

1 **ANALYSIS OF MILK AND FERTILITY TRAITS IN HOLSTEIN FRIESIAN CATTLE**  
2 **ON THE PLATEAU, JOS NIGERIA**

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16 **Authors' contributions**

17 *This work was carried out in collaboration between all authors. Author ORO designed the study.*

18 *Author OMA performed the statistical analysis. Author SIO wrote the protocol. Author SDO clean the data.*

19 *Author AOG wrote the first draft of the manuscript. Author LU managed the literature searches. Author*

20 *OH managed the data extraction. Author IBA managed the data collection. All authors read and approved*

21 *the final manuscript.*

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23

24 **ABSTRACT**

25 The data set for the estimation of genetic parameters for milk and fertility traits of 650 cows

26 calved between 1992 and 2015 was obtained from the database of Integrated Dairies Limited,

27 Jos, Nigeria. The analytical model included the effects of herd-year-season, sire, cow and

28 residual effects. Sire, cow, and residual effects were random while all other effects were fixed.

29 Heritability estimates for calving interval (CI), conception rate (CR), number of services per

30 conception (NSC) and no return rate at 56 days (NRR56 days) were low and ranged between

31 0.028 (CR) and 0.166 (NSC) in the third parity. Milk yield had high heritability and repeatability

32 estimates across parities. The coefficient of variation was highly variable, and ranged from

33 14.86-43.67%. Thus, there was no indication of an adverse genetic relationship between fertility

34 and milk production in this population and overall genetic parameters imply a good practical

35 management on the Plateau will be essential for improving milk without deteriorating the  
36 efficiency of fertility traits in Holstein Friesian cattle.

## 37 **INTRODUCTION**

38 Fertility is one of the non-yield traits which is of great economic importance in dairy herds. The  
39 quest to profiteer by improving milk yield over the last decades through the use of selective  
40 breeding and omics technology by dairy scientist had been a source of concern due to its  
41 snowballing effect on fertility traits. The genetic gain in milk production per cow on daily basis  
42 had extended fertility traits by 1% increment [1]. In Italy, the genetic gain in milk yield per cow  
43 on yearly basis is 112 kg in Holstein-Friesian with an extension in calving interval by 1.4 day per  
44 year [2]. Despite the huge variations in breeding practice across the countries under diverse  
45 production systems and divergent climatic conditions, all had synergistic effect on the extension  
46 of fertility traits [2]. This lack of a unique measure of fertility is due to the diverse type of  
47 information available to assess the reproductive success [3]. If results of artificial inseminations  
48 in each insemination cycle are available, traits such as days open (DO), interval from calving to  
49 first insemination, number of inseminations per conception, the interval between first and last  
50 insemination or conception rate have been used. When information of result of inseminations is  
51 not available, calving interval (or an approximate measure of days open obtained from calving  
52 interval and average pregnancy duration in the population) provide a measure of the overall  
53 reproductive efficiency in each parity and it is widely used because it can be easily obtained from  
54 milk recording schemes [12]. However, this measure is highly influenced by farmer interventions  
55 (mainly, voluntary waiting period) and by problems regarding to the low quality of fertility  
56 measurements such as censored records [5]. Therefore, a wide number of statistical models have  
57 been used in the genetic evaluations of fertility traits with no clear consensus as to what approach

58 is best for each trait. One of the features shared by most fertility traits is that several measures  
59 are available along the cows productive life. Treatment of longitudinal traits in animal breeding  
60 has followed several approaches from the simplest repeatability model [3] to the most complex  
61 multiple trait models [7]. Other studies have found evidence of differences in patterns of  
62 response to fertility traits along parities [6] in some fertility traits. However, none of the previous  
63 studies have dealt with the combined selection for fertility level and fertility persistency along  
64 lactation. In this study, relationships between fertility traits in different parities were quantified.  
65 Attention was paid to the effect of selection on the estimates of genetic parameters for milk and  
66 fertility traits.

## 67 **MATERIALS AND METHODS**

68 The Jos Plateau is a plateau located near the centre of Nigeria. It covers 8600 km<sup>2</sup> and is bounded  
69 by 300-600 m escarpments around much of its circumference. With an average altitude of 1280  
70 m, it is the largest area over 1000 m in Nigeria, with a high point of 1829 m, in the Shere Hills.  
71 A total of 4405 records from 650 cows collected from parity 1 to 3 during the period 1992 to  
72 2015 were used in this study sired by 55 bulls on the Jos Plateau.

73 Milk yield was adjusted for lactation length at 305<sup>th</sup> days by multiplicative correction factors

74 Fat corrected milk (FCM) = [(0.4\*milk yield (kg) + [(15\*fat yield (kg)] [10].

75 Fertility traits were computed using fertility chart which was then preprocessed in VAMMP  
76 dairy management software interface. The traits were:

77 Calving Interval (CI) was defined as the period (in days) between the first and the next calving.

78 Number of service per conception (NSC) was defined as the number of service or matings to  
79 effect a pregnancy

80 Conception rate was calculated by dividing the number of pregnant cows by the total number of  
81 inseminations.

82 Variance components for milk and fertility were estimated through univariate analysis using an  
83 animal model considering the effects of herd, number of calving and contemporary group as  
84 fixed, and the permanent environmental, animal additive genetic and residual effects as random.

85 The contemporary group included herd and year of calving

86 The model used [10] can be described as:

$$87 \quad y = Xb + Wpe + Za + e$$

88 in which  $y$  = vector of observations;  $b$  = vector of fixed effects (herd, number of calving, and  
89 season).  $pe$  = vector of random permanent environmental effects;  $a$  = vector of random animal

90 effects;  $e$  = vector of random residual effects;  $X$ ,  $W$ , and  $Z$  = incidence matrices that establish

91 relationships between the records and the effects. It is assumed that permanent environmental,

92 animal, and residual effects are independently distributed with mean zero and constant variance:

$$93 \quad V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

94 Considering that  $A =$  relationship matrix,  $I\sigma_e^2 = R$ , then  $V(y) = ZAZ'\sigma_a^2 + WI\sigma_{pe}^2W' + R$ .

95 Heritability was estimated as the ratio of the additive genetic variance to total phenotypic

96 variance; and repeatability, as the ratio of the sum of the additive genetic variance plus

97 permanent environmental variance to phenotypic variance, as described by Falconer and Mackay

98 (2001):

$$99 \quad h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

$$100 \quad W^2 = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

101 To estimate genetic and environmental correlations, a multi-trait animal model was used which  
 102 included herd, number of calving and contemporary group (which included year of calving) as  
 103 the fixed effects, and the permanent environmental and additive genetic direct effects as random.

104 The matrix model used was:

$$105 \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

106 in which  $y_i$  = vector of N observations;  $b_i$  = vector of fixed effects (herd, number of calving,  
 107 contemporary group);  $pe_i$  = vector of random permanent environmental effects;  $a_i$  = vector of  
 108 random animal effects;  $e_i$  = vector of random residual effects;  $X$ ,  $W$ , and  $Z$  = incidence matrices  
 109 establishing relationships between the records and the fixed and random effects, respectively. It  
 110 is assumed that random permanent environmental, animal and error effects are independently  
 111 distributed with mean of zero and variance:

$$112 V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G_0 \otimes A & 0 & 0 \\ 0 & Q_0 \otimes I & 0 \\ 0 & 0 & R_0 \otimes I \end{bmatrix}$$

113 in which  $\otimes$  = direct or Kronecker product;  $I$  = identity matrix equal to number of observations;  $A$   
 114 = relationship matrix among all animals in the pedigree;  $G_0$  = variance and covariance matrix of  
 115 random animal effects;  $\sigma_{aii}^2$  = animal additive genetic variance for trait  $i$ ;  $\sigma_{ajj}^2$  = animal additive  
 116 genetic variance for trait  $j$ ;  $\sigma_{aij} = \sigma_{aji}$  = animal additive genetic covariance between traits  $i$  and  $j$ ;  
 117  $Q_0$  = variance and covariance matrix of random permanent environmental effects;  $\sigma_{peii}^2$  =  
 118 permanent environmental variance for trait  $i$ ;  $\sigma_{pejj}^2$  = permanent environmental variance for trait  
 119  $j$ ;  $\sigma_{peij} = \sigma_{peji}$  = permanent environmental covariance between traits  $i$  and  $j$ ;  $R_0$  = variance and  
 120 covariance matrix of residual effects;  $\sigma_{eii}^2$  = residual variance for trait  $i$ ;  $\sigma_{ejj}^2$  = residual variance  
 121 for trait  $j$ ; and  $\sigma_{eij} = \sigma_{eji}$  = residual covariance between traits  $i$  and  $j$ [11].

## 122 RESULTS

123 Table 1 shows the least squares means for milk and fertility traits at different parities. Milk yield  
 124 and calving intervals differs significantly ( $p<0.05$ ) between parities. The coefficient of variation  
 125 was highly variable, which ranged from 14.86-43.67%. The phenotypic mean of milk yield and  
 126 calving interval linearly increased at consecutive parities and this change only was statistically  
 127 significant ( $p<0.01$ ) between parities. An increasing trend for milk yield and calving interval has  
 128 also been found in other studies [1, 6]. The descriptive statistics for calving interval indicate that  
 129 cows in earlier parities had more chances for good fertility performance than cows in later  
 130 parities. The number of records decreased from parity 1 to 3 due to voluntary and involuntary  
 131 culling of cows. This may reflect differences in management conditions for varied values  
 132 reported at different parities.

133

Table 1: Least squares means of milk and fertility traits at different parities

Parameters	Parities			CV
	1	2	3	
No of records	4500	2899	2006	
Milk yield (kg)	876.11(87.23) <sup>c</sup>	1288 (77.29) <sup>b</sup>	1602 (120.50) <sup>a</sup>	14.86
Calving interval (days)	138 (26.4) <sup>b</sup>	129 (22.4) <sup>a</sup>	128 (21.1) <sup>a</sup>	16.44
Number of services per conception	2.07	2.10	2.00	43.67
Conception rate	59.4	55.0	54.6	32.01
No return rate at 56 days	80.1	77.5	74.0	40.12

CV-Coefficient of variation; <sup>abc</sup>Means with different superscript are significantly different ( $P<0.05$ ); standard deviation is given in brackets.

134

135 Table 2 shows the genetic and environmental correlations for milk yield and fertility traits at  
 136 different parities in Holstein Friesian cattle in the study area. This value (+0.40) is the genetic  
 137 correlation value between calving rate (CR) and milk yield (MY) while +0.34 is the genetic  
 138 correlation value between NRR56days and calving interval (CI) in parity 1. No significant  
 139 genetic and phenotypic correlations were found between herd fertility and milk yield in the

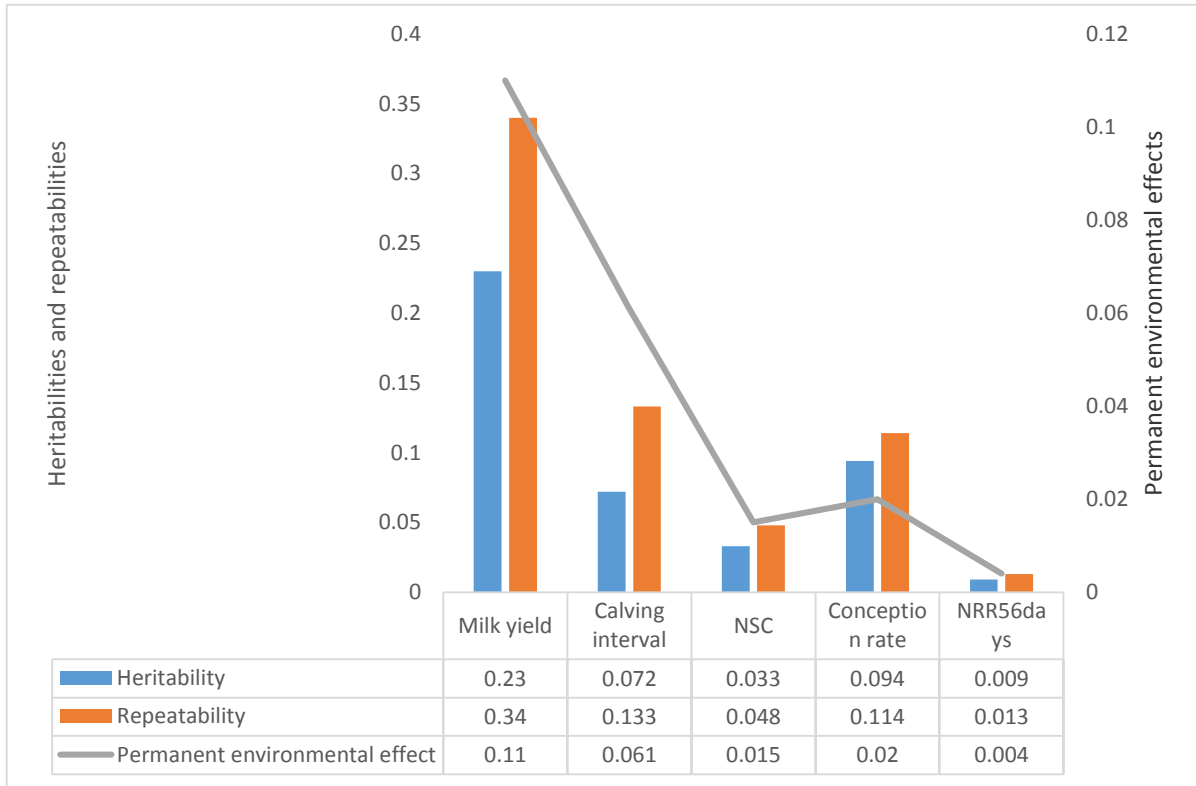
140 second parity. Milk yield showed significant genetic correlation between calving interval and  
 141 number of services per conception in the third parity. Significant phenotypic positive correlation  
 142 was found between milk yield and number of services per conception (+0.28). The highest  
 143 negative correlation was found between calving rate and non return rate at 56 days (-0.72) in  
 144 parity 3.  
 145

Table 2: Genetic correlations (above diagonal) and environmental correlations (below diagonal) for milk yield and herd fertility traits in Holstein Friesian cattle at different parities

<b>Parity 1</b>					
Traits	MY	CI	NSC	CR	NRR56days
MY	1	-0.19	0.08	0.40	0.09
CI	0.13	1	0.04	0.18	0.34
NSC	0.02	0.19	1	0.19	-0.13
CR	0.45	0.14	-0.12	1	0.10
NRR56days	-0.09	0.08	0.05	-0.10	1
<b>Parity 2</b>					
MY	1	-0.12	0.03	0.04	0.08
CI	0.19	1	0.19	0.10	0.12
NSC	0.03	0.12	1	0.03	-0.02
CR	0.04	0.18	-0.10	1	0.16
NRR56days	-0.08	0.15	0.03	0.05	1
<b>Parity 3</b>					
MY	1	0.48	0.20	0.12	0.06
CI	0.19	1	0.11	0.09	0.14
NSC	0.28	-0.11	1	0.07	-0.13
CR	0.07	0.16	-0.12	1	0.10
NRR56days	-0.02	-0.12	0.19	-0.72	1

146 CR-Conception rate, MY-Milk yield, CI-Calving interval, NSC-Number of services per conception, CR-Calving  
 147 rate, NRR56days-No return rate at 56days  
 148

149 Figures 1, 2 and 3 shows the permanent environmental effect, heritability and repeatability for  
 150 milk yield and herd fertility variable. The permanent environmental effect, heritability and  
 151 repeatability had the highest values for milk yield in the second parity as compared to first and  
 152 third parity.

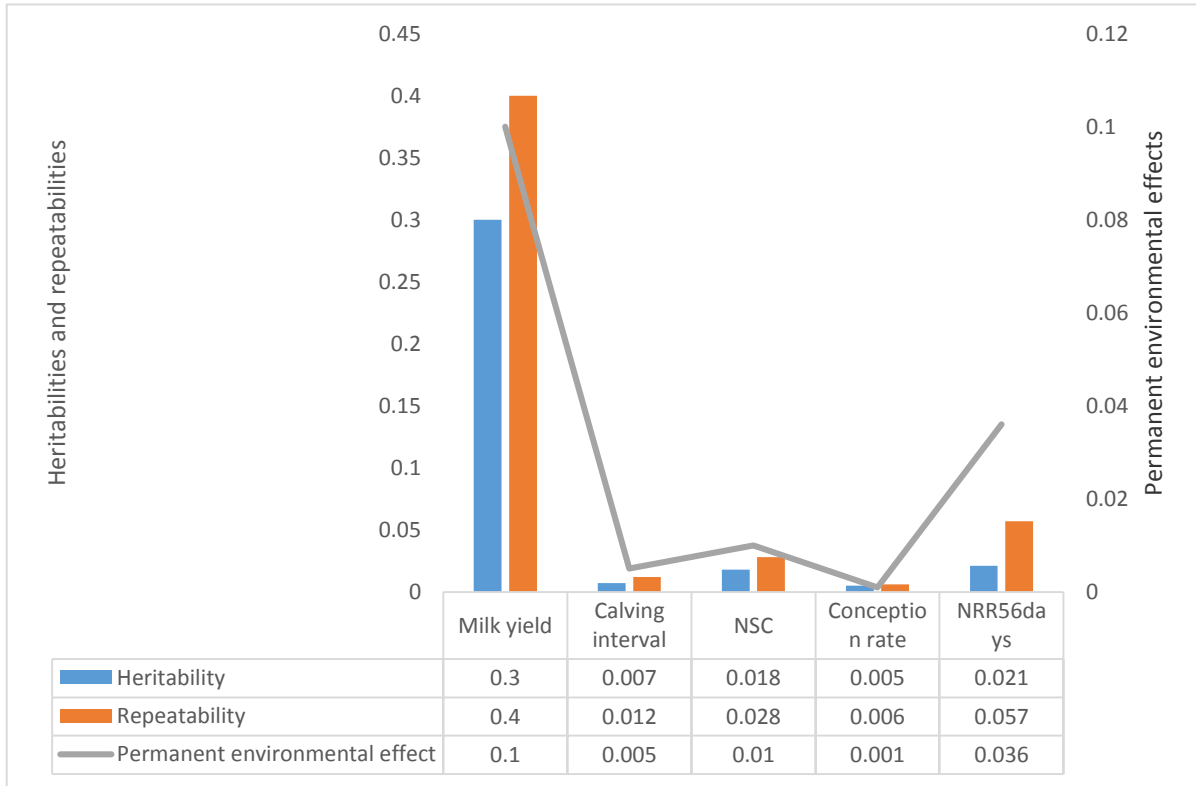


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Figure 1: Genetic parameter estimates for milk and fertility traits in parity 1

UNDER PEEL





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Figure 2: Genetic parameter estimates for milk and fertility traits in parity 2

UNDER PEER REVIEW

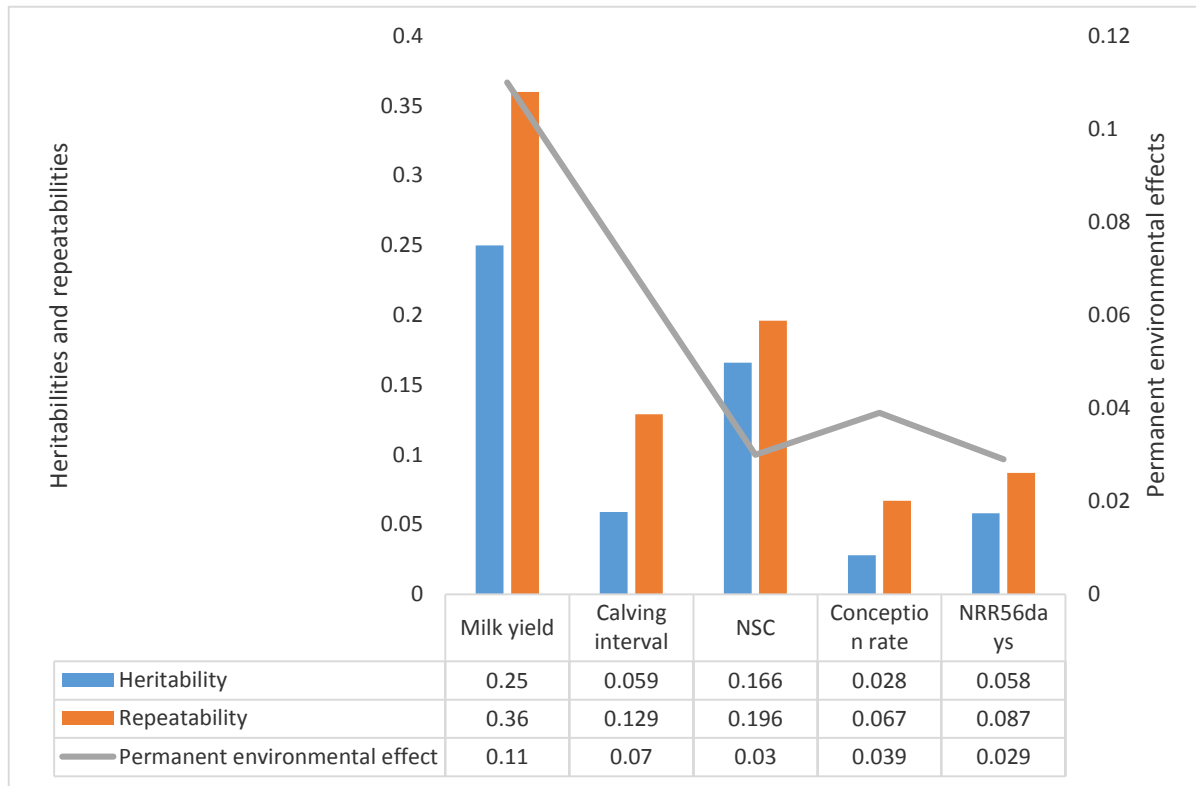


Figure 3: Genetic parameter estimates for milk and fertility traits in parity 3

## DISCUSSION

Genetic values for herd fertility variables were non linear and low from the first to the third parity. The changes were primarily due to the sire of cow component as a great deal of the inseminations in different parities comes from the same sires. These results confirm the findings of [4], who found low genetic correlations for number of services per period for sire of cow in heifers and first parity cows (0.20). Genetic correlations between sire of cow and sire of insemination for parity 2 and 3 were close to values found by [5, 8]. Although it would be tempting to improve fertility in cows via indirect selection on non-return rate of sires, the results indicate that this would not be effective for the improvement of conception rate in heifers and first parity cows. Indirect selection on non-return rates of sires would have a moderately positive effect on conception rates of older cows. This change may be related to the increase in metabolic

180 rate when the cows start producing milk. The differences in repeatability estimates obtained  
181 indicate that some herd fertility parameters are more useful for characterization of herdmanship  
182 than others. For milk production repeatability of herd yearly averages of 0.85 to 0.90 have been  
183 found [1] which is higher than the estimates reported in this study. The deviations observed may  
184 be caused by the variations in sample size, statistical model and location of the study.

## 185 **CONCLUSION**

186  
187 The use of fertility traits in selection index programs can reduce genetic slippage caused by  
188 correlated selection response of milk production in Holstein Friesian cattle. Genetic correlations  
189 between milk yield and fertility traits were not robust and less than 0.6 across parities. However,  
190 these estimates are likely to be associated with large sampling variance because of the small data  
191 set and poor connectedness.

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