Measure of departure from average marginal homogeneity for the analysis of collapsed ordinal square contingency tables

Mana Aizawa¹, Kouji Yamamoto² and Sadao Tomizawa³

¹Department of Information Sciences, Faculty of Science and Technology, Tokyo
University of Science, Noda City, Chiba, 278-8510, Japan,
e-mail: aizawa.m01@gmail.com

²Department of Biostatistics, School of Medicine, Yokohama City University, 3-9
Fukuura, Kanazawa-ku, Yokohama, 236-0004, Japan
e-mail: kouji_y@yokohama-cu.ac.jp

³Department of Information Sciences, Faculty of Science and Technology, Tokyo
University of Science, Noda City, Chiba, 278-8510, Japan,
e-mail: tomizawa@is.noda.tus.ac.jp

SUMMARY

In clinical research, collected data are often classified into ordered categories using a set threshold to evaluate efficacy and safety of treatment. Data can be summarized as a shift table, which displays the change in the frequency of subjects across specified categories from the baseline to post-baseline. Although ordered categories are sometimes recombined into three categories, the combined patterns vary. To consider various collapsed patterns comprehensively, this paper proposes a new measure that represents the degree of departure from average marginal homogeneity, and can distinguish between two kinds of marginal inhomogeneity. Additionally, applications of the proposed measure to clinical data are discussed.

Key words: Collapsed table, marginal homogeneity, measure

1. Introduction

In clinical research, collected data are often classified into ordered categories using a set threshold to evaluate efficacy and safety of treatment. In particular, laboratory data are often classified into categorical values using predetermined thresholds. Table 1, which is taken from Nogid et al. (2018), shows an example. These data represent shifts in renal function categories

from the baseline to the end of therapy in patients treated with telavancin or vancomycin. The row values and column values describe the creatinine clearance (CrCl) level at the end of treatment and at the baseline, respectively. For such data, it is interesting to evaluate the equality of the row and column marginal distributions.

Table 1. Shifts in the renal function categories from the baseline to the end of therapy in patients treated with (a) telavancin and (b) vancomycin; taken from Nogid et al. (2018)

End of therapy CrCl category (mL/min)		Baseline CrCl category (mL/min)							Total
		(1)	(2)	(3)	(4)	(5)	(6)	(7)	
(a) Telavancin	(1)	60	15	8	11	5	6	4	109
	(2)	8	21	10	6	3	1	9	58
	(3)	6	12	19	11	5	4	3	60
	(4)	1	5	16	15	7	5	12	61
	(5)	2	4	8	10	13	8	12	57
	(6)	3	1	3	3	12	10	12	44
	(7)	0	1	7	3	16	12	256	295
	Total	80	59	71	59	61	46	308	684
(b) Vancomycin	(1)	50	10	2	1	4	2	7	76
	(2)	15	16	11	2	2	1	9	56
	(3)	9	24	11	10	4	1	10	69
	(4)	4	11	19	14	9	3	11	71
	(5)	3	5	8	6	12	6	11	51
	(6)	2	3	1	9	14	6	19	54
	(7)	0	3	9	13	15	32	249	321
	Total	83	72	61	55	60	51	316	698

CrCl indicates creatinine clearance.

(1): ≤ 30 , (2): $> 30-40$, (3): $> 40-50$, (4): $> 50-60$, (5): $> 60-70$, (6): $> 70-80$, (7): > 80 .

To analyze the marginal homogeneity in a square contingency table which has the same row and column classifications, Stuart (1955) proposed the marginal homogeneity (MH) model. If the MH model holds in Table 1, then the distribution of the CrCl value at the end of treatment is the same as that at the baseline.

If the MH model does not hold, one of our interests is to apply the extended models. On the other hand, measuring the degree of departure from marginal homogeneity is also of great interest. In addition, for several data sets, it is meaningful to compare the degree of departure from marginal homogeneity. For nominal square contingency tables, Tomizawa and Makii

(2001) proposed a measure to express the degree of departure from marginal homogeneity. For ordinal square contingency tables, Tomizawa et al. (2003) proposed a measure which represents the degree of departure from marginal homogeneity. This measure ranges from 0 to 1. The measure is 0 if and only if the MH model holds, and 1 if and only if the degree of departure from the MH model is maximum.

There are two kinds of departures, or marginal inhomogeneities (i.e., whether all observations concentrate in the lower left triangle cells or the upper right triangle cells in the table). These marginal inhomogeneities indicate different and opposite maximum departures from marginal homogeneity. Therefore, it is also important to distinguish between the two kinds of inhomogeneity. Yamamoto et al. (2011) proposed a measure to represent the degree of departure from average marginal homogeneity, which can distinguish between the two kinds of inhomogeneity. Ando (2019) developed an index for visually measuring the marginal inhomogeneity, which can concurrently define degrees of departure from marginal homogeneity corresponding to the extended marginal homogeneity (EMH) model (Tomizawa, 1984) and the marginal logit model (McCullagh, 1977).

To simplify the interpretation of the results, the categories for the ordinal square contingency table are often divided into three categories (e.g., mild, moderate and severe). However, for laboratory data similar to those in Table 1, various thresholds should be considered. Further, in clinical research, the data are often classified into four or more categories in guidelines. In such a case, consideration should be given to merging the categories without breaking categories which follow the original guidelines. Thus, it is also important to consider dividing the items that have already been classified into four or more categories into three categories. For the reasons above, it is meaningful to assess various collapsed patterns comprehensively. Yamamoto et al. (2020) proposed a measure for the degree of departure from marginal homogeneity for a collapsed table. However, its measure cannot distinguish between the two kinds of marginal inhomogeneity.

This paper proposes a new measure to express the degree of departure from average marginal homogeneity by adopting collapsed 3×3 tables. The proposed measure can distinguish between the two kinds of inhomogeneity.

2. Measure of departure from marginal homogeneity for collapsed 3×3 table

Consider an $r \times r$ square contingency table with the same ordered row and column classifications. Let p_{ij} denote the probability that an observation will fall in cell (i, j) ($i = 1, \dots, r; j = 1, \dots, r$). The MH model is defined as

$$p_{i\cdot} = p_{\cdot i} \quad \text{for } i = 1, \dots, r,$$

where $p_{i\cdot} = \sum_{k=1}^r p_{ik}$ and $p_{\cdot i} = \sum_{k=1}^r p_{ki}$. This model indicates that the row and column marginal distributions are equal.

An $r \times r$ ordinal square contingency table can be collapsed into a 3×3 table $(r-1)(r-2)/2$ ways by choosing cut points after the s th and t th rows and after the s th and t th columns for $1 \leq s < t \leq r-1$. Each collapsed 3×3 table is defined as T_{st} ($1 \leq s < t \leq r-1$). This means that r categories in the original $r \times r$ table are included in three categories by dividing at the cut points s and t . Then, the table T_{st} ($1 \leq s < t \leq r-1$) has the three new categories. In a collapsed table T_{st} ($1 \leq s < t \leq r-1$), let $G_{ij}^{(s,t)}$ indicate the corresponding probability for row value i ($i = 1, 2, 3$) and column value j ($j = 1, 2, 3$). That is,

$$\begin{aligned} G_{11}^{(s,t)} &= \sum_{i=1}^s \sum_{j=1}^s p_{ij}, & G_{12}^{(s,t)} &= \sum_{i=1}^s \sum_{j=s+1}^t p_{ij}, & G_{13}^{(s,t)} &= \sum_{i=1}^s \sum_{j=t+1}^r p_{ij}, \\ G_{21}^{(s,t)} &= \sum_{i=s+1}^t \sum_{j=1}^s p_{ij}, & G_{22}^{(s,t)} &= \sum_{i=s+1}^t \sum_{j=s+1}^t p_{ij}, & G_{23}^{(s,t)} &= \sum_{i=s+1}^t \sum_{j=t+1}^r p_{ij}, \\ G_{31}^{(s,t)} &= \sum_{i=t+1}^r \sum_{j=1}^s p_{ij}, & G_{32}^{(s,t)} &= \sum_{i=t+1}^r \sum_{j=s+1}^t p_{ij}, & G_{33}^{(s,t)} &= \sum_{i=t+1}^r \sum_{j=t+1}^r p_{ij}. \end{aligned}$$

The MH model can also be expressed as

$$G_{i\cdot}^{(s,t)} = G_{\cdot i}^{(s,t)} \quad \text{for } i = 1, 2, 3; 1 \leq s < t \leq r-1,$$

where

$$G_{i\cdot}^{(s,t)} = \sum_{j=1}^3 G_{ij}^{(s,t)}, \quad G_{\cdot i}^{(s,t)} = \sum_{j=1}^3 G_{ji}^{(s,t)}.$$

Namely, the MH model can be restated as

$$H_{1(k)}^{(s,t)} = H_{2(k)}^{(s,t)} \quad \text{for } k = 1, 2; 1 \leq s < t \leq r-1,$$

where

$$H_{1(k)}^{(s,t)} = \sum_{u=1}^k \sum_{v=k+1}^3 G_{uv}^{(s,t)}, \quad H_{2(k)}^{(s,t)} = \sum_{u=1}^k \sum_{v=k+1}^3 G_{vu}^{(s,t)}.$$

Assume that $H_{1(k)}^{(s,t)} + H_{2(k)}^{(s,t)} \neq 0$ for $1 \leq s < t \leq r-1$ and $k = 1, 2$. Let

$$\Delta_{st} = \sum_{k=1}^2 (H_{1(k)}^{(s,t)} + H_{2(k)}^{(s,t)})$$

and

$$H_{1(k)}^{*(s,t)} = \frac{H_{1(k)}^{(s,t)}}{\Delta_{st}}, \quad H_{2(k)}^{*(s,t)} = \frac{H_{2(k)}^{(s,t)}}{\Delta_{st}} \quad (k = 1, 2).$$

The MH model may be expressed as

$$H_{1(k)}^{*(s,t)} = H_{2(k)}^{*(s,t)} \quad \text{for } k = 1, 2; 1 \leq s < t \leq r-1.$$

Consider the measure Υ_{MH} defined by

$$\Upsilon_{MH} = \frac{1}{\binom{r-1}{2}} \sum_{1 \leq s < t \leq r-1} \Upsilon_{st},$$

where

$$\Upsilon_{st} = \frac{4}{\pi} \sum_{k=1}^2 (H_{1(k)}^{*(s,t)} + H_{2(k)}^{*(s,t)}) (\theta_k^{(s,t)} - \frac{\pi}{4}),$$

$$\theta_k^{(s,t)} = \arccos \left(\frac{H_{1(k)}^{(s,t)}}{\sqrt{(H_{1(k)}^{(s,t)})^2 + (H_{2(k)}^{(s,t)})^2}} \right).$$

The submeasure Υ_{st} ($1 \leq s < t \leq r-1$) describes the degree of departure from marginal homogeneity for a collapsed table T_{st} with fixed s and t ($1 \leq s < t \leq r-1$). The range of $\theta_k^{(s,t)}$ is $0 \leq \theta_k^{(s,t)} \leq \pi/2$. Therefore, the ranges of Υ_{MH} and Υ_{st} are between -1 and 1 .

The measure Υ_{MH} has the following characteristics:

- (i) $\Upsilon_{MH} = -1$ if and only if $H_{2(k)}^{(s,t)} = 0$ for all $1 \leq s < t \leq r-1$ and $k = 1, 2$ (i.e., $p_{ji} = 0$ for all $i < j$ ($1 \leq i < j \leq r$)). Hereinafter, this is called L-marginal inhomogeneity;
- (ii) $\Upsilon_{MH} = 1$ if and only if $H_{1(k)}^{(s,t)} = 0$ for all $1 \leq s < t \leq r-1$ and $k = 1, 2$ (i.e., $p_{ij} = 0$ for all $i < j$ ($1 \leq i < j \leq r$)). Hereinafter, this is called U-marginal inhomogeneity.

In addition, $\Upsilon_{MH} = 0$ indicates that the weighted average of $(\theta_k^{(s,t)} - \pi/4)$ is equal to 0. Thus, $\Upsilon_{MH} = 0$ indicates average marginal homogeneity. Note that if marginal homogeneity holds, then average marginal homogeneity holds. However, the converse is not the case.

Υ_{MH} indicates whether the departure from average marginal homogeneity is toward L-marginal inhomogeneity or U-marginal inhomogeneity. As Υ_{MH} approaches -1 , the departure from average marginal homogeneity becomes greater toward L-marginal inhomogeneity. On the other hand, as Υ_{MH} approaches 1 , it becomes greater toward U-marginal inhomogeneity.

Furthermore, the submeasure Υ_{st} for fixed s and t ($1 \leq s < t \leq r-1$) has the following characteristics.

- (iii) $\Upsilon_{st} = -1$ if and only if $H_{2(k)}^{(s,t)} = 0$ for $k = 1, 2$. That is, L-marginal inhomogeneity holds in the collapsed table T_{st} ;
- (iv) $\Upsilon_{st} = 1$ if and only if $H_{1(k)}^{(s,t)} = 0$ for $k = 1, 2$. That is, U-marginal inhomogeneity holds in the collapsed table T_{st} ;
- (v) $\Upsilon_{st} = 0$ if and only if average marginal homogeneity holds in the collapsed table T_{st} .

Υ_{st} indicates whether the departure from average marginal homogeneity is toward L-marginal inhomogeneity or U-marginal inhomogeneity in the collapsed table T_{st} .

3. Relationship between the measure and the extended marginal homogeneity model

Consider the relationship between Υ_{MH} and the EMH model. The EMH model is defined as

$$H_{1(k)}^{(s,t)} = \tau H_{2(k)}^{(s,t)}$$

for $k = 1, 2$ and $1 \leq s < t \leq r - 1$. When $\tau = 1$, the EMH model is equivalent to the MH model. If the EMH model holds in an $r \times r$ table, both $\theta_1^{(s,t)}$ and $\theta_2^{(s,t)}$ in the measure Υ_{MH} can be expressed as

$$\arccos \left(\frac{\tau}{\sqrt{\tau^2 + 1}} \right).$$

Namely, Υ_{MH} can be expressed as

$$\Upsilon_{MH} = \frac{4}{\pi} \arccos \left(\frac{\tau}{\sqrt{\tau^2 + 1}} \right) - 1.$$

Therefore, $\Upsilon_{MH} = 0$ if and only if $\tau = 1$. That is, marginal homogeneity holds. As τ approaches ∞ , Υ_{MH} approaches -1 , while the measure Υ_{MH} approaches 1 as τ approaches 0 . Thus, when the EMH model holds in the table, Υ_{MH} represents the degree of departure from marginal homogeneity toward L-marginal inhomogeneity or U-marginal inhomogeneity.

Note that when the EMH model holds, the measure Υ_{MH} is equivalent to the measure Ψ (Yamamoto et al., 2011) defined by

$$\Psi = \frac{4}{\pi} \sum_{i=1}^{r-1} (G_{1(i)}^* + G_{2(i)}^*) \left(\theta_i - \frac{\pi}{4} \right)$$

where

$$\theta_i = \arccos \left(\frac{G_{1(i)}}{\sqrt{G_{1(i)}^2 + G_{2(i)}^2}} \right)$$

and

$$\begin{aligned} G_{1(i)} &= \sum_{s=1}^i \sum_{t=i+1}^r p_{st}, & G_{2(i)} &= \sum_{s=1}^i \sum_{t=i+1}^r p_{ts}, \\ \Delta &= \sum_{i=1}^{r-1} (G_{1(i)} + G_{2(i)}), & G_{1(i)}^* &= \frac{G_{1(i)}}{\Delta}, & G_{2(i)}^* &= \frac{G_{2(i)}}{\Delta} \end{aligned}$$

for $i = 1, \dots, r - 1$.

Figure 1 shows the relationships between the parameter τ in the EMH model and the measures Υ_{MH} and Ψ when the EMH model holds.

In addition, if the EMH model holds in the collapsed table T_{st} , Υ_{st} can be expressed as

$$\Upsilon_{st} = \frac{4}{\pi} \arccos \left(\frac{\tau}{\sqrt{\tau^2 + 1}} \right) - 1$$

for fixed s and t ($1 \leq s < t \leq r - 1$). Therefore, $\Upsilon_{st} = 0$ if and only if $\tau = 1$. That is, marginal homogeneity holds in the collapsed table T_{st} . If the EMH model holds in a collapsed table T_{st} , Υ_{st} represents the degree of departure from marginal homogeneity toward L-marginal inhomogeneity or U-marginal inhomogeneity in the collapsed table T_{st} .

Figure 1. Relationships between τ in the EMH model and measures Υ_{MH} and Ψ when the EMH model holds

4. Approximate confidence interval for the measure

Let n_{ij} denote the observed frequency in the i th row and j th column of an $r \times r$ table ($i = 1, \dots, r$ and $j = 1, \dots, r$). Assuming that a multinomial distribution is applicable to the table, we consider the approximate variance for the estimated measure and a large-sample confidence interval for Υ_{MH} using the delta method. The sample version measure Υ_{MH} (i.e., $\hat{\Upsilon}_{MH}$) is given by Υ_{MH} when $\{p_{ij}\}$ is replaced by $\{\hat{p}_{ij}\}$, where $\hat{p}_{ij} = n_{ij}/n$ and $n = \sum \sum n_{ij}$. Using the delta method, $\sqrt{n}(\hat{\Upsilon}_{MH} - \Upsilon_{MH})$ has an asymptotically normal distribution (as $n \rightarrow \infty$) with mean 0 and variance $\sigma^2[\Upsilon_{MH}]$, where

$$\sigma^2[\Upsilon_{MH}] = \sum_{i=1}^r \sum_{j=1}^r D_{ij}^2 p_{ij},$$

where

$$D_{ij} = \frac{1}{\binom{r-1}{2}} \sum_{s=1}^{r-2} \sum_{t=s+1}^{r-1} \left[\sum_{k=1}^2 (A_k^{(s,t)} C_{ij(k)}^{(s,t)} + B_k^{(s,t)} C_{ji(k)}^{(s,t)}) \right],$$

$$A_k^{(s,t)} = \frac{4}{\pi \Delta_{st}} \left\{ \theta_k^{(s,t)} - \frac{H_{1(k)}^{(s,t)} + H_{2(k)}^{(s,t)}}{(H_{1(k)}^{(s,t)})^2 + (H_{2(k)}^{(s,t)})^2} H_{2(k)}^{(s,t)} \right\} - \frac{1 + \Upsilon_{st}}{\Delta_{st}},$$

$$B_k^{(s,t)} = \frac{4}{\pi \Delta_{st}} \left\{ \theta_k^{(s,t)} + \frac{H_{1(k)}^{(s,t)} + H_{2(k)}^{(s,t)}}{(H_{1(k)}^{(s,t)})^2 + (H_{2(k)}^{(s,t)})^2} H_{1(k)}^{(s,t)} \right\} - \frac{1 + \Upsilon_{st}}{\Delta_{st}},$$

and

$$C_{ij(k)}^{(s,t)} = \begin{cases} I(1 \leq i \leq s, s+1 \leq j \leq r) & (k=1) \\ I(1 \leq i \leq t, t+1 \leq j \leq r) & (k=2) \end{cases},$$

where $I(\cdot)$ is the indicator function. Note that $C_{ii(k)}^{(s,t)} = 0$ for $k=1, 2$.

For the submeasure Υ_{st} , using the delta method, $\sqrt{n}(\hat{\Upsilon}_{st} - \Upsilon_{st})$ has an asymptotically normal distribution (as $n \rightarrow \infty$) with mean 0 and variance $\sigma^2[\Upsilon_{st}]$, where

$$\sigma^2[\Upsilon_{st}] = \sum_{k=1}^2 \left[(A_k^{(s,t)})^2 H_{1(k)}^{(s,t)} + (B_k^{(s,t)})^2 H_{2(k)}^{(s,t)} \right].$$

Let $\hat{\sigma}^2[\Upsilon_{MH}]$ denote $\sigma^2[\Upsilon_{MH}]$ when $\{p_{ij}\}$ is replaced by $\{\hat{p}_{ij}\}$. Namely, $\hat{\sigma}[\Upsilon_{MH}]/\sqrt{n}$ is the estimated standard error of $\hat{\Upsilon}_{MH}$. Moreover, $\hat{\Upsilon}_{MH} \pm z_{p/2} \hat{\sigma}[\Upsilon_{MH}]/\sqrt{n}$ is the approximate 100(1 - p)% confidence interval for Υ_{MH} , where $z_{p/2}$ is the percentage point from the standard normal distribution corresponding to a two-tail probability equal to p .

To evaluate the performance of the confidence interval for Υ_{MH} , we demonstrate a simulation. Table 2(a), 2(b) and 2(c) show the artificial cell probability tables where the value of Υ_{MH} is equal to 0, -0.5, 0.5, respectively. For each experiment, the 95% confidence interval for Υ_{MH} was computed, and we checked whether it contained the true value of Υ_{MH} . In each experiment, the samples are obtained from a population with the artificial cell probability tables in Table 2.

Table 2. Artificial cell probability tables

(a) $\Upsilon_{MH} = 0$				
0.05	0.08	0.02	0.03	0.02
0.03	0.08	0.02	0.07	0.05
0.04	0.03	0.07	0.05	0.01
0.05	0.04	0.06	0.02	0.03
0.03	0.02	0.03	0.03	0.04

(b) $\Upsilon_{MH} = -0.5$				
0.05	0.08	0.04	0.05	0.07
0.04	0.03	0.03	0.08	0.05
0.03	0.01	0.05	0.06	0.02
0.01	0.06	0.03	0.01	0.08
0.02	0.01	0.01	0.04	0.04

(c) $\Upsilon_{MH} = 0.5$				
0.05	0.04	0.03	0.01	0.02
0.08	0.03	0.01	0.06	0.01
0.04	0.03	0.05	0.03	0.01
0.05	0.08	0.06	0.01	0.04
0.07	0.05	0.02	0.08	0.04

Table 3 shows the coverage probability of 1,000,000 experiments with sample sizes of 100, 500, 1000 and 2000. Although it seems to be permissive when the sample size is 100, from Table 3, we see that the coverage probabilities of the confidence interval for Υ_{MH} are close to 95% regardless of the value of the true Υ_{MH} .

Table 3. Coverage probability of 95% confidence interval for Υ_{MH} of 1,000,000 experiments

Sample size	$\Upsilon_{MH} = 0$	$\Upsilon_{MH} = -0.5$	$\Upsilon_{MH} = 0.5$
100	0.931	0.933	0.933
500	0.946	0.946	0.946
1000	0.948	0.948	0.948
2000	0.949	0.948	0.948

5. Examples

Consider the data shown in Tables 1(a) and 1(b).

For Table 1(a), the values of the likelihood ratio chi-squared statistic (G^2) for the MH and EMH models are 15.533 with 6 degrees of freedom (df) and 5.853 with 5 df, respectively. Thus, the MH model fits the data in Table 1(a) poorly; however, the EMH model fits the data in Table 1(a) well. For Table 1(b), the values of G^2 for the MH and EMH models are 7.929 with 6 df and 5.882 with 5 df, respectively. Thus, the MH and EMH models fit the data in Table 1(b) well.

According to Table 4, the estimated value of Υ_{MH} applied in Table 1(a) is -0.257 , and the corresponding confidence interval does not include 0. Therefore, the departure from average marginal homogeneity for the shift in CrCl in patients treated with telavancin is toward L-marginal inhomogeneity. This indicates that the CrCl value tends to be lower at the end of therapy than at the baseline in patients treated with telavancin.

Similarly, the estimated value of Υ_{MH} applied in Table 1(b) is 0.110, and the corresponding confidence interval includes 0. Therefore, average marginal homogeneity may hold in the data for the shift in CrCl in patients treated with vancomycin.

In addition, the confidence intervals for Υ_{MH} for the data in Tables 1(a) and 1(b) do not overlap, demonstrating that the CrCl value from the baseline significantly differs in patients treated with telavancin and those treated with vancomycin.

We also analyze the data in Tables 1(a) and 1(b) using the submeasure Υ_{st} ($1 \leq s < t \leq 6$) (Table 5). For Table 1(a), all the estimated submeasures and the corresponding confidence intervals are negative. Therefore, patients treated with telavancin tend to have a lower CrCl value at the end of therapy than at the baseline when the original seven categories are collapsed into three categories using any pattern.

For Table 1(b), the confidence intervals for the submeasures Υ_{12} , Υ_{23} and Υ_{25} are positive and do not include 0. From Υ_{12} , patients treated with vancomycin tend to have a higher CrCl value at the end of therapy than at the baseline when the original 7 categories are collapsed into 3 categories as (1) ≤ 30 , (2) $> 30 - 40$, and (3) > 40 mL/minute. A similar interpretation is obtained for Υ_{23} when the original 7 categories are collapsed into 3 categories as (1) ≤ 40 , (2) $> 40 - 50$, and (3) > 50 mL/minute, and for Υ_{25} when the original 7 categories are collapsed into 3 categories as (1) ≤ 40 ,

(2) $> 40 - 70$, and (3) > 70 mL/minute. Conversely, the confidence intervals for the other submeasures include 0. Therefore, when we collapse the original 7 categories into 3 categories using the other patterns, average marginal homogeneity may hold in each collapsed table for Table 1(b).

Table 4. Estimates of the measure Υ_{MH} , approximate standard errors for $\hat{\Upsilon}_{MH}$ and approximate 95% confidence intervals for Υ_{MH} , applied to Tables 1(a) and 1(b).

Applied data	Estimated measure	Standard error	Confidence interval
Table 1(a)	-0.257	0.080	(-0.414, -0.101)
Table 1(b)	0.110	0.082	(-0.052, 0.271)

Table 5. Estimates of the submeasure Υ_{st} and approximate 95% confidence intervals for Υ_{st} , applied to Tables 1(a) and 1(b).

Submeasure	For Table 1(a)		For Table 1(b)	
	Estimated value	Confidence interval	Estimated value	Confidence interval
Υ_{12}	-0.417	(-0.580, -0.255)	0.230	(0.045, 0.415)
Υ_{13}	-0.300	(-0.466, -0.135)	0.155	(-0.027, 0.337)
Υ_{14}	-0.331	(-0.498, -0.163)	0.041	(-0.142, 0.224)
Υ_{15}	-0.296	(-0.465, -0.128)	0.101	(-0.079, 0.280)
Υ_{16}	-0.321	(-0.499, -0.144)	0.077	(-0.099, 0.253)
Υ_{23}	-0.259	(-0.418, -0.101)	0.212	(0.053, 0.371)
Υ_{24}	-0.283	(-0.444, -0.123)	0.120	(-0.041, 0.280)
Υ_{25}	-0.255	(-0.416, -0.094)	0.166	(0.008, 0.324)
Υ_{26}	-0.271	(-0.440, -0.102)	0.144	(-0.011, 0.300)
Υ_{34}	-0.199	(-0.359, -0.040)	0.072	(-0.086, 0.230)
Υ_{35}	-0.175	(-0.334, -0.015)	0.116	(-0.039, 0.272)
Υ_{36}	-0.181	(-0.348, -0.014)	0.098	(-0.056, 0.251)
Υ_{45}	-0.193	(-0.355, -0.032)	0.035	(-0.121, 0.191)
Υ_{46}	-0.202	(-0.372, -0.032)	0.019	(-0.134, 0.173)
Υ_{56}	-0.174	(-0.344, -0.004)	0.061	(-0.090, 0.213)

6. Concluding remarks

The proposed measure Υ_{MH} represents the degree of departure from average marginal homogeneity and distinguishes between two kinds of complete marginal inhomogeneity (i.e., U-marginal inhomogeneity and L-marginal inhomogeneity). Since the measure $\hat{\Upsilon}_{MH}$ ranges from -1 to 1 regardless of the dimension and sample size, $\hat{\Upsilon}_{MH}$ is useful to compare the degrees of departure from average marginal homogeneity in several tables. In particular, when the EMH model holds in the table, $\hat{\Upsilon}_{MH}$ represents the degree of departure from marginal homogeneity toward either one of the complete marginal inhomogeneities.

As described above, considering collapsed 3×3 tables can simplify the interpretation. If various thresholds can be considered for clinical data, it is meaningful to equally assess square contingency tables in various collapsed patterns. Therefore, the measure Υ_{MH} , which combines all submeasures Υ_{st} with the same weights, may be useful to interpret such data.

Acknowledgements

The authors would like to thank the referees for their comments.

REFERENCES

- Ando S. (2019): A bivariate index for visually measuring marginal inhomogeneity in square tables. *International Journal of Statistics and Probability* 8:58-65.
- McCullagh P. (1977): A logistic model for paired comparisons with ordered categorical data. *Biometrika* 64: 449-453.
- Nogid B., Lacy M. K., Jacobs M., Bruss J. and Dwyer J. (2018): Time course and extent of renal function changes in patients receiving treatment for staphylococcal pneumonias: an analysis comparing telavancin and vancomycin from the ATTAIN trials. *Pharmacotherapy* 38:990-998.
- Stuart A. (1955): A test for homogeneity of the marginal distributions in a two-way classifications. *Biometrika* 42:412-416.
- Tomizawa, S. (1984): Three kinds of decompositions for the conditional symmetry model in a square contingency table. *Journal of the Japan Statistical Society* 14:35-42.
- Tomizawa S. and Makii T. (2001): Generalized measures of departure from marginal homogeneity for contingency tables with nominal categories. *Journal of Statistical Research* 35:1-24.
- Tomizawa S., Miyamoto N. and Ashihara N. (2003): Measure of departure from marginal homogeneity for square contingency tables having ordered categories. *Behaviormetrika* 30:173-193.

- Yamamoto K., Ando S. and Tomizawa S. (2011): A measure of departure from average marginal homogeneity for square contingency tables with ordered categories. *Revstat: Statistical Journal* 9:115-126.
- Yamamoto K., Iwama I. and Tomizawa S. (2020): Measure of departure from marginal homogeneity for the analysis of collapsed square contingency tables with ordered categories. *Journal of Statistical Theory and Applications* 19:212-222.