1S31, H2S27, H3S21, H3S30, H3S42, H4S3, H4S12, H4S41, H6S9, H6S21, H7S19, H7S28, H7S29, H7S33	32
3	Influential Point (-0,2233 < $DFFITS_i$ > 0,2233	H0S3, H0S4, H0S8, H0S9, H0S12, H0S13, H0S18, H0S22, H1S5, H1S22, H1S25, H1S31, H1S33, H1S37, H1S40, H1S43, H3S17, H3S20, H3S21, H6S21	20

The DFFITS test is not a formal hypothesis test like the t-test or F-test, but rather a diagnostic metric in regression analysis. This test aims to identify influential outliers based on a linear regression prediction model (Zulkarnain et al., 2020). Simply put, this test measures how much the predicted pH value for a sample change if that sample is removed from the analysis to ensure the robustness of the model. The next data iteration stage is carried out by excluding data that have been detected as influential point data from the previous iteration. In the second data iteration stage, 20 data sets identified as influential points were removed from the 321 data sets used in the first iteration stage. The data identified as influential point can be seen in Figure 1. Thus, the total number of data sets used in the second iteration process is 301. The influence of influential points that have been removed from the laboratory measurement sample data set can be seen in the multiple linear regression model in the first, second and final iterations as presented in Table 3.

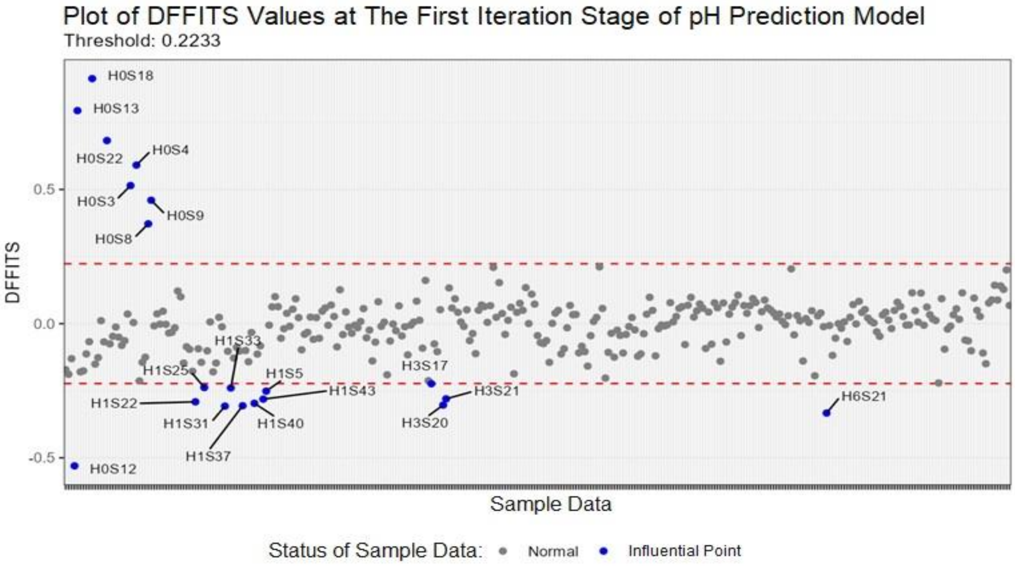

Fig. 1. Plot of $DFFITS_i$ values at the first iteration stage of pH prediction model.

Table 3. Comparison of the results of the first and second stage data iterations and the results of the final stage iteration in the multiple linear regression model for predicting pH of lady finger banana.

No	Differentiator		First Stage Iteration Results	Second Stage Iteration Results	Last Stage (17th) Iteration Results
1	Number of iteration data sets		321	301	178
2	Regression equation model		$\hat{y}_i = 5,3908 + 0,0130R – 0,0224G + 0,0157B$	$\hat{y}_i = 5,3924 + 0,0161R – 0,0258G + 0,0151B$	$\hat{y}_i = 5,8096 + 0,0143R – 0,0263G + 0,0138B$
3	Number of influential point data		20	13	0
4	Intercept (b_0)		5,3908	5,3924	5,8096
5	Slope	R (b_1)	0,0130	0,0161	0,0143
		G (b_2)	-0,0224	-0,0258	-0,0263
		B (b_3)	0,0157	0,0151	0,0138
6	s^2		0,0304	0,0188	0,0072
7	R^2		70,93%	79,52%	82,25%

The influence of the 20 influential point data sets removed from the 321 data sets used in the first iteration stage can be seen in the results of the second iteration stage as presented in Table 3. The s^2 and R^2 values increased from 0.0304 to 0.0188 and from 70.93% to 79.52%, respectively. In the second iteration stage, 13 data sets were still found as influential points. The data iteration on the prediction model for the acidity level (pH) of lady finger banana stopped and reached a convergent state in the 17th iteration stage. In the 17th iteration stage, no outlier data was detected as influential point. The final number of data sets that were free from influential point was 178 data sets. The final result of the iteration process obtained a regression model $\hat{y}_i = 5,8096 + 0,0143R – 0,0263G + 0,0138B$, with a value of $s^2 = 0,0072$ and $R^2 = 82,25\%$.

Brix Prediction Model of Lady Finger Banana

A multiple linear regression model with total dissolved solids (Brix) as the dependent variable and the peel color components Red (R), Green (G) and Blue (B) as independent variables from 321 lady finger banana samples data was formed using the R Studio application. The multiple linear regression model at the initial stage (first iteration) is $\hat{y}_i = 14,4582 + 0,1236R – 0,0708G – 0,0637B$, with $R^2 = 34,24\%$ and $s^2 = 2,0792$. The results of the first iteration of the diagnostic parameter calculation are presented in Table 4.

Table 4. Results of the calculation of the diagnostic parameters of the first stage iteration of the regression model for predicting the Brix of lady finger bananas.

No	Sample Code	Regression Variable				Diagnostic Parameters		
		Brix (x)	R (y_1)	G (y_2)	B (y_3)	t_i	h_{ii}	DFFITS
1	H0S1	21.0	134.6	119.3	35.9	0.322	0.008	0.028
2	H0S2	20.4	136.4	122.9	39.6	0.162	0.007	0.013
3	H0S3	5.8	97.9	112.6	42.2	-5.149	0.031	-0.920
4	H0S4	7.0	110.2	126.8	47.5	-4.578	0.034	-0.856
5	H0S5	16.9	112.8	123.6	46.9	0.106	0.025	0.017
6	H0S6	16.7	95.7	108.9	34.1	0.157	0.031	0.028
7	H0S7	20.1	118.8	119.6	39.9	0.939	0.013	0.108
8	H0S8	7.5	99.2	112.9	41.2	-4.298	0.029	-0.747
9	H0S9	6.3	97.3	109.7	40.7	-4.953	0.029	-0.851
10	H0S10	16.8	100.8	112.6	38.9	0.175	0.027	0.029
11	H0S11	19.8	123.0	123.1	42.2	0.732	0.012	0.082
12	H0S12	5.1	73.5	71.1	52.2	-5.191	0.061	-1.328
13	H0S13	5.0	106.8	123.8	44.7	-5.683	0.033	-1.053
14	H0S14	19.0	104.8	114.5	40.6	1.111	0.023	0.171
15	H0S15	18.0	113.1	121.5	46.5	0.562	0.021	0.083
16	H0S16	18.2	99.7	113.3	37.4	0.876	0.029	0.153
17	H0S17	18.3	107.3	120.5	43.0	0.916	0.027	0.153
18	H0S18	5.0	98.7	114.1	40.6	-5.627	0.032	-1.015
19	H0S19	19.1	132.5	139.7	54.5	0.807	0.030	0.141
20	H0S20	21.0	148.9	138.1	42.9	0.317	0.015	0.039
21	H0S21	19.4	101.8	114.9	39.7	1.481	0.028	0.251
22	H0S22	5.3	106.7	121.0	47.3	-5.510	0.030	-0.967
23	H0S23	19.1	107.6	118.7	41.1	1.165	0.024	0.184
24	H0S24	20.6	131.0	118.6	34.6	0.255	0.009	0.024
25	H0S25	20.6	136.6	119.0	37.6	0.054	0.006	0.004
26	H0S26	20.3	133.4	120.4	38.5	0.162	0.006	0.013
27	H0S27	20.6	122.8	111.9	36.4	0.565	0.008	0.050
28	H0S28	18.6	105.8	116.6	43.2	0.994	0.024	0.156
29	H0S29	20.8	153.1	140.3	45.0	0.107	0.016	0.014
30	H0S30	18.6	98.2	113.9	42.9	1.369	0.032	0.250
31	H1S1	22.4	118.5	109.0	31.1	1.467	0.013	0.166
32	H1S2	18.6	116.8	121.5	41.5	0.461	0.017	0.060
33	H1S3	21.8	153.0	134.3	43.4	0.343	0.011	0.037
34	H1S4	21.4	137.0	123.9	42.7	0.737	0.006	0.056
35	H1S5	17.4	104.8	111.7	38.9	0.180	0.021	0.026
36	H1S6	20.8	136.1	116.5	37.2	0.066	0.006	0.005
37	H1S7	22.2	122.2	113.9	31.6	1.299	0.012	0.143
38	H1S8	21.6	140.1	128.7	36.4	0.624	0.011	0.067
39	H1S9	21.5	123.5	110.1	29.7	0.722	0.013	0.082
40	H1S10	20.2	142.4	117.2	38.2	-0.533	0.007	-0.045
41	H1S11	18.5	128.8	135.6	53.3	0.544	0.026	0.089
42	H1S12	22.0	139.0	128.1	41.2	1.008	0.008	0.093
43	H1S13	20.8	126.3	106.9	33.7	0.228	0.009	0.022
44	H1S14	18.1	107.3	115.5	42.5	0.619	0.021	0.091
45	H1S15	17.0	103.2	111.4	39.7	0.099	0.022	0.015
46	H1S16	22.3	141.8	124.9	42.1	0.886	0.006	0.069
47	H1S17	20.4	120.8	117.6	34.9	0.768	0.012	0.085
48	H1S18	21.1	127.3	116.8	34.9	0.677	0.009	0.064
49	H1S19	21.6	139.5	127.1	38.1	0.653	0.009	0.063
50	H1S20	21.2	128.8	119.0	36.8	0.753	0.008	0.067
51	H1S21	20.3	138.8	133.4	48.1	0.576	0.013	0.065
52	H1S22	18.8	99.6	115.2	40.4	1.350	0.032	0.244
53	H1S23	21.4	141.9	127.0	38.6	0.395	0.009	0.037
54	H1S24	21.3	141.9	123.9	42.7	0.380	0.005	0.028
55	H1S25	17.2	98.3	110.6	39.0	0.442	0.028	0.075
56	H1S26	21.2	136.5	123.6	37.9	0.516	0.008	0.046
57	H1S27	20.4	134.9	116.5	34.8	-0.141	0.008	-0.013
58	H1S28	21.3	149.0	128.8	41.6	0.079	0.009	0.007
59	H1S29	21.9	145.8	129.9	41.9	0.622	0.009	0.058
60	H1S30	22.2	144.1	138.8	39.6	1.093	0.018	0.150
61	H1S31	17.6	94.1	106.8	38.0	0.711	0.031	0.127
62	H1S32	21.0	135.6	124.8	38.1	0.502	0.009	0.047
63	H1S33	21.4	153.1	138.9	52.8	0.587	0.015	0.072
64	H1S34	21.5	128.9	120.7	39.0	1.020	0.008	0.090
65	H1S35	20.4	148.8	126.7	43.9	-0.333	0.007	-0.028
66	H1S36	21.3	141.6	125.8	43.0	0.459	0.006	0.036
67	H1S37	19.0	104.8	113.0	37.7	0.967	0.022	0.145
68	H1S38	22.1	145.6	134.5	43.4	0.924	0.012	0.101
69	H1S39	21.6	134.2	118.6	40.5	0.736	0.005	0.051
70	H1S40	20.0	103.9	113.2	39.5	1.594	0.023	0.245
71	H1S41	21.0	129.0	116.7	36.0	0.542	0.008	0.047
72	H1S42	22.0	116.6	111.5	32.5	1.520	0.013	0.175
73	H1S43	19.9	123.2	129.1	48.5	1.187	0.020	0.170
74	H2S1	20.9	145.0	116.7	38.6	-0.366	0.008	-0.033
75	H2S2	21.3	146.2	121.6	44.3	0.099	0.005	0.007
76	H2S3	20.6	152.9	123.3	38.5	-0.760	0.011	-0.081
77	H2S4	21.0	137.8	115.0	34.3	-0.064	0.009	-0.006
78	H2S5	21.7	134.0	120.5	40.3	0.873	0.006	0.065
79	H2S6	22.5	134.4	119.5	37.5	1.112	0.007	0.091
80	H2S7	22.7	140.4	134.1	43.3	1.540	0.013	0.176
81	H2S8	20.3	129.2	100.8	40.5	-0.183	0.009	-0.017
82	H2S9	21.4	133.2	115.9	37.8	0.526	0.006	0.040
83	H2S10	20.3	140.4	114.5	44.1	-0.301	0.004	-0.020
84	H2S11	22.2	135.7	116.7	36.3	0.728	0.007	0.061
85	H2S12	22.8	133.7	121.6	36.7	1.352	0.008	0.121
86	H2S13	22.7	130.3	117.5	34.4	1.291	0.009	0.121
87	H2S14	21.4	153.1	130.3	42.5	-0.036	0.010	-0.004
88	H2S15	20.6	133.1	110.7	32.7	-0.187	0.010	-0.019
89	H2S16	22.2	160.2	143.9	54.7	0.787	0.020	0.113
90	H2S17	22.7	133.5	118.4	41.6	1.327	0.005	0.089
91	H2S18	22.1	155.9	139.8	52.3	0.763	0.015	0.096
92	H2S19	21.6	150.6	137.9	46.3	0.600	0.014	0.070
93	H2S20	22.1	138.7	121.3	38.1	0.714	0.007	0.058
94	H2S21	21.6	148.1	119.3	42.3	0.007	0.007	0.001
95	H2S22	21.0	145.4	124.2	40.1	-0.025	0.007	-0.002
96	H2S23	20.7	136.1	110.4	32.6	-0.317	0.011	-0.034
97	H2S24	21.6	133.7	110.0	34.4	0.301	0.009	0.029
98	H2S25	20.4	138.0	113.0	33.3	-0.478	0.010	-0.049
99	H2S26	21.7	135.4	110.9	34.8	0.262	0.009	0.025
100	H2S27	21.7	150.5	108.6	24.5	-1.049	0.035	-0.201
101	H2S28	20.6	155.3	123.9	32.0	-1.104	0.019	-0.155
102	H2S29	20.6	152.3	130.3	43.5	-0.332	0.009	-0.032
103	H2S30	20.7	161.3	137.1	44.1	-0.561	0.015	-0.070
162	H4S3	21.0	162.5	140.8	67.1	0.357	0.027	0.060
163	H4S4	22.1	138.7	118.9	50.9	1.022	0.004	0.064
164	H4S5	19.8	131.2	108.3	48.2	-0.068	0.004	-0.004
165	H4S6	20.8	136.5	117.6	49.2	0.435	0.003	0.026
166	H4S7	20.1	133.2	114.1	49.9	0.194	0.004	0.012
167	H4S8	20.2	127.7	97.9	49.2	0.010	0.010	0.001
168	H4S9	20.5	142.2	122.7	65.4	0.649	0.015	0.081
169	H4S10	19.2	145.7	121.7	65.3	-0.237	0.015	-0.029
170	H4S11	19.0	148.9	124.2	64.8	-0.451	0.015	-0.055
171	H4S12	19.6	152.0	130.2	71.3	0.066	0.026	0.011
172	H4S13	19.1	152.1	130.1	66.6	-0.345	0.019	-0.048
173	H4S14	20.3	147.9	113.8	57.6	-0.346	0.010	-0.035
174	H4S15	21.7	149.4	127.3	64.3	0.911	0.015	0.113
175	H4S16	19.9	153.0	128.1	58.4	-0.344	0.011	-0.036
176	H4S17	21.6	140.9	121.0	52.7	0.810	0.005	0.057
177	H4S18	20.3	157.0	133.2	68.2	0.092	0.023	0.014
178	H4S19	20.2	144.9	111.4	56.2	-0.350	0.009	-0.034
179	H4S20	21.9	141.9	121.5	51.1	0.833	0.004	0.056
180	H4S21	19.8	136.3	113.6	51.9	-0.065	0.004	-0.004
181	H4S22	19.2	141.8	118.6	50.5	-0.576	0.004	-0.036
182	H4S23	21.0	153.4	124.5	61.3	0.160	0.012	0.018
183	H4S24	21.0	149.1	116.0	56.3	-0.059	0.009	-0.006
184	H4S25	20.5	156.1	131.5	65.0	0.084	0.018	0.011
185	H4S26	20.3	137.6	107.6	53.8	-0.074	0.007	-0.006
186	H4S27	20.1	146.1	122.3	57.3	-0.039	0.008	-0.003
187	H4S28	21.8	136.2	115.6	52.8	0.989	0.004	0.066
188	H4S29	22.5	140.3	119.5	50.2	1.137	0.004	0.071
189	H4S30	21.6	140.5	120.5	53.1	0.817	0.005	0.058
190	H4S31	20.7	138.5	110.4	60.2	0.374	0.010	0.038
191	H4S32	20.2	152.7	129.0	62.9	0.018	0.015	0.002
192	H4S33	19.9	151.6	125.3	55.8	-0.400	0.008	-0.037
193	H4S34	21.0	144.4	118.1	62.0	0.486	0.011	0.052
194	H4S35	20.1	134.6	111.5	51.9	0.099	0.004	0.007
195	H4S36	20.4	135.7	108.5	47.7	-0.055	0.005	-0.004
196	H4S37	19.5	154.4	131.8	68.3	-0.157	0.022	-0.024
197	H4S38	19.6	148.3	124.9	63.7	-0.139	0.014	-0.016
198	H4S39	19.8	141.8	120.0	55.4	-0.077	0.006	-0.006
199	H4S40	19.4	136.7	115.6	55.3	-0.107	0.006	-0.008
200	H4S41	19.3	158.0	135.9	70.9	-0.255	0.028	-0.043
201	H4S42	21.1	159.2	135.8	65.9	0.379	0.022	0.056
202	H4S43	19.9	147.6	123.2	58.1	-0.183	0.009	-0.017
203	H5S1	21.4	122.9	99.6	45.6	0.841	0.008	0.074
204	H5S2	20.0	120.4	96.6	43.9	0.156	0.010	0.015
205	H5S3	20.6	135.7	107.6	54.7	0.231	0.007	0.020
206	H5S4	19.6	144.2	117.6	55.0	-0.409	0.006	-0.032
207	H5S5	21.5	130.2	108.3	48.2	0.797	0.004	0.051
208	H5S6	19.6	126.7	106.3	49.3	0.068	0.005	0.005
209	H5S7	20.0	144.5	116.9	52.6	-0.335	0.005	-0.024
210	H5S8	19.7	133.7	107.9	54.9	-0.056	0.007	-0.005
211	H5S9	18.3	149.5	125.5	62.1	-0.855	0.012	-0.096
212	H5S10	20.2	145.1	121.6	60.7	0.149	0.010	0.015
213	H5S11	20.4	145.3	120.5	58.6	0.117	0.008	0.011
214	H5S12	20.7	130.5	107.8	45.3	0.305	0.004	0.020
215	H5S13	19.5	127.1	101.5	51.7	-0.076	0.008	-0.007
216	H5S14	19.2	134.8	112.0	47.8	-0.471	0.003	-0.028
217	H5S15	20.5	139.5	117.6	50.4	0.146	0.004	0.009
218	H5S16	19.9	140.9	117.3	53.3	-0.150	0.005	-0.010
219	H5S17	19.0	146.2	122.2	62.9	-0.407	0.012	-0.046
220	H5S18	20.5	154.3	130.0	59.2	-0.030	0.012	-0.003
221	H5S19	20.0	129.8	105.0	42.7	-0.156	0.006	-0.012
222	H5S20	19.1	147.9	123.5	61.6	-0.484	0.011	-0.052
223	H5S21	21.2	151.6	125.6	58.2	0.289	0.010	0.029
224	H5S22	19.3	134.4	109.2	56.4	-0.216	0.007	-0.019
225	H5S23	21.0	135.9	100.2	50.9	0.039	0.012	0.004
226	H5S24	20.5	134.3	109.4	50.7	0.215	0.005	0.015
227	H5S25	20.2	140.3	110.3	56.9	-0.065	0.008	-0.006
228	H5S26	19.6	136.3	112.8	56.9	-0.063	0.007	-0.005
229	H5S27	19.1	150.7	125.4	60.8	-0.613	0.011	-0.066
230	H5S28	19.9	119.9	92.4	55.4	0.354	0.017	0.046
231	H5S29	18.9	151.9	123.6	53.5	-1.038	0.007	-0.090
232	H5S30	21.1	133.1	107.5	58.4	0.735	0.009	0.071
233	H5S31	19.0	131.3	104.8	42.9	-0.725	0.006	-0.056
234	H5S32	21.7	129.9	105.0	43.4	0.664	0.006	0.049
235	H5S33	20.7	132.0	107.1	40.9	0.055	0.006	0.004
236	H5S34	21.1	141.1	109.6	52.1	0.135	0.007	0.011
237	H5S35	19.0	130.1	108.3	48.0	-0.394	0.004	-0.025
238	H5S36	19.2	147.1	120.7	58.7	-0.568	0.009	-0.053
239	H5S37	20.0	125.1	100.0	43.5	-0.022	0.008	-0.002
240	H5S38	19.7	139.9	114.7	55.8	-0.167	0.006	-0.013
241	H5S39	19.6	137.3	116.0	49.9	-0.223	0.003	-0.013
242	H5S40	21.1	130.4	104.9	53.2	0.631	0.007	0.053
243	H5S41	20.8	136.6	114.3	47.9	0.292	0.003	0.017
244	H5S42	19.2	148.9	124.0	57.3	-0.582	0.008	-0.053
245	H5S43	19.2	146.9	123.2	61.6	-0.390	0.011	-0.042
246	H6S1	20.1	130.8	106.9	44.1	-0.085	0.005	-0.006
247	H6S2	19.1	140.5	114.7	56.8	-0.487	0.007	-0.040
248	H6S3	20.4	143.0	116.3	54.5	0.002	0.006	0.000
249	H6S4	20.0	135.4	111.1	52.4	0.006	0.005	0.000
250	H6S5	20.1	133.8	107.9	43.8	-0.240	0.005	-0.017
251	H6S6	20.4	143.0	118.4	57.4	0.145	0.007	0.012
252	H6S7	19.0	139.1	114.2	56.2	-0.492	0.006	-0.039
253	H6S8	20.3	136.6	108.1	50.0	-0.117	0.005	-0.009
254	H6S9	20.0	66.3	54.1	48.2	2.147	0.086	0.657
255	H6S10	21.0	130.6	104.6	42.5	0.236	0.006	0.018
256	H6S11	21.4	148.7	121.2	53.7	0.254	0.006	0.020
257	H6S12	19.6	130.2	107.7	45.3	-0.209	0.004	-0.014
258	H6S13	20.9	146.8	120.1	52.8	0.082	0.006	0.006
259	H6S14	20.3	127.3	102.5	56.3	0.460	0.010	0.046
260	H6S15	19.4	138.9	114.2	51.1	-0.415	0.004	-0.027
261	H6S16	20.0	143.3	118.9	56.8	-0.055	0.007	-0.005
262	H6S17	22.0	120.7	94.1	50.9	1.210	0.013	0.137
263	H6S18	19.9	120.0	91.3	53.7	0.225	0.017	0.029
264	H6S19	21.3	143.2	116.7	57.0	0.487	0.007	0.041

104	H2S31	21.6	138.9	113.1	33.1	0.057	0.011	0.006
105	H2S32	23.2	142.0	115.8	31.2	0.650	0.014	0.076
106	H2S33	20.9	131.6	109.9	35.3	0.085	0.008	0.008
107	H2S34	20.6	156.9	130.6	41.2	-0.664	0.012	-0.074
108	H2S35	21.5	135.9	111.9	27.9	-0.010	0.016	-0.001
109	H2S36	22.9	132.5	124.4	42.8	1.755	0.007	0.152
110	H2S37	22.4	134.0	121.6	38.6	1.168	0.007	0.097
111	H2S38	21.7	123.2	96.5	27.0	0.291	0.022	0.043
112	H2S39	21.1	141.9	113.6	35.0	-0.314	0.010	-0.032
113	H2S40	21.0	138.3	116.5	33.9	-0.086	0.009	-0.008
114	H2S41	20.9	146.8	119.5	33.9	-0.509	0.012	-0.057
115	H2S42	21.5	140.3	106.0	32.3	-0.338	0.017	-0.044
116	H2S43	20.6	149.0	121.3	40.6	-0.548	0.008	-0.049
117	H3S1	22.8	157.9	135.4	50.6	0.804	0.012	0.089
118	H3S2	21.2	138.4	116.7	36.8	0.128	0.007	0.011
119	H3S3	20.2	130.3	104.1	33.8	-0.393	0.011	-0.042
120	H3S4	20.2	153.9	125.1	45.2	-0.746	0.008	-0.068
121	H3S5	20.9	131.6	108.1	31.5	-0.078	0.012	-0.009
122	H3S6	21.6	127.8	105.8	29.8	0.357	0.014	0.042
123	H3S7	21.4	134.7	113.0	29.1	0.055	0.014	0.007
124	H3S8	20.2	131.1	99.5	31.6	-0.696	0.017	-0.092
125	H3S9	20.3	150.9	117.6	33.5	-1.139	0.016	-0.145
126	H3S10	23.9	144.4	121.4	35.3	1.192	0.010	0.119
127	H3S11	22.4	131.0	109.6	36.4	0.895	0.007	0.075
128	H3S12	19.7	159.4	133.7	50.3	-0.880	0.012	-0.096
129	H3S13	21.1	151.0	117.0	34.5	-0.760	0.015	-0.095
130	H3S14	21.1	129.5	98.4	29.7	-0.229	0.020	-0.032
131	H3S15	21.5	163.6	137.2	42.5	-0.356	0.017	-0.047
132	H3S16	19.9	132.8	101.7	27.5	-0.971	0.021	-0.143
133	H3S17	21.2	154.8	117.7	30.2	-1.025	0.024	-0.160
134	H3S18	19.5	159.0	131.5	44.6	-1.202	0.012	-0.131
135	H3S19	21.6	163.7	139.4	46.8	-0.115	0.017	-0.015
136	H3S20	20.3	146.7	108.2	33.3	-1.216	0.019	-0.170
137	H3S21	20.2	108.6	82.2	35.6	0.184	0.026	0.030
138	H3S22	20.1	142.0	111.2	31.4	-0.969	0.015	-0.120
139	H3S23	19.8	142.4	117.2	36.2	-0.783	0.009	-0.073
140	H3S24	20.8	140.4	116.5	33.6	-0.284	0.010	-0.029
141	H3S25	20.1	151.0	120.9	36.9	-1.003	0.012	-0.109
142	H3S26	21.0	156.8	122.5	38.1	-0.843	0.015	-0.103
143	H3S27	22.5	138.8	117.4	36.9	0.745	0.007	0.062
144	H3S28	20.7	157.9	130.7	48.2	-0.444	0.010	-0.045
145	H3S29	21.3	149.9	110.6	32.1	-0.899	0.022	-0.134
146	H3S30	21.1	135.1	100.3	26.2	-0.641	0.026	-0.105
147	H3S31	20.0	138.0	108.8	30.3	-0.912	0.015	-0.114
148	H3S32	19.7	159.7	135.5	54.5	-0.692	0.013	-0.081
149	H3S33	21.9	142.7	121.7	38.8	0.449	0.007	0.037
150	H3S34	22.2	150.8	126.4	42.3	0.363	0.008	0.033
151	H3S35	22.2	159.3	136.1	49.5	0.423	0.013	0.048
152	H3S36	21.1	138.6	117.5	30.7	-0.118	0.013	-0.013
153	H3S37	21.5	155.2	133.5	46.7	0.136	0.011	0.014
154	H3S38	19.4	157.6	129.2	39.5	-1.381	0.013	-0.161
155	H3S39	20.4	142.7	113.9	39.6	-0.533	0.007	-0.045
156	H3S40	20.8	144.9	116.5	42.6	-0.280	0.006	-0.022
157	H3S41	19.9	148.8	115.0	33.7	-1.273	0.015	-0.159
158	H3S42	21.4	152.5	106.0	32.2	-1.137	0.030	-0.199
159	H3S43	19.9	139.4	111.1	38.0	-0.727	0.008	-0.065
160	H4S1	20.9	138.1	119.6	47.4	0.433	0.004	0.026
161	H4S2	19.2	161.6	138.0	66.1	-0.099	0.024	-0.097
265	H6S20	18.2	143.2	118.3	54.0	-1.048	0.005	-0.077
266	H6S21	20.7	111.6	81.5	50.7	0.690	0.026	0.114
267	H6S22	21.0	134.1	106.7	55.0	0.479	0.007	0.042
268	H6S23	20.1	118.4	92.9	51.9	0.445	0.014	0.054
269	H6S24	20.8	126.7	102.8	54.6	0.678	0.009	0.064
270	H6S25	20.9	126.5	101.4	48.4	0.530	0.007	0.045
271	H6S26	18.8	142.3	118.6	58.1	-0.567	0.008	-0.050
272	H6S27	21.7	142.1	117.1	56.8	0.779	0.007	0.064
273	H6S28	19.8	134.8	108.6	57.7	0.020	0.009	0.002
274	H6S29	19.1	142.0	115.1	54.0	-0.653	0.006	-0.049
275	H6S30	19.6	133.1	112.8	51.0	-0.036	0.004	-0.002
276	H6S31	20.5	153.1	128.5	58.7	-0.023	0.011	-0.002
277	H6S32	20.0	147.4	122.4	55.3	-0.236	0.007	-0.020
278	H6S33	20.0	137.9	114.3	62.8	0.301	0.012	0.033
279	H6S34	18.5	134.8	108.6	53.1	-0.733	0.006	-0.056
280	H6S35	18.8	144.1	118.7	57.1	-0.692	0.007	-0.059
281	H6S36	18.9	133.0	106.3	54.2	-0.474	0.007	-0.040
282	H6S37	19.1	133.3	106.2	51.9	-0.486	0.006	-0.038
283	H6S38	20.4	137.3	110.0	55.9	0.154	0.007	0.013
284	H6S39	20.7	137.5	111.7	55.8	0.342	0.007	0.028
285	H6S40	18.9	134.6	109.7	47.3	-0.680	0.004	-0.043
286	H6S41	20.0	144.2	119.8	58.4	-0.038	0.008	-0.003
287	H7S1	19.8	138.6	112.9	55.5	-0.112	0.006	-0.009
288	H7S2	19.6	136.1	110.3	50.5	-0.304	0.005	-0.020
289	H7S3	21.0	129.9	102.8	50.3	0.481	0.007	0.040
290	H7S4	20.2	136.0	109.1	51.1	-0.057	0.005	-0.004
291	H7S5	19.1	121.1	93.2	47.9	-0.329	0.013	-0.037
292	H7S6	20.3	150.6	122.3	51.8	-0.405	0.007	-0.033
293	H7S7	20.2	125.0	97.9	49.3	0.157	0.010	0.015
294	H7S8	20.7	125.2	98.4	50.8	0.468	0.010	0.046
295	H7S9	21.3	113.2	89.0	51.4	1.176	0.018	0.159
296	H7S10	19.8	126.9	98.2	45.6	-0.252	0.009	-0.024
297	H7S11	18.5	126.8	99.3	50.3	-0.672	0.009	-0.064
298	H7S12	18.8	133.6	108.4	54.2	-0.503	0.006	-0.040
299	H7S13	20.5	127.0	99.3	48.6	0.224	0.009	0.021
300	H7S14	19.8	117.1	92.3	48.2	0.227	0.013	0.027
301	H7S15	19.3	131.6	104.4	50.9	-0.363	0.007	-0.029
302	H7S16	18.9	125.6	100.1	49.5	-0.392	0.008	-0.035
303	H7S17	19.1	127.9	102.9	51.5	-0.303	0.007	-0.026
304	H7S18	18.5	136.5	106.8	48.5	-1.040	0.006	-0.081
305	H7S19	21.0	100.4	85.8	69.3	2.306	0.048	0.515
306	H7S20	19.3	106.2	84.5	52.2	0.485	0.024	0.076
307	H7S21	19.6	128.0	101.7	52.6	-0.047	0.008	-0.004
308	H7S22	20.0	110.7	85.7	50.7	0.578	0.021	0.085
309	H7S23	19.5	117.7	91.8	49.8	0.067	0.014	0.008
310	H7S24	19.8	122.5	95.8	48.6	0.052	0.011	0.005
311	H7S25	19.9	131.8	105.2	51.7	-0.063	0.006	-0.005
312	H7S26	20.1	127.5	102.2	51.2	0.185	0.007	0.016
313	H7S27	19.2	115.3	89.4	50.1	0.017	0.017	0.002
314	H7S28	20.0	103.5	76.0	45.9	0.515	0.032	0.094
315	H7S29	19.4	105.3	80.1	52.7	0.465	0.030	0.081
316	H7S30	21.3	113.0	84.2	44.1	0.817	0.021	0.121
317	H7S31	20.1	131.9	105.8	50.7	0.017	0.006	0.001
318	H7S32	19.5	106.9	83.3	50.9	0.468	0.024	0.074
319	H7S33	18.6	151.2	116.0	73.4	-0.812	0.029	-0.139
320	H7S34	19.0	128.4	100.4	46.7	-0.584	0.008	-0.052
321	H7S35	19.7	120.1	92.0	47.4	-0.046	0.014	-0.005

Note: Table rows with different colors represent data samples identified as influential point.

Based on the results of the first iteration of the calculation of diagnostic parameters from the regression model for predicting Brix of lady finger banana as presented in Table 4. It can be confirmed that in the 321 samples data from the measurement of total dissolved solids (Brix) and peel color components (R, G and B) of lady finger banana, there are outlier data, high leverage points and influential points, the details of which are presented in Table 5.

Table 5. Details of data detected as outlier, high leverage points and influential point from the first iteration of the regression results for predicting Brix of lady finger banana.

No	Data Categories Based on Diagnostic Parameter Results	Sample Code of Data	Total
1	Outlier (-1,967 < t_i > 1,967)	H0S3, H0S4, H0S8, H0S9, H0S12, H0S13, H0S18, H0S22, H6S9, H7S19	10
2	High Leverage Point (h_{ii} > 0,0249)	H0S3, H0S4, H0S6, H0S8, H0S9, H0S10, H0S12, H0S13, H0S16, H0S17, H0S18, H0S19, H0S21, H0S22, H0S30, H1S11, H1S22, H1S25, H1S31, H2S27, H3S21, H3S30, H3S42, H4S3, H4S12, H4S41, H6S9, H6S21, H7S19, H7S28, H7S29, H7S33	32
3	Influential Point (-0,2233 < $DFFITS_i$ > 0,2233	H0S3, H0S4, H0S8, H0S9, H0S12, H0S13, H0S18, H0S21, H0S22, H0S30, H1S22, H1S40, H6S9, H7S19	14

The next data iteration stage was carried out by excluding data that had been detected as influential points from the previous iteration. In the second data iteration stage, 14 data sets identified as influential points were removed from the 321 data sets used in the first iteration stage. The data identified as influential points can be seen in Figure 5. Thus, the number of data sets used in the second iteration stage was 307 data sets. The influence of the influential points that had been removed from the laboratory measurement sample data set can be seen in the multiple linear regression model in the first, second, and final iteration stages, as presented in Table 6.

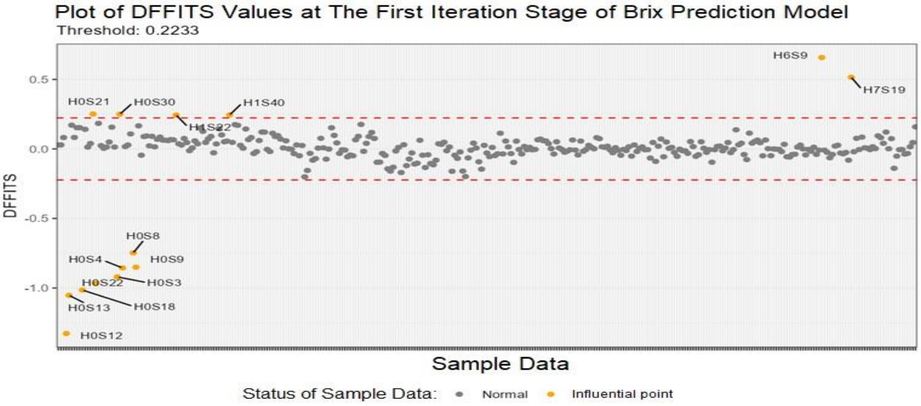

Fig. 2. Plot of *DFFITS*$_i$ values at the first iteration stage of Brix prediction model.

Table 6. Comparison of the results of the first and second stage data iterations and the results of the final stage iteration in the multiple linear regression model for predicting Brix of lady finger banana.

No	Differentiator		First Stage Iteration Results	Second Stage Iteration Results	Last Stage (17th) Iteration Results
1	Number of iteration data sets		321	307	178
2	Regression equation model		$\hat{y}_i$ = 14,4582 + 0,1236R – 0,0708G – 0,0637B	$\hat{y}_i$ = 18,1151 + 0,0406R – 0,0057G – 0,0052B	$\hat{y}_i$ = 22,3332 – 0,0936R + 0,1175G – 0,0521B
3	Number of influential point data		14	23	0
4	Intercept (b_0)		14,4582	18,1151	22,3332
5	Slope	R (b_1)	0,1236	0,0406	-0,0936
		G (b_2)	-0,0708	-0,0057	0,1175
		B (b_3)	-0,0637	-0,0052	-0,0521
6	s^2		4,3229	0,9581	0,5424
7	R^2		34,24%	28,74%	47,57%

The influence of the 14 influential point data sets removed from the 321 data sets used in the first iteration stage can be seen in the results of the second iteration stage as presented in Table 6. The s^2 dan R^2 values decreased from 4,3229 to 0,9581 and from 34,24% to 28,74%, respectively. In the second iteration stage, 23 data sets were still found as influential points. The data iteration on the total dissolved solids (Brix) prediction model for lady finger banana was stopped and reached a convergent state at the 17th iteration stage. At the 17th iteration stage, no data were detected as influential point. The final number of data sets that were free from influential point data was 178 data sets. The final result of the iteration process obtained a regression model $\hat{y}_i$ = 22,3332 – 0,0936R + 0,1175G – 0,0521B, with a value of s^2 = 0,5424 and R^2 = 47,57%.

IV. CONCLUSION

Diagnostic methods can be used to detect outlier, high leverage point and influential point from the laboratory measurement data. The results of the diagnostic method analysis on the 321 data sets of acidity level (pH), total dissolved solids (Brix) and peel color components (Red (R), Green (G) and Blue (B)) measurements of lady finger banana found that there were samples data detected as outlier, high leverage point and influential observation. The data iteration process using diagnostic parameters reached a convergent state at the 17th iteration stage, with the final result being 178 data sets of acidity level (pH), total dissolved solids (Brix) and peel color components (Red (R), Green (G) and Blue (B)) measurements of lady finger banana that were free from influential point data.

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