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Chi-square and Adjusted Standardised Residual Analysis

F.Z. Okwonu[1], N.A. Ahad[2*], J.S. Apanapudor[1] and F.I. Arunaye[1]

[1]*Department of Mathematics, Delta State University, Abraka, Nigeria.*

[2]*Institute of Strategic Industrial Decision Modelling, School of Quantitative Sciences, Universiti Utara Malaysia, 06010 UUM Sintok, Kedah, Malaysia.*

In hypothesis testing, inference is made by comparing the computed test statistic and the critical value which rely on a specified level of significance and degrees of freedom. This paper examines various study variables to assess whether there exists an interdependency between relationship intimacy and these variables. The chi-square test, likelihood ratio test, the adjusted standardised residual, and the proposed benchmark methods are applied to determine the acceptance or rejection of the null hypothesis and the individual category contribution that enhanced the inference. The comparative analysis involves data collected from a survey conducted before the onset of the Covid-19 pandemic, during the Covid-19 lockdown period, and following the relaxation of post-Covid-19 lockdown measures spanning a duration of six weeks. The findings showed that the null hypothesis cannot be rejected implying that the study variables are independent of relationship intimacy for the periods under study. The adjusted standardised residual and the benchmark methods revealed that sexual intimacy and quarrel are the highest variable contributors to the acceptance of the null hypothesis.

Keywords: adjusted standardised residual; benchmark method; chi-square test; Covid-19; likelihood ratio test

I. INTRODUCTION

The chi-square, symbolised as χ^2, was coined by Karl Pearson in 1900 (Pearson, 1900). It is suitable to test for goodness of fit, independence, and homogeneity. A chi-square test is a nonparametric approach that can be applied to quantitative and qualitative variables (Núñez-Antón *et al.*, 2019). It is a test used to investigate the comparison between the observed and expected frequencies of the data set in each category (Cai *et al.*, 2006). Besides statistical fashion and fixity, the chi-square test is one of the most frequently applied test statistics in all fields of studies. The application of the chi-square test and the student's t-test statistic is competitively innumerable. The chi-square has been applied to different fields of studies (Rosenkrantz, 1997).

In some cases, the likelihood ratio test (G^2) is applied to investigate independence. This test and the chi-square test are often used conveniently to test homogeneity to infer if the data set are well distributed across the population of the study (Czekała *et al.*, 2020; Spitzer *et al.*, 2020; Ahad *et al.*, 2019; Ghosh, 2019; Miller, 2019; Núñez-Antón *et al.*, 2019; Patil, 2018; Koch *et al.*, 2016; Kwasiborski & Sobol, 2011; Košťálová, 2010; Withers, 2009).

Sharpe (2015) has investigated the contribution of each category when the chi-square test is statistically significant using the residual methods and other post hoc tests such as ransacking, partitioning, and category comparison. Sharpe (2015) hinges on the recommendation by Beasley and Schumacher (1995) to investigate category contribution to a statistically significant test. Delucchi (1993) opined that a large deviation between the observed and expected values for a category implies a large contribution to the inference. Agresti (2006) considered Habernan's (1973) selection of |2| and |3| as criteria for analysing small and large cells

*Corresponding author's e-mail: aishah@uum.edu.my

contribution may lead to using both negative and positive deviations to analyse cell contributions for the statistically significant test.

In this paper, we consider utilising the contributions of small and large cell category(ies) in their original form without the modulus to draw an inference. Therefore, we propose a method that identifies cell contributions through the benchmark method. This method utilises data from the standardised residuals to derive the benchmark, which is then compared to the raw data obtained from the standardised residuals. The benchmarking method is data-dependent and can be applied to ascertain the statistical significance or insignificance of the test. The key objective is to discern the individual contributions to the inference.

This study focused on various variables to determine whether relationship intimacy is independent or dependent on these variables. The data used in this study is based on a survey conducted over a specified period encompassing the period of the pre-Covid-19 outbreak, the lockdown period due to the outbreak of Covid-19, and post-Covid-19 lockdown relaxation. We applied the standardised residual, adjusted standardised residual, and the benchmark method to determine the study variables with the highest contributions to accepting or rejecting the null hypothesis.

Section 2 discusses the materials and methods including the controversy of the degrees of freedom of the chi-square test, the chi-square and likelihood ratio test together with the residual computation followed by the proposed benchmark method to determine cell contribution to inference. Section 2 ends with the data collection and analysis. Section 3 consists of the presentation of results and discussion along with the evaluation of the methods employed. The paper's conclusion is presented in Section 4.

II. MATERIALS AND METHOD

This section explains the various techniques used in this study. The discussion begins with a look at the chi-square test, then moves on to the likelihood ratio test, standard and adjusted standardised residuals, the benchmark method, and finally the data collection process.

A. The Chi-square Test

The chi-square test is a nonparametric test, that is distribution-free, with the assumption that the minimum number of counts in each category (cell) should be at least five (Yates, 1934; Yule, 1922; Fisher, 1922). There has been a noteworthy argument regarding the minimum numbers of observed or theoretical values in each category of the contingency tables. One basic condition for applying the chi-square test is that the expected frequency in each category must be “at least” five (Gaunt *et al.*, 2017). Otherwise, adjoining expected frequencies are merged to fulfil this rule of thumb (Agresti, 2006).

Various methods have been proposed to address the issue when the expected frequency is fewer than five, in addition to Yates' correction factor (Yates, 1934; Delucchi, 1983; Bartholomew & Tzamourani, 1999; Bartholomew *et al.*, 2011; Lin *et al.*, 2015). Therefore, it is acknowledged that the chi-square performs very well with respect to accuracy when the number in each category is greater than five.

The chi-square test, originally developed by Karl Pearson, has received criticism and modifications, notably by R. A. Fisher. The first modification was the introduction of the degrees of freedom in the case of the contingency table, and the second was the estimate of the number of the unknown parameter with respect to the theoretical distribution and when the parameter is estimated from the central moment (Fisher, 1922; Fisher, 1924; Cochran, 1954; Baird, 1983; Plackett, 1983; Mirvaliev, 1987; Bolboaca *et al.*, 2011). The modification by Fisher based on the degrees of freedom was opposed by Pearson. Ironically, irrespective of Pearson’s opposition, Fisher’s modification is generally implemented in major statistical software packages (Baird, 1983). The chi-square test has become one of the greatest contributions of Karl Pearson to modern statistics.

A power divergence test, such as the chi-square and the likelihood ratio test, is a unique family of test statistics (Cressie & Read, 1984; 1989). The χ^2 statistic is often applied to determine if the observed data set fits the expected data set and to investigate goodness of fit, homogeneity, and independence between the variables of interest. It is mainly applied to categorical data (Lin *et al.*, 2015; Rana & Singhal, 2015). The χ^2 has numerous applications.

Let O_{ij} denote the observed frequencies distributed into different partitions of the contingency table. If this definition is valid, then O_{ij} is described to follow a multinomial distribution with probability π_i, then the following expression satisfies the multinomial distribution:

$$\pi(O_{ij} = O_{11}, O_{12}, \dots, O_{km}) = \binom{L}{O_{11}, O_{12}, \dots, O_{rc}} \pi_1^{O_{11}}, \dots, \pi_k^{O_{km}}$$

$$= \frac{L!}{O_{ij}!} \pi_i^{O_{ij}}, i = 1,2,3, .. k \quad (1)$$

To validate the null hypothesis, the χ^2 is defined as follows:

$$\chi^2 = \frac{\sum_{i=1}^{r} \sum_{j=1}^{c} (O_{ij} - E_{ij})^2}{E_{ij}}, \quad (2)$$

where i, j denotes the subscript for the rows and columns, $O_{ij} > 0$ as defined and $E_{ij} > 0$ is the expected frequency (Withers, 2009). Simply, the expected frequency can be obtained as:

$$E_{ij} = \frac{r \times c}{L}, \text{ and } \sum O_{ij} = \sum E_{ij} = L,$$

where r and c are the row and column total for each category and L denotes the sample size (Withers, 2009). Relying on the null hypothesis to be investigated, Equation (2) is asymptotically the χ^2 with $l = (r-1)(c-1)$ degrees of freedom when the expected values are large (Kim & Akritas, 2012; Mann & Wald, 1942).

If the χ^2 value is large, it denotes a significant difference between the observed and expected frequencies. On the other hand, if the expected values are larger than the observed values, the value of χ^2 statistic will correspondingly follow (Okwonu, 2015a; 2015b). The squared deviation in the numerator of Equation (2) allows this manifestation to occur. In another consideration, if the χ^2 value is small, it implies that the difference between the observed and expected value is small. In most cases, depending on the degrees of freedom, we may conclude in passing that the null hypothesis cannot be rejected. This may not hold predictively true for large χ^2 values with varying degrees of freedom.

The inference is made based on the comparison between the computed χ^2 and the χ^2 critical value which relies on the degrees of freedom (l) and the level of significance (α). If the null hypothesis is valid, then the limiting probability distribution is the χ^2 distribution (Baird, 1983). The χ^2 is also applied to determine whether a statistical association exists between variables of interest (Withers, 2009).

The following are vital aspect of the χ^2 distribution: (i) the χ^2 test relies on the variation between the observed and expected values from each category, (ii) the expected values are always positive, (iii) the minimum value of the χ^2 is zero and it does not have a negative value due to the squared deviation between the observed and expected frequencies in the numerator of Equation (2), (iv) when the difference between the observed and expected frequency is small, the χ^2 value will be small, hence the null hypothesis is satisfied, (v) if the difference between the observed and the expected frequency is large, the χ^2 value will be large and hence the alternative hypothesis is true, (vi) the rejection or acceptance of the null hypothesis depends on the χ^2 critical value which is based on the level of significance and the degrees of freedom, (vii) the χ^2 does not have maximum value, (viii) the χ^2 curve is asymmetric, (ix) the degrees of freedom are associated with every χ^2 distribution, (x) the sum of the area under the χ^2 curve is equal to one, (xi) the χ^2 is skewed to the right and the χ^2 is a multinomial distribution, (xii) the accuracy of the χ^2 approximation relies on the values in the categories, that is to say, a better approximate value is obtained if the number of observations is more than ten in each category (Baird, 1983).

B. The Likelihood Ratio Test

The likelihood ratio test, denoted by G^2, mimics the chi-square statistic (Delucchi, 1983; Cressie & Read, 1989). The G^2 statistic is also affected when a category (cell frequency) is less than five (Lin *et al.*, 2015). The formula is stated as follows:

$$G^2 = 2 \sum_{i=1}^{r} O_{ij} log_e \left(\frac{O_{ij}}{E_{ij}}\right), j = 1,2, .., c \quad (3)$$

where O_{ij} and E_{ij} are defined previously. The likelihood ratio test was modified by interchanging the observed values in Equation (3) with the expected values. Therefore, the modified likelihood ratio test is given as:

$$MG^2 = \sqrt{4} \sum_{i=1}^{r} E_i log_e \left(\frac{E_i}{O_i}\right) \quad (4)$$

Equations (3-4) share similar properties with Equation (2), and the difference between them is often infinitesimal, while the decision rule is similar.

The greater the G^2 statistic, the more evidence there is that the difference between the observed and expected values is large. On the other hand, if G^2 is small, it indicates that the difference between the observed and expected values is small. The G^2 test is asymptotically distributed as χ_l^2 under the null hypothesis. The χ_l^2 and G^2 tests are considered "asymptotically unbiased test of independence" (Lin *et al.*, 2015). The χ_l^2 and G^2 are continuum defined based on the "power divergence family" (Cressie & Read, 1989; 1984), that is:

$$\delta = \frac{2}{\theta(\theta+1)}\sum_{k=1}^{p} Y_k\left[\left(\frac{Y_k}{L\pi_k}\right)^{\theta} - 1\right], -\infty < \theta < \infty, \theta = 0, \theta = -1,$$

where $\delta = 2LI^{\theta}(Y|L:\pi)$. This illustrates the difference and similarities between the χ_l^2 and G^2. Wilks (1938) showed that the G^2 has a limiting χ_l^2 distribution. Both test statistics are consistent, and as the sample size increases, the power of the test approaches unity (Wilks, 1938).

C. Standardised and Adjusted Standardised Residuals

Residual computation is vital to determine the category of interest with the largest difference, that is the difference between the observed and expected value. The residual values tell us about the contribution of each category to the eventual computed chi-square value (Sharpe, 2015). The concept of residual was coined to determine the categories (cells) with the highest contribution to inference (Sharpe, 2015; Delucchi, 1976). A residual is defined as:

$$R_{ij} = (O_{ij} - E_{ij}), \tag{5}$$

where O_{ij} *and* E_{ij} are defined. If either of O_{ij} *or* E_{ij} is large, it is assumed that R_{ij} for that category will also be large. For the residual, the sign direction is vital which may indicate a positive or negative contribution to the analysis. This greatly depends on the values of the observed and expected frequencies. To overcome this deficiency, another procedure is advanced to ameliorate the large difference that may occur. The standardised residual (Haberman, 1973) is applied to ameliorate the deficiency, that is:

$$\theta_i = \frac{R_{ij}}{sqrt(E_{ij})} \tag{6}$$

The standardised residual is used to identify patterns and can be applied to several comparative analyses. It is uniquely applied to determine the contribution of each observation based on the deviations of the numerator. Another unifying procedure to analyse individual cell contribution which relies on cell value definition is the adjusted standard residual, defined as:

$$\omega_i = \frac{R_{ij}}{\sqrt{E_{ij}(\beta\times\delta)}} = \frac{R_{ij}}{\gamma}, \tag{7}$$

where $\beta = \left(1 - \frac{r_{ij}}{L}\right)$ *and* $\delta = \left(1 - \frac{c_{ij}}{L}\right)$. Every ω_i is distributed approximately as a standard normal deviate with the assumption that γ is different from one (Haberman, 1973). This implies that depending on the expected value, γ may be greater than or equal to one. Equations (5-7) help determine the individual contributions of the cell variables being analysed, which can lead to the rejection or acceptance of the null hypothesis (Sharpe, 2015). The rule of thumb based on Equation (7) is that for the null hypothesis to be fitted, ω_i values must be within $|2|$ for few cells and $|3|$ for many cells (Sharpe, 2015; Liski, 2007; Haberman, 1973). The denominator of Equation (7) can be referred to as the estimated standard error.

The sum of the residual is zero, while the sum of the standardised residuals will often give a value that depends on the sign directions. The sum of the squared standardised residuals equals the computed chi-square statistic, that is:

$$\sum_{i=1}^{k} {\theta_i}^2 = \chi^2$$

The sum of the adjusted standardised residuals gives a value that depends on the sign directions.

D. Benchmark Method

Haberman (1973) and Sharpe (2015) used the adjusted standardised residual based on the absolute value of two for small cells and three for large cells to determine the percentage of cell contribution to the rejection of the null hypothesis. In this discussion, we propose the benchmark method to determine the cell contribution to the acceptance or rejection of the null hypothesis. This method uses the values of the standardised residual (θ_i) as raw data to compute the mean ($\bar{\theta}$) and the standardised residual variance (S_θ^2), that is:

$$\bar{\theta} = \frac{\sum_{i=1}^{n}\theta_i}{n}, n = r \times c, \quad 8)$$

$$S_{\theta}^{2} = \frac{\sum_{i=1}^{n}(\theta_i - \bar{\theta})^2}{n-1} \quad (9)$$

The proposed benchmark is:

$$\Delta = \frac{S_{\theta}^{2}}{\sqrt{\chi_{l}^{2}(\alpha)}}, \quad (10)$$

where $\chi_{l}^{2}(\alpha)$ is the chi-square critical value based on a specified level of significance and degrees of freedom. The proposed benchmark method is a combination of the computed mean ($\bar{\theta}$) and the standardised residual variance (S_{θ}^{2}) as the numerator and the denominator are simply the square root of the chi-square based on certain degrees of freedom.

Equation (10) is a proposed method to determine the contribution of each object. This Equation (10) is similar to the performance benchmark discussed in Okwonu *et al.* (2022) and Okwonu *et al.* (2023). Equation (10) was proposed as a benchmark method to address the limitations of the standardised residual (Haberman, 1973) and the residual (Sharpe, 2015) with regard to cell contributions and sign directions, specifically concerning Equations (5-6). The benchmark value is always positive compared to the residual and the standardised residual which have positive and negative directions. As such the proposed method seeks to determine the cell with better cell contributions. It uniquely classifies cell contribution as positive or negative based on the values from Equations (5-6). Therefore, the proposed method is suitable and dependable to determine the performance of the study.

To determine the cell with the highest contribution, we compare the standardised residual value (θ_i) with the benchmark (Δ), that is:

$$\nabla = \theta_i \geq \Delta \quad (11)$$

The results obtained by using the computed chi-square and the critical chi-square value in the denominator of Equation (10) are comparable. In this case, the user may apply both to identify the most effective cell contribution.

Table 1. Study variables.

Variable
Dinner
Sexual intimacy
Quarrel
Living together

Hypothesis testing was conducted based on the following hypothesis statement.

H_0: Relationship intimacy is independent of the study variables.

H_1: Relationship intimacy is dependent on the study variables.

The null hypothesis is rejected if the computed chi-square value is greater than the critical value obtained from the chi-square distribution table using a specified α level of significance with l degrees of freedom. Otherwise, we do not reject the null hypothesis if the computed chi-square value is less than the critical value obtained from the chi-square distribution table. The p-value approach was also applied to validate the decision of critical value.

E. Data Collection and Analysis

The data set was collected to investigate the impact of the study variables as shown in Table 1 on relationship intimacy. We deliberately included the Covid-19 lockdown period with a comparative analysis to pre- (normal times) and post-Covid-19 lockdown relaxation for six weeks. The participants participated of their own accord. Among the respondents, approximately 69.2% were married individuals, while 30.8% were mature adults in relationships who were not married. The average age of male participants is 40.63 years, and the female is 35.55 years with an overall average age of 36.67 years. About 58.2% of females and 41.8% males responded in the survey. The observed and expected values for pre-Covid-19 for six weeks are displayed in Table 2. Table 5 contains the six weeks observed and expected values during Covid-19 lockdown, and Table 8 contains six weeks observed and expected values after Covid-19 lockdown relaxation. The survey was carried out in December 2020 and January 2021.

III. RESULT AND DISCUSSION

The statistic values pertaining to the methods during the six weeks pre-Covid-19 outbreak, Covid-19 lockdown, and post-Covid-19 lockdown relaxation are reported in Tables 3, 6, and 9, respectively. In addition, the chi-square critical value at 5% level of significance, degrees of freedom, and p-value are reported in the above-mentioned tables. Since the computed statistic values are less than the chi-square critical value, we were not able to reject the null hypothesis implying that relationship intimacy is independent of the study variables.

Thompson *et al.* (2000) and MacDonald *et al.* (2000) advanced the residual approach to further investigate individual cell contribution when the null hypothesis is rejected. We adopted this procedure to investigate the highest variable contributor to the acceptance of the null hypothesis. To do this, we adopted suitable procedures such as the standardised residual, the adjusted standardised residual, and the benchmark method. These procedures enabled us to have a baseline idea on which of these variables contributed higher values to the acceptance of the null hypothesis. We concurred that the concept was discussed when the null hypothesis was rejected. Thus, applying it when the null hypothesis is accepted may give further clarification of individual contributions to the acceptance of the null hypothesis.

Tables 4, 7, and 10 itemised the contributions of the different variables of interest to the acceptance of the null hypothesis. The tables demonstrate that males and females have different variables that enhanced the acceptance of the null hypothesis. From the results, we observed that any category with comparative observed and expected values produces comparative residual values that correspond with the deviations. Applying these procedures to validate the inference of the χ^2, G^2, MG^2 against the chi-square, the critical value may provide useful information. The concept postulated by Sharpe (2015), Agresti (2006), and Haberman (1973) states that if the absolute value of ω_i has a value exceeding two for small categories or three for large categories, it shows a lack of fit of the null hypothesis. The implication of the sign direction in analysing the adjusted standardised residual is that the positive sign indicates a variable with the highest contribution, whereas the negative sign shows a variable with a negative contribution to inference.

Table 2. Observed and expected values for six weeks before Covid-19 outbreak.

Gender	Dinner	Sexual Intimacy	Quarrel	Living together	Row Total
Male	36 *(35.80)*	34 *(33.56)*	17 *(19.24)*	28 *(26.40)*	115
Female	44 *(44.20)*	41 *(41.44)*	26 *(23.76)*	31 *(32.60)*	142
Column Total	80	75	43	59	257

Table 3. Statistics for decision analysis for six weeks before Covid-19 outbreak.

χ^2	G^2	MG^2	$p-value$	${\chi^2}_{5\%}$	df
0.660	0.664	0.669	0.88	7.81	3

Table 4. Variable contribution to relationship intimacy before Covid-19 outbreak.

	Gender	Dinner	Sexual intimacy	Quarrel	Living together
Residual	Male	0.202	0.439	-2.241	1.599
	Female	-0.202	-0.439	2.241	-1.599
Standardised residual	Male	0.033	**0.076**	-0.511	**0.311**
	Female	-0.030	-0.068	**0.459**	-0.280
Adjusted standardised residual	Male	0.055	**0.121**	-0.753	**0.477**
	Female	-0.055	-0.121	**0.753**	-0.477

Table 4 indicates that the values in bold contributed more to the acceptance of the null hypothesis. For males, living together and sexual intimacy contributed to the acceptance of the null hypothesis, while for females, quarrel contributed to the acceptance of the null hypothesis. Therefore, living together, sexual intimacy, and quarrel are the highest gender base contributions to the acceptance of the null hypothesis.

Table 5. Observed and expected values for six weeks during Covid-19 lockdown.

Gender	Dinner	Sexual Intimacy	Quarrel	Living together	Row Total
Male	31 *(31.90)*	34 *(32.81)*	19 *(20.50)*	29 *(27.79)*	113
Female	39 *(38.10)*	38 *(39.19)*	26 *(24.50)*	32 *(33.21)*	135
Column Total	70	72	45	61	248

Table 6. Statistics for decision analysis for six weeks during the Covid-19 lockdown.

χ^2	G^2	MG^2	$p-value$	${\chi^2}_{5\%}$	df
0.425	0.425	0.426	0.93	7.81	3

Table 7. Variable contribution to relationship intimacy during Covid-19 lockdown.

	Gender	Dinner	Sexual intimacy	Quarrel	Living together
Residual	Male	-0.895	1.194	-1.504	1.206
	Female	0.895	-1.194	1.504	-1.206
Standardised residual	Male	-0.159	**0.208**	-0.332	**0.229**
	Female	**0.145**	-0.191	**0.304**	-0.209
Adjusted standardised residual	Male	-0.254	**0.335**	-0.498	**0.357**
	Female	**0.254**	-0.335	**0.498**	-0.357

During the Covid-19 lockdown, sexual intimacy and living together contributed to the acceptance of the null hypothesis for males while dinner and quarrel contributed to the acceptance of the null hypothesis for females. Therefore, based on Table 7, we conclude that different study variables contributed to the acceptance of the null hypothesis for males and females.

Table 8. Observed and expected values for six weeks after Covid-19 lockdown relaxation.

	Dinner	Sexual Intimacy	Quarrel	Living together	Row Total
Male	34 (33.22)	33 (31.88)	16 (17.96)	27 (26.94)	110
Female	40 (40.78)	38 (39.12)	24 (22.04)	33 (33.06)	135
Column Total	74	71	40	60	245

Table 9. Statistics for decision analysis for six weeks after Covid-19 lockdown relaxation.

χ^2	G^2	MG^2	$p-value$	${\chi^2}_{5\%}$	df
0.493	0.496	0.499	0.92	7.81	3

Table 10 indicates that after lockdown relaxation, sexual intimacy and dinner contributed more to the acceptance of the null hypothesis for males, while quarrel contributed more for females. Therefore, we conclude that after Covid-19 lockdown relaxation, dinner, sexual intimacy, and quarrel contributed more to the acceptance of the null hypothesis. See Table 13 for details.

The proposed benchmark method identified the highest contribution to inference. In Table 11, the number reported is the number of variables with the highest contributors to the acceptance of the null hypothesis. See Table 13 for periodic analysis. Comparing the analysis in Table 11 with those of Tables 4, 7, and 10, we conclude that the benchmark method is equivalent to the adjusted standardised residual in terms of identification. We compared the identification strength further by applying the benchmark method to the results by Sharpe (2015) in Table 12. The table indicates that Landis *et al.* (2013) identified five major contributors to the rejection of the null hypothesis (19.34 > 18.89), while DeViva (2014) identified two major contributors (8.88 > 7.81).

Table 10. Variable contribution to relationship intimacy after Covid-19 lockdown relaxation.

	Gender	Dinner	Sexual intimacy	Quarrel	Living together
Residual	Male	0.776	1.122	-1.959	0.061
	Female	-0.776	-1.122	1.959	-0.061
Standardised residual	Male	**0.135**	**0.199**	-0.462	0.012
	Female	-0.121	-0.179	**0.417**	-0.011
Adjusted standardised residual	Male	**0.217**	**0.318**	-0.681	0.018
	Female	-0.217	-0.318	**0.681**	-0.018

Table 11. Variable contribution to the acceptance of the null hypothesis.

Methods	Table4	Table 7	Table 10
ω_i	3 (37.5%)	4 (50%)	3 (37.5%)
∇	2 (25%)	4 (50%)	3 (37.5%)

Table 12. Comparison of variable contribution to inference (Sharpe, 2015).

Methods	(Landis *et al.*, 2013)	(DeViva, 2014)
ω_i	5 (33.3%)	3 (50.0%)
∇	5 (33.3%)	2 (33.3%)

Table 13. Highest contribution to inference based on adjusted standardised residual.

Study period	Gender	Dinner	Sexual intimacy	Quarrel	Living together
Pre-Covid-19	Male	--	0.121	--	0.477
	Female	--	--	0.733	--
Covid-19 lockdown	Male	--	0.335	--	0.357
	Female	0.254	--	0.498	--
Post- Covid-19 lockdown relaxation	Male	0.217	0.318	--	--
	Female	--	--	0.681	--

This study has shown that relationship intimacy is independent of the study variables. The test statistic applied accepted the null hypothesis. The study shows that for females, the main contributory factor is quarrel, while for males the main contributory factors are sexual intimacy and living together. The study also reveals that after the relaxation of lockdown, living together never contributed to the acceptance of the null hypothesis for males. During the lockdown period, the numerical strength of quarrel reduces compared to the pre- and post-Covid-19 contribution to inference. For males, sexual intimacy contributed more during lockdown followed by post- and pre-Covid-19 period. The analysis shows that each gender is consistent with their contribution to the acceptance of the null hypothesis before Covid-19 outbreak, during Covid-19 lockdown, and after Covid-19 lockdown relaxation. In general, the output in Table 4, Table 7, and Table 10 mimic the result by Sharpe (2015), DeViva (2014), and Landis *et al.* (2013). The benchmark method clearly and uniquely identified the variable contribution to inference in Table 13.

IV. CONCLUSION

The difference between large observed and small expected values yields large positive contributions, whereas the opposite results in a negative contribution to the eventual residual value. The sign directions only affect the analysis of the residual methods but not the eventual chi-square value. This means that negative residual value should be completely ignored in cell contribution analysis. On the other hand, the residual method is useful to identify cell signs direction contribution while the benchmark method uniquely identifies the major variable contributors to inference. Before the Covid-19 outbreak, quarrels, and living together contributed more to the acceptance of the null hypothesis. During the Covid-19 lockdown, in terms of gender, sexual intimacy and living together contributed more to males, while dinner and quarrel contributed more to females. After Covid-19 lockdown relaxation, quarrel was the highest contributor to inference. Therefore, we conclude that quarrel was the highest contributor to the acceptance of the null hypothesis.

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