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A proposed method for cleaning data from outlier values using the robust RFCH method in structural equation modeling

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Abstract

The GLS and ML methods are the most common methods for estimating SEM but require multivariate normality. Therefore, methods robust to standard errors and quality of fit indexes to Chi-square have been proposed: MLR and they are considered superior to ML and GLS methods analyzing ordinal data. When we have a five-way Likert scale, the data is treated as continuous by calculating the covariance matrix as inputs for ML, GLS, and MLR. However, outliers are familiar because modeling requires a large sample size, either because of the input of data or answers more than is expressed within a particular category. Their presence affects even methods with robust corrections, where the accuracy of estimating parameters, standard errors, and fit indicators may be compromised the quality of fit indexes and inappropriate solutions, where a robust algorithm is proposed to clean the data from the outlier, as this proposed algorithm calculates the robust correlation matrix robust RFCH Reweighted Fast Consistent and High Breakdown, which consists of several steps and has been modified by taking the clean data before calculating the robust RFCH correlation matrix. It was also suggested to make a comparison between the three methods before the treatment process with the presence of outlier values and note the extent of their impact on the methods and after using the robust RFCH method, and note the extent of improvement in estimations, standard errors and the overall quality of fit indexes for each of the Chi-square index, CFI, TLI, and RMSEA, SRMR and CRMR, with the robust corrections in the Chi-square index for each of the methods MLR. Through the simulation experiment, the researcher reached the power of the proposed method robust RFCH in improving the quality of parameter estimation, standard errors, and overall fit indexes quality.

Keywords: outlier, robust RFCH, SEM, fit indexes, methods estimation

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1. Introduction

SEM approaches are widely utilized in situations where variables are hypothesized to have interrelationships. The method that relies on SEM techniques is sometimes termed latent variables modeling. These modeling employ path analyses, confirmatory factor analyses (CFA), full structural regression models (SR models), and latent growth modeling (LGM), investigate causal relationships between one or so more independent variables (IVs), which can be discrete or continuous, and one or more dependent variables (DVs), which can be discrete or continuous. A latent variable (factor) and a measurable variable are both possible for IVs and DVs. Furthermore, A diagram can be used to illustrate how a model is supposed to work. According to built theories and empirical evidence, the application of SEM is especially adept at solving complex relationships among variables in social science studies, management, nature, and other sciences. Causal inference with the SEM involves testing hypotheses on the model and estimating parameter values. In such cases, the findings are considered accurate if the data meet all the assumptions necessary by the estimating method

Multivariate normality is of concern when working with SEM data because that defines which estimation method is to be used. Data from the actual world are rarely (if ever) distributed around a normal curve, regardless of their size. The normal theory-based estimate approach should not be applied to samples having multivariate nonnormal distributions, leading to erroneous results. Researchers may transform the raw data to make it closer to the specified standard or eliminate outliers that cause the data to deviate greatly from the normal distribution and distort the covariance matrix.[6, 57]

The survey data for the Likert scale do not have a normal distribution. The presence of outliers leads to an increase in the deviation of the data from the normal distribution, despite the proposal of methods with robust corrections in the standard errors and robust corrections in the Chi-square fit index that deal with the nonnormal distribution, but all of these methods Sensitive to outlier values as it leads to a distortion in the estimation of parameters and the model and illogical solutions, in addition to its impact on the fit index that leads to the rejection of valid models.

Therefore, the researchers recommend addressing the problem of outlier data before using estimation methods. For this reason, a robust method has been proposed to address the problem of outlier data through the use of a proposed RFCH robust algorithm to trim the data from outlier values and the use of both classical methods and methods with robust corrections in standard errors and fit indexes where These robust correction methods work with data that has nonnormal distribution but is also sensitive to outliers. The proposed algorithm for cleaning the data from the outlier and calculates a robust RFCH matrix of an outlier, where the researcher made a simple modification to the algorithm by taking the final data he reached by going through several estimators before calculating the matrix to be used these robust data in all method estimation.

The researcher found in [6] that the outlier values are one of the factors that lead to wrong conclusions and inappropriate solutions, and ignoring them leads to negative correlations or variances, or greater than one, where he recommended to evaluate and estimate the structural model with and without the outlier. He also presented an experimental example with and without the outlier. In [5, 16], the researcher evaluated the effect of outliers on the CFI fit index, where a modification was made to the construction of the CFI index by using a robust matrix method to estimate the covariance matrix represented by Minimum Covariance Determinant Estimator (MCD)matrix and the Minimum Volume Ellipsoid and called the new fit indicators as CFI-MCD and CFI-MVE The results showed that the results were superior to methods CFI based on ML. In [49] suggested integrating the robust RFCH estimator into the LARS method because it is sensitive to outliers by replacing the non-robust estimators with their robust ones. It was tested with a numerical example and a

simulation study. In [55], the researcher studied the effect of outliers on the estimators and tests in analyzing the covariance structure by using the normal theory-based maximum likelihood (ML) and the asymptotically distribution-free (ADF) method. The researcher found that a small percentage of the values lead to a bias in the standard errors and test statistics, and the model was rejected even if it was defined correctly. He recommended the use of two methods, the first using The classical methods after deleting outliers and the second using robust methods

2. The Problem

The problem of ordinal data is not distributed normally for two reasons: the responses on a paragraph are more than the rest of the paragraphs or because of data entry. These two reasons affect the estimation methods and fit indexes. And The problem of an outlier, as the outlier values affect the estimation of parameters, standard errors, and the quality of fit indexes, although there are methods that deal with no normal distribution, the methods are not strong for outlier values, so they require treatment before using the method of estimation.

3. Objective

The research aims to address the problem of outliers when we have a Likert scale questionnaire form, so there are responses of individuals on a paragraph more than others and errors in data entry because the modeling requires a large sample size. The entry error is very likely. Studying the effect of an outlier on estimation methods ML,MLR and GLS, and using the same estimation methods after treatment using robust estimation RFCH. This research aims to study the effect of the sample size and the degree of distribution on the model's overall fit indexes. And A comparison between the methods and selecting the best method for dealing with the data as an ordinal five-point Likert scale.

4. Outlier

An outlier is an observation that is quite remote from the majority of the data. Outliers can be created by typing or recording errors. In that case, a data collection can contain a substantial proportion of outliers. Outliers should always be investigated to see if they follow a pattern, if they are due to recording errors, or if a different model may satisfactorily describe them. Errors in recording can occasionally be addressed, and variables that were left out can be included [33]. The multivariate normal assumption is commonly employed in SEM estimation. Multivariate outliers, kurtosis, and skewness are detected by several SEM software. Transformations may be attempted if skewness is significant, but skewness remains high even after transformations are applied. It is generally believed that some variables are not normally distributed in the populace, or a variable is not distributed normally in the population. So the researcher should select an estimating method that takes into account nonnormality [45]. error outliers include outlying observations produced by something other than not being part of the population of interest (an error in the sampling technique). Extremely large or little data values within the same construct. Extremely rare outliers that have a significant impact on model fit.

5. The Proposed Method for Processing Data from Outlier Values Represented by Estimation Reweighted Fast Consistent and High Breakdown (RFCH)

Olive and Hawkins [32], developed Reweighted Fast Consistent and High breakdown (RFCH) estimators of location and scatter, which was faster than the fast MCD developed by Rousseeuw and

Driessen [38]. The attractive feature of the RFCH technique is that not only its computation is very fast, which is even faster than Fast MCD [60], but it is $\sqrt{n}$ Consistent estimators. The RFCH utilizes the $\sqrt{n}$ Consistent DGK [19] estimator and high breakdown Median Ball (MB) [34] estimators as attractors.

Mahalanobis defined Mahalanobis Distance (MD) to measure the deviation of a data point from its center. Let us write the i^{th} vector of predictor variables as:

$$X_i^{'} = (1, X_1, X_2, \ldots, X_P) = (1, x_i)$$

where x_i Is a p -dimensional row vector. The mean vector and the variance-covariance matrix are calculated as:

$$\bar{x} = \frac{1}{n \sum_{i=1}^{n} x_i \text{ and } C} = \left(\frac{1}{n-1}\right) \sum_{i=1}^{n} \left(x_i - \bar{x}\right) \left(x_i - \bar{x}\right)^{'}, \qquad \text{respectively.}$$

Subsequently, the (MD) for each observation is written as Equation:

$$MD_i = \sqrt{\left(x_i - T(X)\right)^{'} C(X)^{-1} \left(x_i - T(X)\right)} \; i = 1, 2, \ldots, n \tag{5.1}$$

where $T(X)$ is the mean vector $(\bar{x})$ and $C(X)$ is the variance-covariance matrix (C).
The RFCH algorithms can be summarized as follows:

The DGK Algorithm Steps

(i) Compute the p -dimensional row vector of location and (pxp) the $(T(X), C(X))$ covariance matrix, 0 of the original data and use it as the initial or starting point $(T_{0,\text{ Start}}, C_{0,\text{ Start}})$For calculating the initial Mahalanobis Distance (5.2).

$$MD_{i0,\text{DGK}} = \sqrt{\left(x_i - T_{0,\text{ Start}}\right)^{'} \left(C_{0,\text{ Start}}\right)^{-1} \left(x_i - T_{0,\text{ Start}}\right)} \; i = 1, 2, \ldots, n \tag{5.2}$$

(ii) Sort the $MD_{i0,\text{DGK}}$ in increasing order. Then calculate its median, MED $= median\left(MD_{i0,\text{DGK}}\right)$. The observation corresponding to the Mahalanobis Distance less than the median will be in the remaining half dataset (m observations), defined as Equation (5.3)

$$\widetilde{X}_{1,\text{DGK}} = \left\{X_{\text{jl}} : MD_{i0,\text{DGK}} \leq \text{MED}\right\}, j = 1, 2, \ldots, k, l = 1, 2, \ldots, m \tag{5.3}$$

where k is the number of predictor variables.

(iii) Consider $C_{0,\text{DGK}} = C_{0,\text{ Start where }} C_{0,\text{ Start is the original dataset's scatter matrix,}}$ then recompute the location and scatter estimators for the $\widetilde{X}_{1,\text{DGK}}$ dataset to obtain the first attractors $(T_{1,\text{DGK}}, C_{1,\text{DGK}})$.

(iv) Stop the process if the diagonal elements of $C_{1,\text{DGK}} = C_{0,\text{ Start}}$, otherwise repeat steps 1 to 3 until convergence where at convergence, the final location and scatter estimates $(T_{K,\text{DGK}}, C_{K,\text{DGK}})$ is acquired from the $\widetilde{X}_{K,\text{DGK}}$Where K is the final step at which convergence takes place.

The MB Algorithm Steps

(i) Let an identity matrix be the scatter matrix, denoted as $C = I_p$. Then compute Mahalanobis Distance based on the median vector, median (X) and C as Equation (5.4):

$$MD_i = \sqrt{(x_i - Med(X))' (C)^{-1} (x_i - Med(X))}, i = 1, 2, \ldots, n \tag{5.4}$$

where $Med(X) = median(X)$
Let the median of MD_i be the cut-off point, which is denoted by L_{cut} (Equation (5.5)),

$$L_{cut} = median(\ MD_i) \tag{5.5}$$

Where $Lcut \neq 0.5$. Determine the $\widetilde{X}_0$ for half of the dataset (m) whose MD_i is less than or equal to the Lcut, such that (Equation (5.6))

$$\widetilde{X}_0 = \{X_{\text{jl}} : MD_i \leq \text{Lcut}\}, j = 1, 2, \ldots, k, l = 1, 2, \ldots, m \tag{5.6}$$

(ii) Compute the p-dimensional row vector of location and the (pxp) covariance matrix of scattering estimators of the $\widetilde{X}_0$ and use it as the initial or starting point $(T_{0,\text{ Start}}, C_{0,\text{ Start}})$For calculating the initial Mahalanobis Distance (Equation (5.7)).

$$MD_{0i,\text{MB}} = \sqrt{(x_i - T_{0,\text{ Start}})' (C_{0,\text{ Start}})^{-1} (x_i - T_{0,\text{ Start}})}, i = 1, 2, \ldots, n \tag{5.7}$$

determined the remaining half dataset by using a new cut-off point as Equation:

$$\widetilde{X}_{1,\text{MB}} = \{X_{\text{jl}} : MD_{0i,\text{MB}} \leq \text{ Lcut } 0\}, j = 1, 2, \ldots, k, l = 1, 2, \ldots, m \tag{5.8}$$

where$Lcut0 = median\,(MD_{0i,\text{MB}})$.

(iii) Based on the $\widetilde{X}_{1,\text{MB}}$, calculate the attractor $(T_{1,\text{MB}}, C_{1,\text{MB}})$.

(iv) If the diagonal elements of $C_{1,\text{MB}} = C_{0,\text{ Start}}$ stop the process, otherwise recalculate the $MD_{1,\text{MB}}$ based on attractor $(T_{1,\text{MB}}, C_{1,\text{MB}})$ and iterate the Steps 2 to 3 until the convergence is aChieved at the final attractor $(T_{K,\text{MB}}, C_{K,\text{MB}})$ and final remaining set $\widetilde{X}_{K,\text{MB}}$

The RFCH Algorithm Steps

The RFCH consists of three steps where; in the first step, the Fast Consistent and High breakdown (FCH) attractors of Olive and Hawkins [32] is determined based on the final attractors of DGK and MB estimators that adhere to the following rules:

(i) The T_{FCH} and C_{FCH} are determined as Equation (5.9):

$$T_{FCH} = \begin{cases} T_{K,\text{DGK}} & \text{if } \sqrt{|C_{K,\text{DGK}}|} < \sqrt{|C_{K,\text{MB}}|} \\ T_{K,MB} & \text{Otherwise} \end{cases} \tag{5.9}$$

And Equation (5.10)

$$C_{FCH} = \begin{cases} \frac{Med\left(MD_i\left(T_{K,\text{DCK}}, C_{K,\text{DGK}}\right)\right)}{x^2(p,0.5)} \times C_{K,\text{DGK}}, & \text{if } \sqrt{|C_{K,\text{DGK}}|} < \sqrt{|C_{K,\text{MB}}|} \\ \frac{\text{Med}\left(MD_i\left(T_{K,\text{MB}}, C_{K,\text{MB}}\right)\right)}{x^2(p,0.5)} \times C_{K,\text{MB}}, & \text{otherwise} \end{cases} \tag{5.10}$$

where $x^2_{(p,0.5)}$ is Chi-square distribution with p degrees of freedom and significance level 0.5. The $(T_{\text{FCH}}, C^*_{\text{FCH}})$ are the consistent estimators of the FCH attractors according to Theorem 1 of Olive and Hawkins [32],

$$\text{where } C^*_{\text{FCH}} = \frac{Med\left(MD_i\left(T_{\text{FCH}}, C_{\text{FCH}}\right)\right)}{x^2(p, 0.5)} * C_{\text{FCH}}.$$

(ii) Construct a new set of data, $\widetilde{X}_{\text{FCH}}$ by using the following Equation (5.11),

$$\widetilde{X}_{\text{FCH}} = \left\{X_{\text{jl}} : MD_i\left(T_{\text{FCH}}, C^*_{\text{FCH}}\right) \leq x^2{}_{(p,1-\alpha)}\right\}, \qquad j = 1, 2, \ldots, k, l = 1, 2, \ldots, m, \tag{5.11}$$

where $MD_i\left(T_{\text{FCH}}, C^*_{\text{FCH}}\right)$ is the Mahalanobis Distance based on the location and scatter of FCH estimators in (i) . Then compute the location and scatter estimators for the $\widetilde{X}_{\text{FCH}}$ dataset to obtain the RFCH attractors, $(T_{1,\text{RFCH}}, C_{1,\text{RFCH}})\cdot$ Again, following Theorem 1 of Olive and Hawkins [32], $C^*_{1,\text{RFCH}}$ is defined as Equation (5.12),

$$C^*_{1,\text{RFCH}} = \frac{Med\left(MD_i\left(T_{1,\text{RFCH}}, C_{1,\text{RFCH}}\right)\right)}{x^2(p, 0.5)} * C_{1,\text{RFCH}} \tag{5.12}$$

Subsequently, the Mahalanobis Distance based on is computed, and a new set of data is constructed using the following Equation;

$$\begin{gathered}\widetilde{X}_{2,\text{RFCH}} = \left\{X_{\text{jl}} : MD_i\left(T_{1,\text{RFCH}}, C^*_{1,\text{RFCH}}\right) \leq x^2(p, 1-\alpha)\right\}, \\ j = 1, 2, \ldots, k, l = 1, 2, \ldots, m\end{gathered} \tag{5.13}$$

Following the same process, $(T_{2,\text{RFCH}}, C_{2,\text{RFCH}})$ estimators are calculated based on the $\widetilde{X}_{2,\text{RFCH}}$ dataset. Afterward, $C^*_{2,\text{RFCH}}$ is defined as in Equation (5.14) by applying Theorem 1 of Olive and Hawkins [32]

$$C^*_{2,\text{RFCH}} = \frac{Med\left(MD_i\left(T_{2,\text{RFCH}}, C_{2,\text{RFCH}}\right)\right)}{x^2(p, 0.5)} * C_{2,\text{RFCH}} \tag{5.14}$$

(iii) Repeat steps (i)-(ii) with the new cut-off point until convergence to get the final attractors $(T_{\text{RFCH}}, C_{\text{RFCH}})$ and $\widetilde{X}_{\text{RFCH}}$, Subsequently, the Mahalanobis Distance based on is computed, and a new set of data is constructed using the following Equation (5.15)

$$\begin{gathered}\text{clean data robust} = \widetilde{X}_{3,\text{RFCH}} = \left\{X_{\text{jl}} : MD_i\left(T_{2,\text{RFCH}}, C^*_{2,\text{RFCH}}\right) \leq x^2(p, 1-\alpha)\right\}, \\ j = 1, 2, \ldots, k, l = 1, 2, \ldots, m\end{gathered} \tag{5.15}$$

Upon convergence, the RFCH produced the final $(T_{\text{RFCH}}, C_{\text{FCH}})$ estimators which are $\sqrt{n}$ Consistent according to [32, 30, 48, 60, 59, 38, 19, 34, 33].

6. Structural Equation Models (SEM)

An important two-part of models employed in SEM includes measurement models and structure models. CFA is used to correct for indicator measurement error, shaping the latent variables (factors). A model in which the exogenous variable x and the endogenous variables y are being measured is defined as

$$\begin{aligned} x &= \mathbf{\Lambda}_x \xi + \delta \\ y &= \Lambda_y \eta + \varepsilon \end{aligned} \tag{6.1}$$

The full structural Equation model is defined as

$$\begin{aligned} \eta &= \mathbf{B}\eta + \mathbf{\Gamma}\xi + \zeta \\ (\mathbf{I} - \mathbf{B})\,\eta &= \mathbf{\Gamma}\xi + \zeta \\ \eta &= (\mathbf{I} - \mathbf{B})^{-1}(\mathbf{\Gamma}\xi + \zeta) \end{aligned} \tag{6.2}$$

The covariance matrix is obtained as follows by

$$\Sigma(\theta) = \begin{bmatrix} \mathbf{\Lambda}_y(\mathbf{I} - \mathbf{B})^{-1}[\mathbf{\Gamma}\mathbf{\Phi}\Gamma' + \mathbf{\Psi}](\mathbf{I} - \mathbf{B})^{-1}\mathbf{\Lambda}_y' + \mathbf{\Theta}_\varepsilon & \mathbf{\Lambda}_y(\mathbf{I} - \mathbf{B})^{-1}\mathbf{\Gamma}\Phi\mathbf{\Lambda}_x' \\ \mathbf{\Lambda}_x\mathbf{\Phi}\Gamma'(\mathbf{I} - \mathbf{B})^{-1}\mathbf{\Lambda}_y' & \mathbf{\Lambda}_x\Phi\mathbf{\Lambda}_x' + \mathbf{\Theta}_\delta \end{bmatrix} \tag{6.3}$$

Therefore the matrix of covariance was proven [46, 13, 7].

7. Estimation of Model Parameters

7.1. The maximum likelihood function for SEM (ML)

Several frequently used estimation methods for structural equation modeling have already been well established and are commonly employed. Maximum likelihood estimators are the most often used normal theory estimators in SEM (ML). The vast majority of the most widely used software packages rely on ML as their default estimator. The iterative process with a variational minimization technique aims to generate a function that can expect the target value. The fit function may be defined differently. The first approach uses a log-likelihood ratio fit that minimizes a multivariate normality assumption to address the problem. The second technique is based on a form general of the for least-squares fit function.

An examination of a multivariate normal population through the use of a random sample would indicate that a random sampling procedure called Wishart distribution (Wishart 1928) allows calculating the probability of selecting a sample with variance-covariance matrix S.

$$S = \frac{1}{N-1}\sum_{i=1}^{N}(x_{ij} - \overline{x}_j)(x_{ij} - \overline{x}_j)' = \frac{1}{n}\sum_{i=1}^{N}(x_{ij} - \overline{x}_j)(x_{ij} - \overline{x}_j)' \tag{7.1}$$

The maximization of the equation is equivalent to the minimization of the function in brackets:

$$F_{ML}(\theta) = \ln|\hat{\Sigma}| + \mathrm{tr}(S\hat{\Sigma}^{-1}) - \ln|S| - (p+q) \tag{7.2}$$

While q denotes the X variable and p denotes the Y variable.
While θ is the parameter vector, $\hat{\Sigma}$ is the covariance matrix implied by the model,

F_{ML} denotes the fitting function's value as determined at the final estimates.,

$|\Sigma|$ is the determinant of a matrix, while tr is the matrix's trace [7].
Efficient and consistent estimates of unknown parameters are achieved by minimizing the Eq. (7.2).

$$\hat{\theta}_{ML} = \arg\min F_{ML}(S, \hat{\Sigma}(\hat{\theta}) = \ln|\hat{\Sigma}(\hat{\theta})| + \mathrm{tr}|\hat{\Sigma}(\hat{\theta})| - \ln|S| - (k) \tag{7.3}$$

As equation (7.3) shows, at the minimum of the fit function $F_{ML}(\theta)$, $\hat{\theta}_{ML}$ contains parameter estimates $\hat{\Lambda}$, Φ, and Ψ, where $\hat{\Lambda}$ is a matrix of estimated factor loadings, Φ is an estimated factor covariance, and $\hat{\Psi}$ is the covariance matrix of error variables. Γ is the matrix structural regression of the endogenous and latent exogenous variables, B regression between endogenous factors latent. Standard errors

are defined as the square roots of the diagonal elements of the approximation asymptotic covariance produced from ML under multivariate normality assumption:

$$\operatorname{acov}(\hat{\Theta})_{ML} = \left(\frac{2}{N-1}\right)\left\{E\left[\frac{\partial^2 F_{ML}}{\partial\theta\partial\theta'|_{\theta=\theta_0}}\right]\right\}^{-1} = n^{-1}\left(\Delta'\Gamma^{-1}\Delta\right)^{-1} \tag{7.4}$$

where $\Gamma = \Gamma_{(ij,kl)} = \sigma_{ik}\sigma_{jl} + \sigma_{il}\sigma_{jk}$ *and* $\Delta = (\partial\sigma(\theta)/\partial\theta')_{|\theta=\theta_0}$.

And Is the model's partial derivatives matrix as respects the parameters Estimates of parameters provided by ML are desirable asymptotic, such as unbiased, consistency and efficiency in addition In SEM, A fundamental aspect of modeling is determining how well a model fits a situation Model fit is evaluated using the Chi-square goodness. which is a function of the fit and may be calculated as follows:

$$T_{ML} = (N-1)\,F_{ML}, \quad df = s - t \tag{7.5}$$

Represent s is the number of non-duplicated components in the observable covariance matrix $s = \frac{1}{2}k(k+1)$ and t is the count of unknown parameters and a χ^2 distribution with $s-t$ degrees of freedom [18, 7, 40, 53, 3, 2].

7.2. Generalized least squares(GLS)

The generalized least squares (GLS) method, based on normal theory, first debuted in 1970 (e.g., Anderson, 1973)[11], and has since been widely used. Suppose $\{x_1, \ldots, x_n\}$ are samples of x such that all x_i are (iid) according to $\mathrm{N}[0, \Sigma]$. The covariance matrix is

$$S = (n-1)^{-1}\sum_{i=1}^{n}(x_i - \overline{x})(x_i - \overline{x})' \tag{7.6}$$

This is the most basic finding for constructing the theory of Covariance Structure Analysis under the normally distributed assumption. A result is obtained by Equation (7.7)

$$\begin{aligned} n^{1/2}\operatorname{vec}(S-\Sigma) = n^{\frac{1}{2}}k^{-'}\operatorname{vecs}(S-\Sigma) &\xrightarrow{L} N\left[0, 2k^{-'}k'(\Sigma\otimes\Sigma)kk^{-}\right] \\ &= N[0, 2D(\Sigma\otimes\Sigma)D] \end{aligned} \tag{7.7}$$

Another important matrix $D(k^2 \times k^2)$ is defined by $D = kk^{-} = k\left(k'k\right)^{-1}k'$.

The GLS function is expressed in terms of the residual quadratic form:

$$(vecs(S-\Sigma))'\left(2n^{-1}k'(\Sigma_0\otimes\Sigma_0)k\right)^{-1}(vecs(S-\Sigma)) \tag{7.8}$$

Because Σ If unknown, we will substitute by $k*k$ positive definite matrices V. A discrepancy was identified and explored via [10], known as the Generalized Least Squares (GLS). the GLS function is

$$F_{\mathrm{GLS}}(\theta) = \frac{1}{2}\left[vec(S-\Sigma(\theta))'(V\otimes V)vec(S-\Sigma(\theta))\right] = \frac{1}{2}tr[(S-\Sigma(\theta))V]^2 \tag{7.9}$$

. The constant positive definitive matrix V is a $k \times k$ or the stochastic matrix V that is more likely than not to converge in probability to the constant positive definitive matrix V^*. It is represented by the symbol V*, where $vec()$ is a vectorization operator that turns a matrix into a vector by staking rows of the matrix, where $\otimes$ is the Kronecker product [28]. When V converges in probability to Σ^{-1}. [10, 11], demonstrated that the GLS estimator $\hat{\theta}_{\mathrm{GLS}}$ that minimizes $F_{\mathrm{GLS}}(\theta)$ is asymptotically identical to $\hat{\theta}_{ML}$ and $T_{GLS} = (n-1)F_{\mathrm{GLS}}\left(\hat{\theta}\right)$, and $df = s-t$ degree of freedom with χ^2 distribution is used to describe $nF_{GLS}(\theta) \xrightarrow{L} \chi^2_{s-t}$ [24, 26, 35].

7.3. Maximum likelihood robust function for SEM (MLR)

Because the assumption of normality is invalid, ML estimates for parameters are not asymptotically effective. Due to faulty asymptotic covariance matrix assumption, the $Cov(\theta)ML$ from equation $acov(\hat{\Theta})_{ML} = (\frac{2}{N-1})\{E[\frac{\partial^2 F_{ML}}{\partial\theta\partial\theta'|\theta=\theta_0}]\}^{-1} = n^{-1}\left(\Delta'\Gamma^{-1}\Delta\right)^{-1}$ is no longer consistent with the corresponding true covariance matrix, resulting in incorrect standard error estimations. An affirmative, creative response is to be expected." It has been shown by [56, 58], that Modeling parameters with MLR have a comparable estimation method to ML. Still, additional adjustments are made to ensure robustness against nonnormal data. The correction of SB scaling (Satorra and Bentler, 1994) and [54] can be applied if the model is unspecified or data is the outlier.

Browne's (1982, 1984) original residual-based test statistics T_B Has a theoretical benefit: if the sample size is large enough, the distribution of the test statistics is known exactly. The estimate $\hat{\theta}$: is given as follows:

$$T_B\left(\hat{\theta}\right) = n\hat{e}'\dot{\sigma}_c\left(\hat{\theta}\right)\left[\dot{\sigma}_c'\left(\hat{\theta}\right)S_Y\dot{\sigma}_c\left(\hat{\theta}\right)\right]^{-1}\dot{\sigma}_c'\left(\hat{\theta}\right)\hat{e} \tag{7.10}$$

where $\dot{\sigma}(\theta) = \partial\sigma(\theta)/\partial\theta$ or $\dot{\sigma}(\theta) = \partial vech\Sigma(\theta)/\partial\theta$ represents the Jacobian matrix $s \times t$. There is now an $s \times (s-t)$ matrix $\dot{\sigma}_c(\theta)$ with columns that are orthogonal with those of $\dot{\sigma}(\theta)$. To guarantee that the model is accurately identified at $\hat{\theta}$, we assume that $\dot{\sigma}(\theta)$ has complete rank in the vicinity of $\hat{\theta}$, represented by $\dot{\sigma} = \dot{\sigma}(\hat{\theta})$. And $\hat{e} = s - \sigma(\hat{\theta})$ represents the disparity between the data and any consistent estimator-estimated model.

[54] proposed the TYB test statistic, a modified residual-based test statistic. The concept originates in the regression literature, where model residual cross-products estimate asymptotic covariance matrix and standard errors [22]. With the ofΓ replace S_Y, the following decomposition can be used to obtain a consistent estimate $\hat{\theta}$

$$\hat{\Gamma} = \frac{1}{n}\sum_{i=1}^{N}\left[Y_i - \sigma(\hat{\theta})\right]\left[Y_i - \sigma(\hat{\theta})\right]' = S_Y + \frac{N}{n}[\bar{Y} - \sigma(\hat{\theta})][\bar{Y} - \sigma(\hat{\theta})]' \tag{7.11}$$

Replacing S_Y in (7.10) by $\hat{\Gamma}$, the Yuan-Bentler residual-based statistic is given by:

$$T_{\mathrm{YB}}(\hat{\theta}) = T_B(\hat{\theta})/\left[1 + NT_B(\hat{\theta})/n^2\right)\Big] \tag{7.12}$$

Additionally, the approximate theoretical result of the χ^2 distribution with $(s-t))$ degrees of freedom are also realized asymptotically.

However $T_{\mathrm{YB}}(\hat{\theta}) < T_B(\hat{\theta})$, given any consistent estimate $\hat{\theta}$, it is believed that the problem of over rejection will be reduced by using T_{YB}. Because the denominator in (7.12) is nearly always bigger than one, which tends to minimize inflation, it will be small and help reduce it though. [22] observed that nominal T_{YB} has a high rate of model acceptance even in the face of limited sample size [47, 43].

Another way to express the correction for standard errors. There is always a need to rescue the standard errors. Note Asparouhov and Muthén (2005) methods that the parameter covariance matrix under the multivariate normality assumption is defined by Equation $\mathrm{acov}(\hat{\Theta})_{ML}$, whereas the robust parameter covariance matrix has a sandwich-like form under non-normality, as shown in Equation (7.13)

$$cov(\sqrt{N}\hat{\theta}) = \left(\hat{\Delta}'\Gamma^{-1}\hat{\Delta}\right)^{-1}\hat{\Delta}'\Gamma^{-1}\hat{\Gamma}^{*}\Gamma^{-1}\hat{\Delta}\left(\hat{\Delta}'\Gamma^{-1}\hat{\Delta}\right)^{-1} \tag{7.13}$$

is the matrix above of model derivatives evaluated at the parameters estimates And $\hat{\Gamma}^*$ is the kurtosis matrix of the data, or a distribution-free estimate of the asymptotic covariance matrix of

sample covariances [10]. The typical element $\hat{\Gamma}^*$, is $\hat{\Gamma}^*_{ij,kl} = s_{\text{ijkl}} - s_{ij}s_{\text{kl}}$ Where s_{ijkl} is the fourth central moment of the data observed, and s_{ij}, s_{kl} are covariances of samples. [36] The inverse matrix of Fisher information $\left(\hat{\Delta}'\Gamma^{-1}\hat{\Delta}\right)^{-1}$ Which is similar to Equation (7.13), forms the outer "bread" of the sandwich, and the inner part (i.e., the "meat") is $\hat{\Delta}'\Gamma^{-1}\hat{\Gamma}^*\Gamma^{-1}\hat{\Delta}$, where $\hat{\Gamma}^*$ It is the same as the ADF asymptotic covariance matrix, which can be defined based on Equation $\mathbf{\Gamma}^* = \Gamma^*_{ij,kl} = \sigma_{\text{ijkl}} - \sigma_{ij}\sigma_{\text{kl}}$. And this matrix of covariance is sometimes called the "covariance matrix for a sandwich" [53, 39, 10, 54], rewrite the

$$acov(\hat{\theta}) = N^{-1}A_{MLR}B_{MLR}A_{MLR}, \tag{7.14}$$

8. Model Evaluation

Researchers use total fit indices from studies in applied SEM to make decisions on model-data fit. is applied to the primary hypothesis $\Sigma(\theta) = \Sigma$. If the model-estimated variance/covariance matrix, $\hat{\Sigma}$ Is not significantly different from the actual data covariance matrix, S, then we say the model fits the data well. All research has found the following: The overall model fit is evaluated before parameter estimations are interpreted. The results of the sample estimates are unreliable until the model has been validated [7, 1, 23].

8.1. Root Mean Square Error of Approximation (RMSEA) Index

Some practical research considers the (RMSEA) to be one of the most useful and reliable measures of model fit. The RMSEA was first created by (Steiger & Lind, 1980)). If the population covariance matrix were available, the RMSEA would tell you how well the hypothesized model would fit the population covariance matrix with randomly selected parameter valuesThe RMSEA fit index is determined as follows

$$RMSEA_{ML,n} = \sqrt{\max\left(0, \frac{F(S, \Sigma(\hat{\theta}))}{df} - \frac{1}{n-1}\right)} = \sqrt{\max\left(0, \frac{T_{,n} - df}{(n-1)df}\right)} \tag{8.1}$$

$F(S, \Sigma(\hat{\theta}))$ denotes that the fit function is minimized, while max denotes the maximum value of the bracketed values, and The number of known parameters is s. In contrast, the number of independent parameters is$t$. The degree of freedom is denoted by $df = s - t$, and the sample size is denoted by n [41]. A good fit index is when the value is less than 0.05. In equation (8.5), when the sample size is large compared to the model size, RMSEA produces superior estimate performance. When the sample size is large, the term [1/(n – 1)] approaches 0 asymptotically [37, 12, 51, 36].

8.2. Comparative Fit Index (CFI)

Bentler (1990) suggested the CFI as another incremental fit index. For the ML-based CFI, the following are the population and sample definitions:

$$CFI_n = 1 - \frac{F_{0,M}}{F_{0,B}} = 1 - \frac{T_M - df_M}{T_B - df_B}, \ or \ \ 1 - \frac{\max\left[\left(T_M - df_M\right), 0\right]}{\max\left[\left(T_M - df_M\right), \left(T_B - df_B\right), 0\right]} \tag{8.2}$$

If the population and the sample values of the ML discrepancy of the model are $F_{0,B}$ and $\hat{F}_B$; if the baseline model. χ^2_B represent Chi-square of the baseline model, $\hat{F}$ represents the minimum fit function and χ^2_M represent Chi-square of the target model.

This test compares your model's predicted covariance matrix against the null model's observed covariance matrix. The CFI value ranges from 0 to 1. A CFI score close to 1 suggests that the model is well fitted. The cut-off for a satisfactory fit for a CFI value is > 90 [1], suggesting that your model can recreate 90% of the covariance in the data. CFI is unaffected by sample size [17, 41, 42, 15].

8.3. Tucker Lewis Index (TLI)

TLI, the incremental fit index developed by Tucker and Lewis (1973) originally, was a reliability coefficient named after [1]. To compare nested or non-nested models inside any sample or compare a particular model across samples with differing sizes, the researchers employed TLI (sometimes called NNFI, or Nonnormed Fit Index)[1]. TLI is defined as

$$TLI_{M,n} = 1 - \frac{T_M - df_M}{T_B - df_B} \times \frac{df_B}{df_M} \quad = 1 - [(\lambda_M/df_M)/(\lambda_B/df_B)] \tag{8.3}$$

$T_{ML,B}$ represent Chi-square of the baseline model, $\hat{F}_{ML,M}$ represent the minimum fit function and $T_{ML,M}$ Represent Chi-square of the target model. The TLI approaches 1 for a correctly described model; however, the TLI can surpass the range of 0 to 1. The poorer the fit of the model, the smaller the value being modeled. When the TLI number was larger, the model was more suited. Most studies choose 0.97 as the cut-off threshold, but values of 0.95 or above are usually acceptable. [14, 22, 51].

8.4. Robust Model-fit Indexes with methods robust estimation

The robust Chi-square statistic, resilient to no normal data, corrects the other Chi-square-based goodness-of-fit indices such as RMSEA, CFI, and TLI. According to [36]. Another method is using nonnormal data from the robust RMSEA. When requested to use Yuan and Bentler's robust ML technique (1999), these programs print a robust RMSEA, different from Equation (8.1). This robust RMSEA is calculated according to the equation below:

$$\text{RMSEA}_{PR,n} = \sqrt{\max(0, \frac{T_{YB,n} - df}{(n-1)df})} \tag{8.4}$$

This equation is obtained by simply replacing $T_{ML,n}$;n in Equation (8.2) and (8.3) with $T_{YB,n}$. one can replace T with T_{ML}, T_{MLR}, For the CFI and the TLI,

$$CFI_{YB,n} = 1 - \frac{T_{YB,M} - df_M}{T_{YB,\ B} - df_B} \tag{8.5}$$

$$TLI_{YB,n} = 1 - \frac{T_{\underline{YB},M} - df_M}{T_{\underline{YB},\ B} - df_sB} \times \frac{df_B}{df_M} \qquad [8,\ 9] \tag{8.6}$$

while F_M and d_M are the fit function and degrees of freedom, respectively. Model Baseline denotes B. [8, 52, 22].

9. Residual-Based Fit Indices

9.1. Residual Matrix

. Residual matrix To examine the hypothesis that $\Sigma = \Sigma(\theta)$ you must calculate $\Sigma - \Sigma(\theta)$. A nonzero member in a null matrix indicates model definition error. To find S, you would use $\Sigma(\theta)$ as a substitution for Σ, and then you would use $S - \Sigma(\theta)$ to form $\Sigma - \Sigma(\theta)$ has elements, where each element is calculated as $\Sigma - \Sigma(\theta)$. The sample correlation is $r_{ij} - \hat{\rho}_{ij}$, while the model predicted correlation is $r_{ij} - \hat{\rho}_{ij}$. While this fix adequately tackles scaling discrepancies, it neglects sampling inaccuracy. the correlation residuals the following [21, 7].

$$r_{ij} - \hat{\rho}_{ij} = \frac{s_{ij}}{\left(s_{\text{ii}} s_{\text{jj}}\right)^{1/2}} - \frac{\hat{\sigma}_{ij}}{\left(\hat{\sigma}_{\text{ii}} \hat{\sigma}_{\text{jj}}\right)^{1/2}},\ (i, j = 1, \ldots, p) \tag{9.1}$$

9.1.1. Standardized Root Mean square Residual (SRMR)

This formula is known as the "Root Mean Square Residual" (SRMR). Dr. Bentler created SRMR in 1995, [3]. It is a covariance residual-based indicator of fit, calculated as the covariance residuals difference between observed and model projected covariances. Residuals should ideally be approaChing zero as long as the researcher's model fits the data adequately. SRMR resulted in a correlation matrix for the sample and predicted covariance matrix and then applies the procedure for calculating mean total correlation residuals. Thus, SRMR accounts for both the actual and anticipated correlations [25]. SRMR is calculated the sample estimate and population its are as follows:

$$SRMR = \sqrt{\frac{1}{s}\sum_{i=1}^{p}\sum_{j=1}^{i}\frac{\left(\sigma_{ij}^{*}-\sigma_{0,ij}\right)^{2}}{\sigma_{\mathrm{ii}}^{*}\sigma_{y}^{*}}} \tag{9.2}$$

Where $s = k(k+1)/2$). And $\sigma_{ij}^{*}, \sigma_{0,ij}$, are elements of $\Sigma^{*}$and Σ_0 Respectively. SRMR value has 0 or 1, with 0 being the optimum fit and 1 representing the worst fit. [15, 25, 41].

9.1.2. Correlation Root Mean Square Residual (CRMR)

Another standardized effect size of overall misfit suitable for covariance structure models is the correlation root mean square residual (CRMR):

$$CRMR = \sqrt{\frac{1}{s-p}\sum_{i<j}\left(\rho_{ij}-\rho_{ij}^{0}\right)^{2}} \tag{9.3}$$

Where $s = k(k+1)/2)$ and p represent vector sample variances. If you have an unknown correlation between variables, ρ_{ij} describes the correlation between variables i and j and ρ_{ij}^{0} indicates the correlation for the model fit. For the sake of ease of interpretation, standardized effect sizes are preferred to unstandardized effect sizes. [29, 31, 44].

10. Characteristics of the Research Summary

The features of the research summary dictate how the quality of the simulation findings is evaluated. The preceding robustness analysis used the following study summary data. The term "relative bias" refers to the bias of parameter estimators calculated by the equation following

$$Bias\left(\hat{\theta}_i\right) = \frac{\bar{\hat{\theta}}_i - \theta_i}{\theta_i}, \tag{10.1}$$

where θ_i denotes the population value for i^{th} parameter and $\hat{\theta}_i$ Denotes the mean of the i^{th} parameter estimations across all replications. For parameter estimation, the mean absolute relative bias is

$$\frac{1}{t}\sum_{i=1}^{t}\left|Bias\left(\hat{\theta}_i\right)\right|, \tag{10.2}$$

The number of parameters in the model is denoted by t. The relative bias of estimators for parameter standard errors θ_i It is defined as Represent t is the number of parameters in the model. The relative bias of estimators for the standard error of parameter estimates θ_i is calculated by equation

$$Bias\left(se\left(\hat{\theta}_i\right)\right) = \frac{\overline{se\left(\hat{\theta}_i\right)} - sd\left(\hat{\theta}_i\right)}{sd\left(\hat{\theta}_i\right)}, \tag{10.3}$$

where $sd\left(\hat{\theta}_i\right)$ Denotes the standard deviation of the estimates for the parameter I, and (se(i)) denotes the mean of the standard error estimates for the parameter I across all replications. For standard error estimation, the mean absolute relative bias is

$$\frac{1}{t}\sum_{i=1}^{t}\left|Bias\left(se\left(\hat{\theta}_i\right)\right)\right|,(Harwell,2018) \tag{10.4}$$

11. Simulation at the Population Level

The simulation was conducted to answer the research objectives and problems of the research. The simulation design, data generation and analysis procedures and evaluation of the results will be described. Continuous data were generated using the R program according to the method of [50, 36] for a multivariate normal distribution with skewness and kurtosis of 0 and 0 and a distribution of Medium normal with skewness and kurtosis 2 and 7, and the number of variables required for the variance-covariance matrix as defined in the model, and then a set of thresholds are determined to convert each continuous variable into an ordered categorical variable, as the number of categories is equal to 5, and this is common in research. It is Generating data with different sample sizes, in addition to 500 replicates for each group with a 20% contamination average for each sample size, randomly, where the proposed modified robust system is applied to clean the data from an outlier. The following table shows the design of the simulation experiment for the model, sample sizes, and distributions.
Table (1) shows a summary of the simulation design

Table 1: The statistical attributes of prediction models.

Design factors	***Levels***
Estimation methods	*ML,MLR,GLS*
Model size/number of indicators	*12*
Sample size	*200,400,600,800,1000*
Number of variable categories	*5–category*
Variable distribution	*moderate non-normality Normally*
Fit index	*X2,RMSEA,TLI,CFI,SRMR,CRMR*

11.1. Simulation population parameter models

The first model consists of four factors and 12 variables; each factor has three variables. We have three exogenous factors and one endogenous factor, and the indicators are loaded on the first three factors at 0.70. with making the indicators for one factor, they are generated random normality, with a mean equal to 0.5 and standard deviation 0.05, the scheme The following describes the design of a simulation experiment for a model The model consists of two parts, measurement the model, which is represented by the following mathematical equations

$$\begin{aligned}
X_{31} &= \lambda x_{31}X_1 + \delta_3 & X_{153} &= \lambda x_{153}X_3 + \delta_{15}\\
X_{41} &= \lambda x_{41}X_1 + \delta_4 & X_{163} &= \lambda x_{163}X_3 + \delta_{16}\\
X_{51} &= \lambda x_{51}X_1 + \delta_5 & X_{173} &= \lambda x_{173}X_3 + \delta_{17}\\
X_{102} &= \lambda x_{102}X_2 + \delta_{10} & Z_{31} &= \lambda z_{31}Z_1 + \delta_3\\
X_{112} &= \lambda x_{112}X_2 + \delta_{11} & Z_{41} &= \lambda z_{41}Z_1 + \delta_4\\
X_{122} &= \lambda x_{122}X_2 + \delta_{12} & Z_{51} &= \lambda z_{51}Z_1 + \delta_5
\end{aligned} \tag{11.1}$$

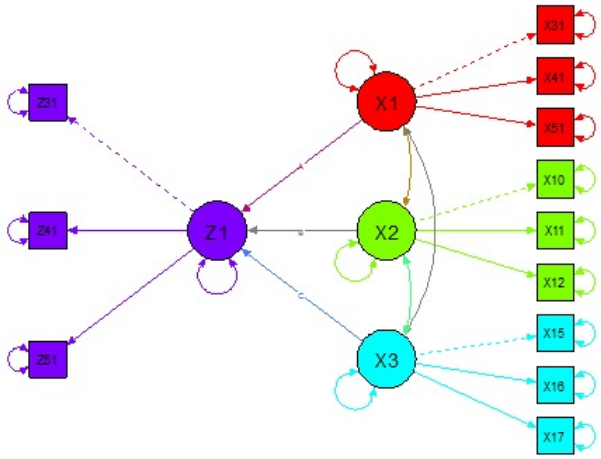

Diagram (1) the design of a model of the hierarChical model paths for the estimated parameters

As for the structural model, it is written in the following format

$$Z_1 = \gamma_{11}X_1 + \gamma_{12}X_2 + \gamma_{13}X_3 + \zeta_1 \tag{11.2}$$

The parameters λx_{11} ... λy_{51} , $\gamma_{11} \ldots . \gamma_{13}$are unknown, and their estimation is required. The factor loads of the standard model, the measurement errors on the measured variable, and the structural model parameters represent a pathway analysis between the underlying variables.

11.2. Analysis of the Simulation Results

The results of the simulation experiment for the model and the estimation methods shown in the theoretical side are presented with outliers, studying and their impact on parameters, standard errors and indicators of quality of conformity, and using the proposed robust method to clean the data from outlier by using robust RFCH, which pass in several stages.

11.3. The absolute bias average for standard errors

To determine the overall fit of the standard errors of the parameters, the total absolute bias average of the standard errors were calculated as shown in Table (2), which represents the bias for both factor loading, structural coefficients, correlations, by three methods estimation with the presence of outlier values and using the proposed method robust RFCH and according to the distribution normal and moderate distribution non-normality, as it was noted that the relative bias of errors decreased in all sample sizes and all methods, which indicates the quality of the proposed method to clean the data from an outlier in addition to the effect of an outlier on standard errors.

It was noted that the value of the standard error bias average when the data are distributed normality with skew 0 and kurtosis 0 for the ML method before cleaning and with all sample sizes between 0.4773 - 0.3347, while the CML values after using the proposed method between 0.16465 - 0.19672, and from this result, it was found that there is a clear difference using the method robust RFCH, as the errors decreased and became less than using the ML method directly

As for the MLR method, Table (2) shows that the bias average for standard errors before cleaning ranged between 0.4246 - 0.309, while the CMLR after using the proposed method ranged between 0.14512 - 0.19314, and we note through this result that there is a clear difference using the robust RFCH method; Since the errors are less than if the ML method was used directly, it was also shown through the use of the two methods that the robust maximum possibility method gives a biased

Table 2: Represents the absolute bias average of the standard errors of the model.

Dist.	***Sample size***	***200***	***400***	***600***	***800***	***1000***
	ML	*0.4773*	*0.3553*	*0.3531*	*0.3347*	*0.3507*
	CML	*0.16465*	*0.17193*	*0.19672*	*0.1851*	*0.18667*
	MLR	*0.4246*	*0.309*	*0.3091*	*0.3142*	*0.3147*
skew=0 , kurtosis =0	*CMLR*	*0.14512*	*0.1703*	*0.19314*	*0.1843*	*0.18683*
	GLS	*0.5534*	*0.357*	*0.4144*	*0.4252*	*0.4161*
	CGLS	*0.1795*	*0.17544*	*0.19827*	*0.1888*	*0.18861*
	ML	*0.4975*	*0.4748*	*0.3958*	*0.3911*	*0.3978*
	CML	*0.2587*	*0.20606*	*0.2107*	*0.2154*	*0.2288*
	MLR	*0.4261*	*0.3961*	*0.3364*	*0.339*	*0.3437*
skew =2, kurtosis =7	*CMLR*	*0.18392*	*0.1733*	*0.19374*	*0.1906*	*0.1948*
	GLS	*0.5732*	*0.4933*	*0.4573*	*0.43195*	*0.4441*
	CGLS	*0.3137*	*0.21026*	*0.2068*	*0.2052*	*0.22897*

average with standard errors less than the ML method, due to the use of a correction in the robust standard errors

It was noted through the results in Table (2) of the GLS estimation method that the bias average for standard errors before cleaning ranged between 0.5534 - 0.357, while the values of GLS after using the proposed method ranged between 0.19827 - 0.1795, and from this result, we note that there is a clear difference using the robust RFCH method; Since the standard errors are smaller than if using the GLS method directly, and by comparing the results after cleaning, it was found that the MLR method gives a lower bias average than the ML and GLS methods and that the GLS method gives the highest bias when we treat the data as continuous using the covariance matrix And covariance as inputs to estimation methods.

When the data are generated with a moderate non-normality distribution with skew two and kurtosis seven, as shown in Table (2), the absolute bias average for standard errors before and after the cleaning was higher than the absolute bias average for standard errors when generated with a normal distribution, and all estimation methods after cleaning using the method The proposed method gave fewer bias results

11.4. Bais parameter estimation

The total quality of the estimated parameters was calculated by calculating the absolute bias average for the parameters before and after cleaning with the presence of outlier using the proposed method, as it was noted through Table (3) that all the parameters estimated using the robust RFCH were very small compared to the contaminated data and for all methods. However, the bias differed according to the method and the sample size. It was found that the bias values of the parameters for each of the ML and MLR methods are the same; Because the corrections were in the standard errors, it was also noted that the methods ML,MLR were superior when we deal with the data as continuous with all sample sizes after and before cleaning from methods GLS.

It was noted through the data that was normality generated with outlier and cleaned using the proposed method that the overall bias average of the parameters is much smaller than the data that were assumed by the nonnormal distribution so that the performance of the robust and weighted methods without outlier is better for both two distributions, in addition to that the evaluation of the model through the relative bias average For standard errors and estimated parameters, the quality of the proposed method is evaluated after cleaning from the outlier through the residual matrix, which

Table 3: The absolute bias average for the parameters of the model.

Dist.	*Sample size*	*200*	*400*	*600*	*800*	*1000*
skew=0 , kurtosis =0	*ML*	*30.0729*	*7.04054*	*6.0129*	*3.4046*	*1.44173*
	CML	*2.062*	*0.22853*	*0.1869*	*0.19393*	*0.18904*
	MLR	*30.0729*	*7.04054*	*6.0129*	*3.4046*	*1.44173*
	CMLR	*2.062*	*0.22853*	*0.1869*	*0.19393*	*0.18904*
	GLS	*315.7394*	*58.5182*	*17.6838*	*7.29491*	*3.16684*
	CGLS	*2.3757*	*0.23815*	*0.19659*	*0.19639*	*0.19508*
skew =2, kurtosis = 7	*ML*	*187.49*	*10.0617*	*7.0563*	*3.67284*	*1.93096*
	CML	*3.27994*	*0.28411*	*0.2571*	*0.2784*	*0.24505*
	MLR	*187.49*	*10.0617*	*7.0563*	*3.67284*	*1.93096*
	CMLR	*3.27994*	*0.28411*	*0.2571*	*0.2784*	*0.24505*
	GLS	*86.574*	*5.25011*	*3.5016*	*3.66378*	*0.91395*
	CGLS	*3.3621*	*0.29455*	*0.2667*	*0.2882*	*0.24648*

represents the difference between the real parameter and the estimated parameter; As it requires that all of them be close to zero, so the residual matrix of the model will be drawn before and after cleaning and for all methods and one sample size through drawing the histogram, which is required to be close to the normal distribution. Whereas the Figures (1), (2) and (3) represent the residual matrix for the data generated by skew 2 and kurtosis 7, while the figures (4), (5) and (6) represent the residual matrix for the data generated by skew 0 and kurdosis 0.

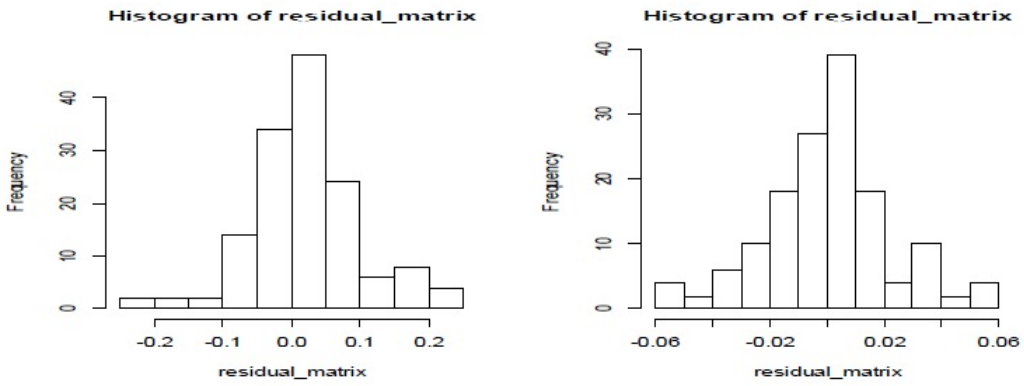

Figure 1: A: residual matrix for ML method for contaminated data by skew 2 and kurtosis 7 of a model, for B: residual matrix for ML method for clean data

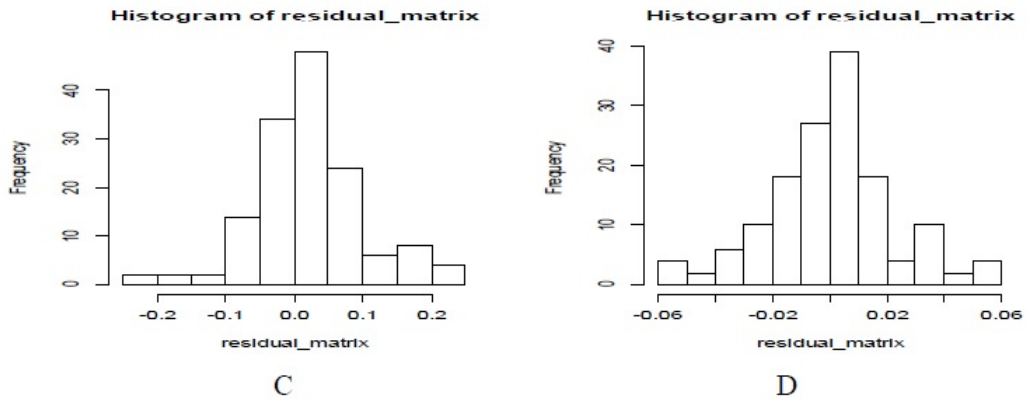

Figure 2: C: Residual matrix for MLR method for contaminated data by skew 2 and kurtosis 7 of a model, D: Residual matrix for MLR method for clean data

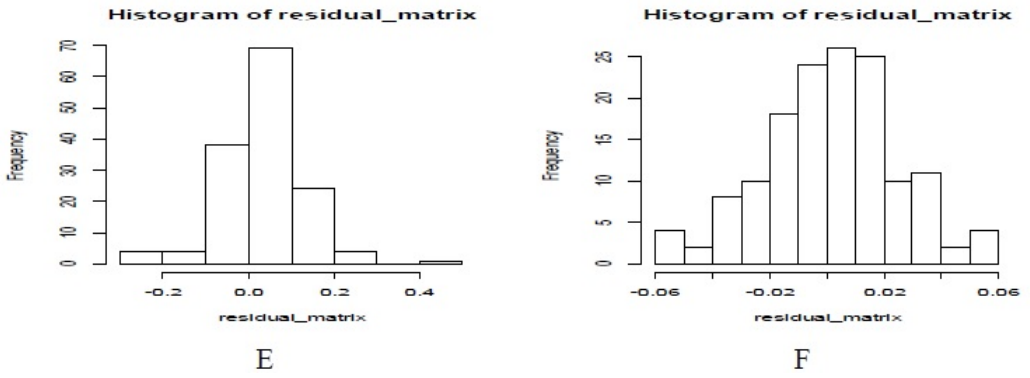

Figure 3: E: residual matrix for GLS method for contaminated data by skew 2 and kurtosis 7 of a model, F: residual matrix for GLS method for clean data

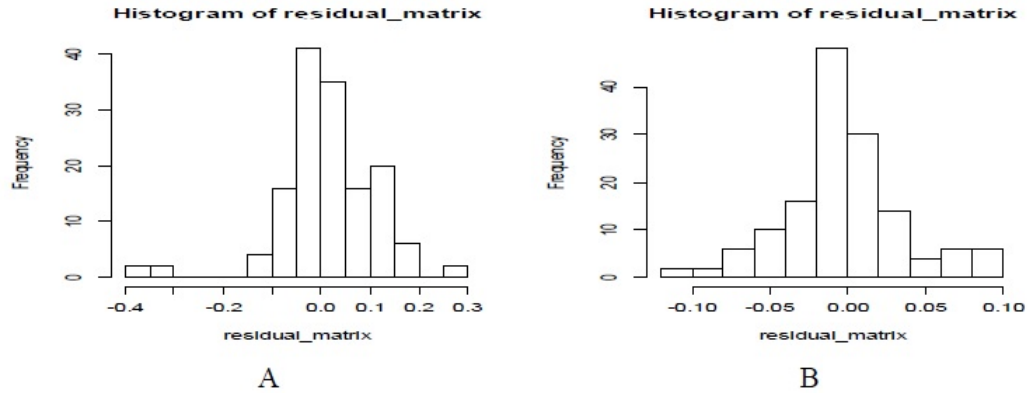

Figure 4: A: residual matrix for ML method for contaminated data by skew 0 and kurtosis 0 of a model, B: residual matrix for ML method for clean data

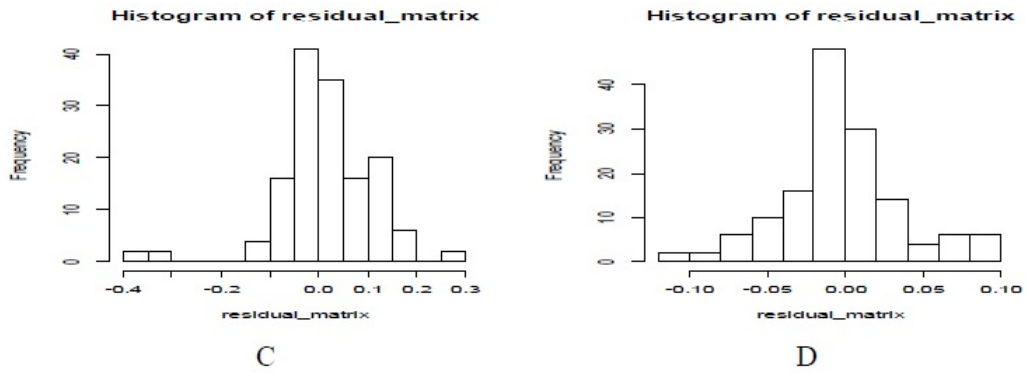

Figure 5: C: residual matrix for MLR method for contaminated data by skew 0 and kurtosis 0 of a model, D: residual matrix for MLR method for clean data

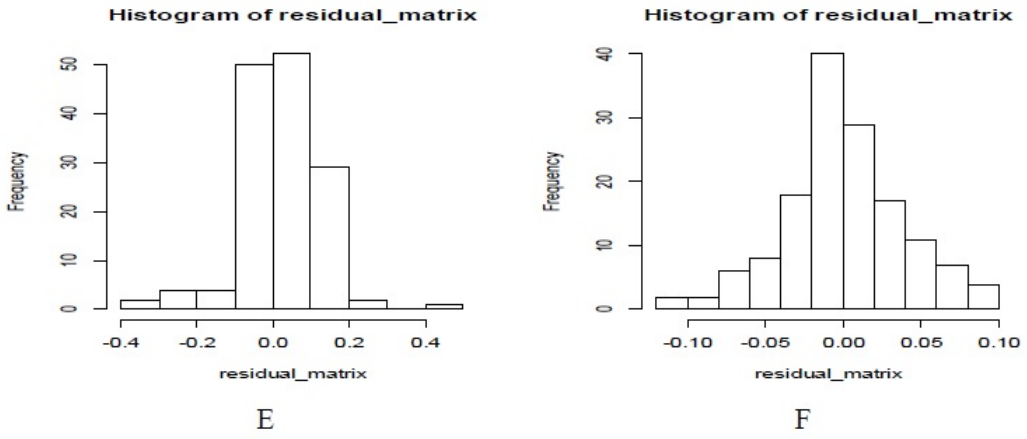

Figure 6: E: residual matrix for GLS method for contaminated data by skew 0 and kurtosis 0 of a model, F: residual matrix for GLS method for clean data

11.5. The goodness of fit indices with estimations methods

The model is evaluated in addition to the absolute bias average of the model as a whole, related to loading factors, structural coefficients, and covariance, through the overall quality of fit indices of the model, as the issue of model fit indexes has received a lot of research and study in recent decades with any other aspect of SEM modeling.

The basic fit indices used by most researchers will be presented. The extent to which they affect outlier values and the ability of the proposed method robust RFCH to improve the quality of fit indexes of the model, as well as study the effect of sample size on the fit indicators, as well as the shape of the distribution, and this will be known through the model.

11.5.1. fit indexes for model

Through the simulation results of the previous model, the data follow the two distributions of first: skewness 2, kurtosis 7, and second: skewness 0, kurtosis 0, in the presence of an outlier. They are cleaned by the proposed method robust RFCH from outlier and use five sample sizes: 200, 400, 600, 800, and 1000. It was noticed through the tables (4)(5)(6)(7) (8) (9)(10) that the fit indicators are collapsing and outside the cut-off limits even in the case of a large samples size, while using the same data after the proposed method to clean the data from the outlier within the cut-off limits,

which indicates that An improvement in the model by reducing errors as happened with parameters and standard errors, as well as it was noted that the fit indexes of differing according to the estimated method Because some methods use the correction robust Chi-square, in addition, some fit indicators are based on the Chi-square correction robust.

11.5.2. Chi-square Fit Index

It is observed from the simulation results of the ML estimation method that it increases with increasing sample size; Because the fit indicator is sensitive to the sample size, and its value ranges between 119.1042-381.553 when no normal data are distributed and in the presence of outlier values, while using the proposed method to clean the data from the outlier robust RFCH the value of the Chi-Square decreased, and it became between 47.582-49.0987. It also shows that the results obtained with a normal distribution are smaller than nonnormal distribution, whether the data contains outlier or without outlier for clean data, which fit indicates that the fit index is affected by the sample size and the degree of distribution; The Chi-square value after cleaning for the normal distribution ranged between 46.96701-45.59924.

The MLR method uses the Chi-square correction of the robust based on (Yuan& Bentler). Its value is greater than the ML method when the data is distributed according to the normal distribution. In comparison, its value was less when the nonnormal data is distributed, which indicates the robustness of the correction to deal With nonnormal data. Likewise, with the rest of the methods, the value differed according to the method and the correction used for the method, and all Chi values decreased after using the proposed method RFCH as shown in Table (4).

Table 4: The Chi-square fit index for the model.

Dist.	***Sample size***	***200***	***400***	***600***	***800***	***1000***
	methods	*Chisq*	*Chisq*	*Chisq*	*Chisq*	*Chisq*
skew=0 , kurtosis =0	*ML*	*107.0608*	*160.1475*	*214.1313*	*271.8662*	*326.6604*
	CML	*46.96701*	*46.12237*	*45.83765*	*45.94457*	*45.59924*
	MLR	*113.5882*	*168.4422*	*223.9806*	*283.9359*	*340.6213*
	CMLR	*49.01496*	*47.08533*	*46.42495*	*46.40169*	*45.97737*
	GLS	*80.20922*	*116.3932*	*151.4148*	*187.9886*	*222.2941*
	CGLS	*43.2932*	*44.6198*	*44.74189*	*45.15475*	*44.847*
skew =2, kurtosis = 7	*ML*	*119.1042*	*184.4172*	*243.1821*	*319.2162*	*381.553*
	CML	*49.09878*	*48.25171*	*47.58237*	*47.82839*	*48.07935*
	MLR	*123.5459*	*190.701*	*246.6004*	*322.1167*	*383.7285*
	CMLR	*49.76983*	*48.12665*	*47.21022*	*47.28411*	*47.41331*
	GLS	*87.91792*	*128.5561*	*167.6598*	*213.6098*	*251.0348*
	CGLS	*47.8485*	*46.80773*	*46.46408*	*46.95684*	*47.25539*

11.5.3. RMSEA Fit Index

This is the most fitting indicator based on the estimation technique; It was noticed through the Table (5) when using the proposed method and for all sample sizes that the RMSEA values had decreased, and became within the ideal limits close to zero, and it was also noted that the value of RMSEA with the increase in the sample size approached to zero using the RFCH method, and that the use of robust corrections for Chi Square in the RMSEA index gave better results, as it was noted that the MLR method provided better results than the ML method for nonnormal distributions and for all sample sizes, in order to use a robust correction in the ML estimation method, where the

RMSEA values for clean data after using the proposed method ranged from -0.0061 to 0.014, while the MLR method ranged Between 0.0162-0.005, while the GLS method was between 0.01932- 0.005554, and that all these values for the data are not distributed normallywith skwenses 2 and kortossis 7, and we note that the best fit indicator is for MLR when the data is treated as continuous. And when the data is distributed normality and using the proposed method RFCH , we note the superiority of the ML and GLS on method MLR

Table 5: The RMSEA fit index values for the model.

Dist.	***Sample size***	***200***	***400***	***600***	***800***	***1000***
	methods	*RMSEA*	*RMSEA*	*RMSEA*	*RMSEA*	*RMSEA*
skew=0 , kurtosis =0	*ML*	*0.07638*	*0.075112*	*0.074742*	*0.075262*	*0.075234*
	CML	*0.01243*	*0.008038*	*0.00599*	*0.005314*	*0.004656*
	MLR	*0.07462*	*0.074576*	*0.07257*	*0.073872*	*0.074644*
	CMLR	*0.01484*	*0.008868*	*0.006542*	*0.005682*	*0.004884*
	GLS	*0.06592*	*0.068754*	*0.069174*	*0.069754*	*0.069696*
	CGLS	*0.0068*	*0.006802*	*0.005152*	*0.004684*	*0.004166*
skew =2, kurtosis = 7	*ML*	*0.08355*	*0.082906*	*0.081034*	*0.082832*	*0.082198*
	CML	*0.01485*	*0.01022*	*0.007594*	*0.006808*	*0.006164*
	MLR	*0.077505*	*0.077972*	*0.076068*	*0.077776*	*0.079448*
	CMLR	*0.012225*	*0.01012*	*0.007314*	*0.006308*	*0.005704*
	GLS	*0.07222*	*0.073866*	*0.07361*	*0.074914*	*0.074348*
	CGLS	*0.01932*	*0.018252*	*0.007428*	*0.006806*	*0.005554*

11.5.4. SRMR Fit Index

This fit index is less affected by the Chi-square determinants, an index of the covariance matrix of the residuals. The closer to zero indicates that there is no error and that the recommended minimum is 0.08.

Table 6: The SRMR fit index values for the model.

Dist.	***Sample size***	***200***	***400***	***600***	***800***	***1000***
	methods	*SRMR*	*SRMR*	*SRMR*	*SRMR*	*SRMR*
skew=0 , kurtosis =0	*ML*	*0.07444*	*0.06586*	*0.06289*	*0.061906*	*0.061608*
	CML	*0.05293*	*0.035754*	*0.02901*	*0.02493*	*0.022236*
	MLR	*0.07444*	*0.06586*	*0.06289*	*0.061906*	*0.061608*
	CMLR	*0.05293*	*0.035754*	*0.02901*	*0.02493*	*0.022236*
	GLS	*0.10624*	*0.085974*	*0.080526*	*0.077446*	*0.075852*
	CGLS	*0.06637*	*0.040578*	*0.03163*	*0.026646*	*0.023488*
skew =2, kurtosis = 7	*ML*	*0.07997*	*0.073352*	*0.068788*	*0.069336*	*0.068038*
	CML	*0.04919*	*0.034852*	*0.028522*	*0.024632*	*0.022186*
	MLR	*0.07997*	*0.073352*	*0.068788*	*0.069336*	*0.068038*
	CMLR	*0.04919*	*0.034852*	*0.028522*	*0.024632*	*0.022186*
	GLS	*0.124815*	*0.100964*	*0.092222*	*0.091134*	*0.088318*
	CGLS	*0.061655*	*0.039472*	*0.0311*	*0.026396*	*0.02347*

The results are shown in Table (6) for all methods, whether normal or nonnormal distribution, as shown in Table (6). And that the GLS method gave the highest values before and after cleaning

and for all sample sizes. In contrast, the ML and MLR method gives the same results, as it was noted that with the increase in the sample size and for all methods after cleaning, it approaches more than zero and the least error for the residuals.

11.5.5. Fit Indexes TLI and CFI

These fit indicators are not affected by the sample size, the high value indicates a perfect fit through the results in the Tables (7), (8) for all methods and all sample sizes and for the two distributions, and the values of the two fit indicators lead to the rejection of the model when the data contains outlier values for most methods. At the same time, the values after using the proposed method RFCH obtained an ideal fit quality and were close to one. We conclude that with the increase in the sample size, the accuracy and robustness of fit indexes increasing, as shown in the tables.

Table 7: The CFI fit index values for the model.

Dist.	***Sample size***	***200***	***400***	***600***	***800***	***1000***
	methods	*CFI*	*CFI*	*CFI*	*CFI*	*CFI*
skew=0 , kurtosis =0	*ML*	*0.90564*	*0.909226*	*0.90965*	*0.909062*	*0.909464*
	CML	*0.98463*	*0.99368*	*0.996446*	*0.997436*	*0.997858*
	MLR	*0.83925*	*0.867324*	*0.858138*	*0.868528*	*0.877658*
	CMLR	*0.98097*	*0.98506*	*0.996088*	*0.997246*	*0.997736*
	GLS	*0.81707*	*0.81862*	*0.820826*	*0.820242*	*0.821664*
	CGLS	*0.98313*	*0.987884*	*0.9931*	*0.99471*	*0.995692*
skew =2, kurtosis = 7	*ML*	*0.90045*	*0.903698*	*0.908426*	*0.905138*	*0.906764*
	CML	*0.987015*	*0.993242*	*0.99581*	*0.996858*	*0.997402*
	MLR	*0.803225*	*0.832418*	*0.842354*	*0.841162*	*0.8721*
	CMLR	*0.97546*	*0.993222*	*0.995944*	*0.997058*	*0.997608*
	GLS	*0.78462*	*0.796402*	*0.802516*	*0.797598*	*0.801988*
	CGLS	*0.979845*	*0.98704*	*0.991298*	*0.993184*	*0.994218*

Table 8: The TLT fit index values for the model.

Dist.	***Sample size***	***200***	***400***	***600***	***800***	***1000***
	methods	*TLI*	*TLI*	*TLI*	*TLI*	*TLI*
skew=0, kurtosis =0	*ML*	*0.87025*	*0.87518*	*0.87577*	*0.874938*	*0.87552*
	CML	*1.03124*	*1.00726*	*1.00422*	*1.003142*	*1.002696*
	MLR	*0.8053*	*0.834066*	*0.825944*	*0.835716*	*0.84453*
	CMLR	*0.99715*	*0.996634*	*1.003064*	*1.002502*	*1.00227*
	GLS	*0.74891*	*0.750638*	*0.7536*	*0.752812*	*0.75476*
	CGLS	*1.00383*	*1.000772*	*1.000802*	*1.000228*	*1.008606*
skew =2, kurtosis =7	*ML*	*0.86309*	*0.867578*	*0.874082*	*0.869602*	*0.871762*
	CML	*0.998345*	*1.000038*	*1.000812*	*1.00036*	*1.000052*
	MLR	*0.76881*	*0.798832*	*0.810234*	*0.807842*	*0.838378*
	CMLR	*0.98534*	*1.0003*	*1.001404*	*1.000962*	*1.000648*
	GLS	*0.70395*	*0.720076*	*0.72845*	*0.72169*	*0.727774*
	CGLS	*1.007905*	*1.000706*	*1.000208*	*1.000618*	*1.00015*

In addition, the TLI and CFI fit indicators for the normal distribution, whether for contaminated

data and clean data, after using the proposed method give greater results than if the data distribution is no normal.

11.5.6. CRMR Fit Index

This fit indicator expresses the matrix of correlations, which is the square root of the residuals matrix, and the smaller the result indicates the quality of fit the residuals correlation matrix, as it was noted from Table (9) that all values after cleaning and for all methods using the proposed method give better results.

Table 9: The CRMR fit index values for the model.

Dist.	***Sample size***	***200***	***400***	***600***	***800***	***1000***
	methods	*CRMR*	*CRMR*	*CRMR*	*CRMR*	*CRMR*
skew=0 , kurtosis =0	*CML*	*0.05751*	*0.038896*	*0.031554*	*0.027102*	*0.024174*
	MLR	*0.08087*	*0.07159*	*0.068344*	*0.067318*	*0.066976*
	CMLR	*0.05751*	*0.038896*	*0.031554*	*0.027102*	*0.024174*
	GLS	*0.09273*	*0.078714*	*0.074568*	*0.072602*	*0.07206*
	CGLS	*0.06145*	*0.04003*	*0.032136*	*0.027506*	*0.024468*
skew =2, kurtosis = 7	*ML*	*0.08698*	*0.079744*	*0.074758*	*0.07538*	*0.07398*
	CML	*0.053465*	*0.037868*	*0.030968*	*0.026766*	*0.024132*
	MLR	*0.08698*	*0.079744*	*0.074758*	*0.07538*	*0.07398*
	CMLR	*0.053465*	*0.037868*	*0.030968*	*0.026766*	*0.024132*
	GLS	*0.10481*	*0.08931*	*0.082652*	*0.082534*	*0.080756*
	CGLS	*0.057105*	*0.038972*	*0.03155*	*0.02717*	*0.024432*

The Table also noted that when the data is distributed normally, the results of the fit indexes decrease. The results are better than if the distribution was nonnormal and for all methods, that the closer the distribution is to normal, the better performance of the fit index, and the quality of fit the model is obtained despite the use of methods And corrections are robust when we deal with the data as not being distributed normally by skew and kurtosis. Still, the effect of an outlier leads to a decrease in the quality of the fit index, while the proposed method improved the quality of the fit index and reduced errors.

12. Conclusions

We conclude from the simulation results that the outlier affects all methods with robust corrections standard errors and the classical methods. Using the proposed method RFCH, the absolute bias rate for standard errors and parameters and model decreases significantly, indicating the algorithm's quality to clean outliers, improve the quality of parameters, and reduce errors. We conclude that the degree of distribution affects the absolute bias rate for parameters and standard errors. It is less accurate when the data is not distributed normally.

It is continuous when dealing with the data, especially if we have a five-point Likert scale and above through the covariance matrix as an input to ML, MLR and GLS. We conclude that the best method is MLR, to use robust corrections in standard errors. At the same time, it was noted that the absolute bias rate for ML and MLR are equal because of the Correction of standard errors. By simulating different sample sizes and with an increase in the sample size, at a contamination rate of 20%, the absolute bias rate of errors increases due to the percentage of contamination, but with the

use of the proposed method for cleaning from an outlier, we conclude that the standard errors after cleaning and with the same sample size obtain stability, which indicates the quality of the method.

Through the total quality based on the fit indexes, we conclude that all fit indexes after using the proposed method are within the ideal cut-off limits after cleaning. We conclude that the Chi-square value is biased by the sample size, as it rises with the increase in the sample size and the degree of distribution, so it is not recommended to rely on it. Through the simulation results, all the fit indexes are affected by the sample size, so we notice an increase in the accuracy of the quality of the fit indexes after using the proposed method for clean data as the sample size increases. Whereas TLI and CFI are close to one, so modeling requires a large sample size.

Through the results, we conclude that the quality of fit indexes is affected by the degree of distribution. When the data are distributed in a normal distribution and free of an outlier, the fit indexes are more ideal than no normal distribution. By drawing the residual matrix for all methods, we conclude that after cleaning using the proposed method, the residuals approach zero and the normal distribution. The simulation results were observed at some sample sizes, especially when generating data with a normal distribution. After the cleaning process, the quality of fit indexes of the GLS method is better than that of the MLR that uses a robust correction for YB, while in the same sample sizes and before the cleaning process for contaminated data, the GLS method gives a fit indexes Bad and that the MLR method gives a perfect fit index and is higher than GLS, which indicates a robust YB correction against outlier and a violation of the distribution assumption. Through the results of the CRMR and SRMR fit indexes, these two indicators do not depend on the Chi-square correction but rather represent the matrix of covariance and correlations for the standard residuals. Thus, we conclude that the best methods are the maximum likelihood methods and robust after and before cleaning from the outlier in the proposed way.

We recommend applying the proposed method and methods to continuous and mixed data. We recommend contaminated ama the data with other ratios and generating data for other distributions to verify the quality of the proposed method. We recommend using RFCH as input matrix instead of covariance matrix when data is continuous and polychoric when data is ordinal

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