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Orthogonal Decomposition of the Anti-Symmetry Model via Anti-Two-Ratios-Parameter Symmetry Model for Square Contingency Tables

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Abstract. This paper proposes the anti-two-ratios-parameter symmetry (ATRPS) model for square contingency tables with ordered categories. The proposed model provides a parsimonious two-parameter extension of the anti-symmetry model, separates a global ratio effect from an anti-diagonal-distance effect, contains the anti-conditional symmetry and anti-linear-diagonals-parameter symmetry models as special cases, and is nested within the anti-diagonals-parameter symmetry model. By applying a column-reversal transformation, we show that the anti-symmetry model holds if and only if the ATRPS, anti-global symmetry, and anti-marginal mean equality models hold simultaneously; equivalently, it holds if and only if the ATRPS and AGSME models hold simultaneously. We also establish an asymptotic orthogonal decomposition of the likelihood ratio statistic. An analysis of grip strength data illustrates the proposed methodology and shows that the departure from anti-symmetry is almost entirely attributable to the AGSME component.

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1. Introduction

Square contingency tables with a common set of ordered row and column categories arise frequently in the analysis of agreement, mobility, and directional association (see, e.g., [1, 2] for general treatments). For such tables, symmetry-type models provide a mathematically tractable way to describe structured relations among cell probabilities. In the ordinary main-diagonal setting, the symmetry (S) model [3], the conditional symmetry (CS) model [4], the diagonals-parameter symmetry (DPS) model [5], the linear diagonals-parameter symmetry (LDPS) model [6], and the two-ratios-parameter symmetry (TRPS) model [7] form a well-studied hierarchy. Among these, the TRPS model is especially notable because it introduces a two-parameter multiplicative structure that separates a global

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directional effect from a distance-from-diagonal effect. A landmark result of Caussinus [8] showed that the S model holds if and only if both the quasi-symmetry and marginal homogeneity models hold, establishing the principle that symmetry can be decomposed into interpretable components. Extending this philosophy, Tahata and Tomizawa [9] showed that the S model holds if and only if the TRPS, global symmetry (GS), and marginal mean equality (ME) models hold simultaneously, and they further obtained an asymptotic orthogonal decomposition of the corresponding likelihood ratio statistics, formulated precisely in Section 4. For comprehensive reviews of symmetry models and their decompositions, see Tomizawa and Tahata [10] and Tahata and Tomizawa [11]. Related developments for square tables with ordered categories also include local-odds-based symmetry formulations; see, for example, Altun [12]. Thus, in the main-diagonal setting, the TRPS model plays both a modeling role and a decomposition role.

For anti-diagonal analysis, the natural comparison is no longer between (i, j) and (j, i) but between (i, j) and its counterpart (j^*, i^*) under anti-diagonal reflection, where $i^* = R + 1 - i$ and $j^* = R + 1 - j$. This formulation is appropriate when the relevant structural index is the sum $i + j$ rather than the difference $i - j$, because cells on the same anti-diagonal are precisely those with common value of $i + j$. Such anti-diagonal structures arise naturally when the categories encode complementary or opposing extremes; for instance, in grip strength tables where $(1, 1)$ represents "both hands strongest" and (R, R) represents "both hands weakest," these cells lie at opposite ends of the same anti-diagonal. Anti-diagonal symmetry-type models have therefore been developed as counterparts of the ordinary symmetry family. In particular, the anti-symmetry (AS) model, the anti-conditional symmetry (ACS) model, the anti-diagonals-parameter symmetry (ADPS) model, and the anti-linear-diagonals-parameter symmetry (ALDPS) model have been proposed and studied for square contingency tables with ordered categories [13–15]. To the best of our knowledge, this is still a comparatively small literature, and no anti-diagonal counterpart of the TRPS model has been available.

Despite this parallel development, the anti-diagonal literature still lacks a direct counterpart of the TRPS model. This gap is mathematically meaningful. The ACS model introduces only a single global ratio and therefore cannot represent how asymmetry changes with anti-diagonal distance. The ADPS model allows a separate ratio for each anti-diagonal distance, but this flexibility comes at the cost of $R - 1$ asymmetry parameters. The ALDPS model imposes a log-linear distance effect and is more parsimonious, but it does not separate the global level effect from the anti-diagonal-distance effect. Accordingly, there is no existing anti-diagonal model that simultaneously has the interpretability of two distinct ratio parameters, the nesting relationships expected from the main-diagonal theory, and the potential to yield a decomposition theory for the AS model parallel to that of TRPS.

The present paper fills this gap by introducing a new anti-two-ratios-parameter symmetry (ATRPS) model, formally defined in Definition 1. The proposed model contains the ACS and ALDPS models as special cases and is nested within the ADPS model. Our first objective is to characterize the AS model through ATRPS together with two auxiliary balance conditions, namely anti-global symmetry (AGS) and anti-marginal mean equality

(AME). Our second objective is to show that this characterization yields an asymptotic orthogonal decomposition of the likelihood ratio statistics associated with these models.

The technical device underlying the theory is a column-reversal transformation that converts the anti-diagonal problem into an ordinary main-diagonal problem. The contribution of the present paper is not a new asymptotic device beyond the TRPS theory, but the establishment of an anti-diagonal formulation in which the relevant objects are intrinsic to the original table. More precisely, the mathematical novelty is the identification of a single bijection that simultaneously preserves all four ingredients required for the decomposition: (a) the paired-cell correspondence $(i,j) \leftrightarrow (j^*,i^*)$, (b) the anti-diagonal distance index $R+1-(i+j)$, (c) the upper/lower anti-diagonal balance condition (AGS), and (d) the anti-marginal mean constraint (AME). Without establishing that one transformation carries over this entire package, the decomposition and orthogonality results do not follow automatically from the main-diagonal theory. Proposition 1 below records these correspondences explicitly. A direct anti-diagonal proof is possible in principle, but it requires repeated re-indexing by constant-sum classes $i+j$ and by reflected pairs $(i,j) \leftrightarrow (j^*,i^*)$; we provide a sketch in Remark 2. Thus, the proposed framework is not merely a restatement in transformed coordinates; rather, it provides an explicit anti-diagonal formulation in which the parameters, constraints, and decomposition components can be read on the scale relevant to the original problem.

The remainder of the paper is organized as follows. Section 2 introduces the ATRPS model and its relation to existing anti-diagonal models. Section 3 establishes a decomposition theorem for the AS model. Section 4 proves the asymptotic orthogonal decomposition of the likelihood ratio statistic. Section 5 presents an application to grip strength data, Section 6 discusses the implications and limitations of the proposed approach, and Section 7 concludes the paper.

2. Models

Let p_{ij} denote the probability that an observation falls in cell (i,j) $(i,j=1,\ldots,R)$, and let

$$A = \{(i,j) \mid i,j = 1,\ldots,R\}.$$

For anti-diagonal analysis, define

$$i^* = R+1-i, \qquad j^* = R+1-j,$$

and

$$E = \{(i,j) \in A \mid i+j < R+1\}.$$

Thus, each cell $(i,j) \in E$ is paired with the reflected cell (j^*,i^*), which lies below the anti-diagonal. For later use, let

$$m = \frac{R(R-1)}{2}.$$

The AS model is defined by

$$p_{ij} = p_{j^*i^*} \qquad ((i,j) \in E). \tag{1}$$

The ACS model is defined by

$$p_{ij} = \gamma p_{j^*i^*} \qquad ((i,j) \in E), \tag{2}$$

where $\gamma > 0$ is an unknown parameter. The ADPS model is defined by

$$p_{ij} = \delta_{R+1-(i+j)} p_{j^*i^*} \qquad ((i,j) \in E), \tag{3}$$

where $\delta_1, \ldots, \delta_{R-1} > 0$ are unknown parameters. The ALDPS model is defined by

$$p_{ij} = \delta^{R+1-(i+j)} p_{j^*i^*} \qquad ((i,j) \in E), \tag{4}$$

where $\delta > 0$ is an unknown parameter [15].

We now propose the anti-two-ratios-parameter symmetry model.

Definition 1. *The anti-two-ratios-parameter symmetry (ATRPS) model is defined by*

$$p_{ij} = \gamma \phi^{R+1-(i+j)} p_{j^*i^*} \qquad ((i,j) \in E), \tag{5}$$

where $\gamma > 0$ and $\phi > 0$ are unknown parameters.

For a paired cell at anti-diagonal distance $k = R+1-(i+j)$, the ratio $p_{ij}/p_{j^*i^*}$ equals $\gamma\phi^k$. Hence γ represents a global asymmetry level, while ϕ controls how the asymmetry changes with distance from the anti-diagonal.

Special cases and nesting relationships. The ATRPS model contains several important models as special cases:

(i) $\gamma = \phi = 1$ gives the AS model;

(ii) $\phi = 1$ gives the ACS model;

(iii) $\gamma = 1$ gives the ALDPS model;

(iv) setting $\delta_k = \gamma\phi^k$ in (3) shows that the ATRPS model is a special case of the ADPS model.

Thus the nesting relationships are

$$\text{AS} \subset \text{ACS} \subset \text{ATRPS} \subset \text{ADPS}, \qquad \text{AS} \subset \text{ALDPS} \subset \text{ATRPS} \subset \text{ADPS}.$$

These relationships are illustrated in Figure 1.

Figure 2 gives a schematic illustration of the anti-diagonal pairing used throughout the paper.

To decompose the AS model, we introduce two additional models. Define

$$\Delta_U = \sum_{i+j<R+1} p_{ij}, \qquad \Delta_L = \sum_{i+j>R+1} p_{ij}.$$

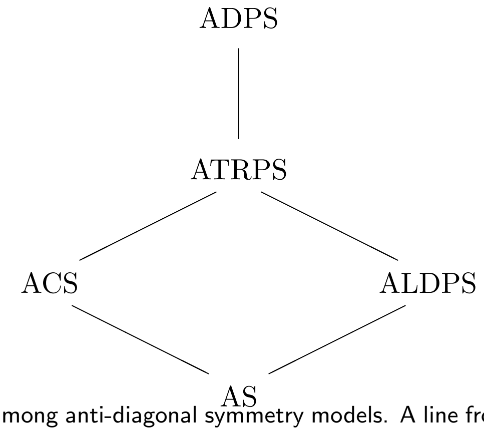

Figure 1: Nesting relationships among anti-diagonal symmetry models. A line from model M_1 (below) to model M_2 (above) indicates that M_1 implies M_2, namely, $M_1 \subset M_2$.

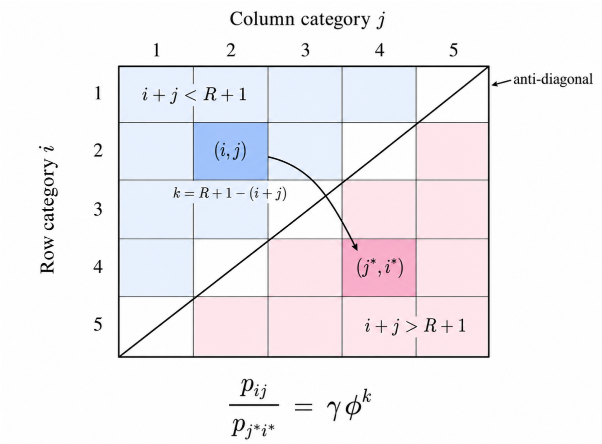

Figure 2: Schematic illustration of anti-diagonal reflection and ATRPS pairing in a 5×5 square contingency table. A cell (i, j) above the anti-diagonal is paired with the reflected cell (j^*, i^*) below the anti-diagonal. The anti-diagonal distance is $k = R + 1 - (i + j)$, and under the ATRPS model the paired-cell ratio is $\gamma\phi^k$.

The anti-global symmetry (AGS) model is

$$\Delta_U = \Delta_L. \tag{6}$$

Next, let X and Y denote the row and column variables. The anti-marginal mean equality (AME) model is

$$E(X) = E(R + 1 - Y). \tag{7}$$

Equivalently,

$$\sum_{(i,j)\in A} \{i + j - (R + 1)\}p_{ij} = 0.$$

Finally, the anti-global symmetry plus anti-marginal mean equality (AGSME) model is the model determined by (6) and (7) simultaneously.

3. Decomposition of the Anti-Symmetry Model

We shall denote the column-reversed table $\{p_{i,R+1-\ell}\}$ by $\{q_{i\ell}\}$. Thus, define the mapping

$$T : \{p_{ij}\}_{1\le i,j\le R} \longmapsto \{q_{i\ell}\}_{1\le i,\ell\le R}, \qquad q_{i\ell} = p_{i,R+1-\ell}.$$

Equivalently, the ℓth column of the transformed table corresponds to the $(R+1-\ell)$th column of the original table. Since T merely permutes the R columns by the involution $\ell \mapsto R+1-\ell$, it is a well-defined bijection on the set of $R\times R$ probability tables; in particular, T^2 is the identity. Under this transformation, the anti-diagonal of the original table (cells with $i+j=R+1$) becomes the main diagonal of the transformed table (cells with $i=\ell$).

The following proposition, which we refer to as the *model correspondence under column reversal*, is the structural core of the paper.

Proposition 1 (Model correspondence under column reversal)**.** *Under the transformation T, the following equivalences hold:*

(i) the AS model for $\{p_{ij}\}$ is equivalent to the S model for $\{q_{i\ell}\}$;

(ii) the ATRPS model for $\{p_{ij}\}$ is equivalent to the TRPS model for $\{q_{i\ell}\}$;

(iii) the AGS model for $\{p_{ij}\}$ is equivalent to the global symmetry (GS) model for $\{q_{i\ell}\}$;

(iv) the AME model for $\{p_{ij}\}$ is equivalent to the marginal mean equality (ME) model for $\{q_{i\ell}\}$.

Proof. For each ℓ, define $j(\ell)=R+1-\ell$. Then

$$i+j(\ell) < R+1 \iff i+(R+1-\ell) < R+1 \iff i<\ell.$$

Moreover,

$$p_{j(\ell)^* i^*} = p_{R+1-j(\ell),R+1-i} = p_{\ell,R+1-i} = q_{\ell i},$$

and

$$R+1-\{i+j(\ell)\} = R+1-\{i+(R+1-\ell)\} = \ell - i.$$

Therefore, for $i<\ell$, the AS relation $p_{ij}=p_{j^*i^*}$ is equivalent to $q_{i\ell}=q_{\ell i}$, which is exactly the S model. Likewise, the ATRPS relation

$$p_{ij} = \gamma\phi^{R+1-(i+j)} p_{j^*i^*}$$

is equivalent to

$$q_{i\ell} = \gamma\phi^{\ell-i} q_{\ell i} \qquad (i<\ell),$$

which is the TRPS model. This proves (i) and (ii).

For (iii),

$$\sum_{i+j<R+1} p_{ij} = \sum_{i<\ell} q_{i\ell}, \qquad \sum_{i+j>R+1} p_{ij} = \sum_{i>\ell} q_{i\ell},$$

so the AGS condition $\Delta_U = \Delta_L$ is identical to the GS condition for the transformed table.

For (iv), using $q_{i\ell} = p_{i,R+1-\ell}$,

$$E(X) = \sum_{i=1}^{R} \sum_{j=1}^{R} i p_{ij} = \sum_{i=1}^{R} \sum_{\ell=1}^{R} i p_{i,R+1-\ell} = \sum_{i,\ell} i q_{i\ell}.$$

Also, define the function $\ell(j) = R + 1 - j$. Then

$$E(R+1-Y) = \sum_{i=1}^{R} \sum_{j=1}^{R} (R+1-j) p_{ij} = \sum_{i=1}^{R} \sum_{j=1}^{R} \ell(j)\, p_{ij} = \sum_{i=1}^{R} \sum_{\ell=1}^{R} \ell p_{i,R+1-\ell} = \sum_{i,\ell} \ell q_{i\ell}.$$

Hence $E(X) = E(R + 1 - Y)$ is equivalent to $E_q(X) = E_q(Y)$, namely the ME model for the transformed table. This establishes (iv), and the proof is complete.

Remark 1. *The model correspondence (Proposition 1) is the key self-contained step in the anti-diagonal argument. It shows that the column-reversal map preserves not only paired-cell relations but also the distance index and the two auxiliary balance constraints. This is precisely why the transformed proof is shorter than a direct proof written entirely in the anti-diagonal indexing.*

The next theorem is the anti-diagonal analogue of the TRPS decomposition theorem of Tahata and Tomizawa [9].

Theorem 1. *The AS model holds if and only if the ATRPS, AGS, and AME models hold simultaneously.*

Proof. First assume that the AS model holds. Then, by definition,

$$p_{ij} = p_{j^* i^*} \qquad ((i, j) \in E),$$

so the ATRPS model holds with $\gamma = 1$ and $\phi = 1$. In addition,

$$\Delta_U = \sum_{i+j<R+1} p_{ij} = \sum_{i+j<R+1} p_{j^* i^*} = \sum_{i+j>R+1} p_{ij} = \Delta_L,$$

which proves AGS. Finally,

$$\sum_{(i,j)\in A} \{i + j - (R + 1)\} p_{ij} = 0$$

because each pair of cells (i, j) and (j^*, i^*) has coefficients $-(R+1-(i+j))$ and $R+1-(i+j)$, respectively, and the paired probabilities are equal under AS. Thus AME also holds.

Conversely, suppose that ATRPS, AGS, and AME hold for the original table $\{p_{ij}\}$. By Proposition 1, the transformed table $\{q_{i\ell}\} = T(\{p_{ij}\})$ satisfies the TRPS, GS, and ME models simultaneously. Theorem 1 of Tahata and Tomizawa [9] then implies that the transformed table satisfies the ordinary symmetry model $q_{i\ell} = q_{\ell i}$ for all $i < \ell$. Applying Proposition 1(i) once more, this is equivalent to the AS model for the original table. Hence the AS model holds.

Since the AGSME model is defined by the AGS and AME constraints jointly, Theorem 1 immediately yields the following corollary.

Corollary 1. *The AS model holds if and only if the ATRPS and AGSME models hold simultaneously.*

Proof. If the AS model holds, then Theorem 1 shows that ATRPS, AGS, and AME all hold, and hence AGSME holds by definition. Conversely, if ATRPS and AGSME hold, then ATRPS, AGS, and AME hold simultaneously, so Theorem 1 yields the AS model.

Theorem 1 and Corollary 1 are useful when the AS model fails to fit. They show that a departure from AS can be assessed through two conceptually distinct components: the structured anti-diagonal asymmetry represented by ATRPS, and the broader imbalance represented by AGSME.

Remark 2 (Direct proof sketch for the converse of Theorem 1)**.** *A direct anti-diagonal proof of the converse can be outlined as follows. Suppose that ATRPS, AGS, and AME hold for* $\{p_{ij}\}$*. Under ATRPS, the ratio* $p_{ij}/p_{j^*i^*} = \gamma\phi^k$ *is constant within each anti-diagonal distance class* $k = R + 1 - (i + j)$*. For each* $k = 1, \dots, R - 1$*, write* $S_k^+ = \sum_{(i,j):\, R+1-(i+j)=k} p_{ij}$ *and* $S_k^- = \sum_{(i,j):\, R+1-(i+j)=k} p_{j^*i^*}$*. Then* $S_k^+ = \gamma\phi^k S_k^-$ *for every* k*. Setting* $w_k = (\gamma\phi^k - 1)S_k^-$*, the AGS constraint yields*

$$\textstyle\sum_{k=1}^{R-1} w_k = 0,$$

and the AME constraint yields

$$\textstyle\sum_{k=1}^{R-1} k\, w_k = 0.$$

Suppose for contradiction that (w_k) *is not identically zero. Since* $\gamma\phi^k$ *is a geometric function of* k*, the sequence* $\gamma\phi^k - 1$ *changes sign at most once on* $\{1, \dots, R - 1\}$*, and because* $S_k^- > 0$ *for all* k *under interior-point conditions, the same is true of* (w_k)*. If* w_k *does not change sign, then* $\sum_k w_k \neq 0$*, contradicting the first equation. Thus* (w_k) *changes sign exactly once: there exists* k_0 *such that* w_k *and* $w_{k'}$ *have opposite signs for* $k \leq k_0 < k'$*. Choosing any such* k_0*, the first equation gives* $\sum_k w_k = 0$*, whence*

$$\textstyle\sum_{k=1}^{R-1} (k - k_0)\, w_k = \sum_{k=1}^{R-1} k\, w_k = 0.$$

But $(k - k_0)w_k \geq 0$ *for every* k *with strict inequality for at least one* k*, because* $k - k_0$ *and* w_k *share the same sign pattern. This is a contradiction. Therefore* $w_k = 0$ *for all* k*, i.e.,* $\gamma\phi^k = 1$ *for* $k = 1, \dots, R - 1$*. Evaluating at any two distinct values of* k *gives* $\gamma = 1$ *and* $\phi = 1$*, hence the AS model.*

4. Orthogonal Decomposition of the Likelihood Ratio Statistic

For a fitted model M, let $G^2(M)$ denote the likelihood ratio chi-squared statistic for testing M against the saturated model, and let $\mathrm{df}(M)$ denote the corresponding degrees of freedom. Table 1 summarizes the degrees of freedom of the models considered in this paper.

Table 1: Degrees of freedom for anti-diagonal models with $m = R(R-1)/2$.

Model	AS	ACS	ADPS	ALDPS	ATRPS	AGS	AME	AGSME
df	m	$m-1$	$m-(R-1)$	$m-1$	$m-2$	1	1	2

Let n_{ij} denote the observed frequency in cell (i,j) and let

$$N = \sum_{i=1}^{R}\sum_{j=1}^{R} n_{ij}.$$

Under multinomial sampling, the log-likelihood for the original table is, up to an additive constant independent of the model parameters (see, e.g., [16] for general theory of goodness-of-fit statistics),

$$\ell_P(p) = \sum_{i=1}^{R}\sum_{j=1}^{R} n_{ij}\log p_{ij}.$$

For the transformed table, define

$$m_{i\ell} = n_{i,R+1-\ell} \qquad (i,\ell = 1,\ldots,R).$$

Then $\sum_{i,\ell} m_{i\ell} = N$ and the log-likelihood becomes

$$\ell_Q(q) = \sum_{i=1}^{R}\sum_{\ell=1}^{R} m_{i\ell}\log q_{i\ell}.$$

Because $q_{i\ell} = p_{i,R+1-\ell}$ and $m_{i\ell} = n_{i,R+1-\ell}$, we have the exact identity

$$\ell_Q(q) = \ell_P(p). \tag{8}$$

In other words, the column-reversal transformation is merely a relabeling of cell indices, so it preserves the multinomial likelihood.

Lemma 1. *Let $\mathcal{M}_P$ be a model for the original table and let $\mathcal{M}_Q = T(\mathcal{M}_P)$ be its image under the column-reversal transformation. Then the likelihood ratio statistic for testing $\mathcal{M}_P$ based on $\{n_{ij}\}$ is identical to the likelihood ratio statistic for testing $\mathcal{M}_Q$ based on $\{m_{i\ell}\}$.*

Proof. By (8), the log-likelihood values at corresponding points are the same. Since T is a bijection,

$$\sup_{p \in \mathcal{M}_P} \ell_P(p) = \sup_{q \in \mathcal{M}_Q} \ell_Q(q).$$

The same statement holds for the saturated model because the saturated model is also preserved under relabeling. Therefore the difference between the maximized saturated and constrained log-likelihoods is identical for the two tables. Hence the two likelihood ratio statistics coincide.

We can now state the main orthogonality result. Throughout, for statistics U_N and V_N, the notation

$$U_N \simeq V_N$$

means that $U_N - V_N = o_p(1)$ under the AS model as $N \to \infty$. In particular, the two quantities have the same first-order asymptotic expansion and hence the same null chi-square approximation. The asymptotic claim inherits the regularity conditions of the underlying multinomial theory and of the TRPS orthogonality result of Tahata and Tomizawa [9]: it is assumed that the true cell probabilities satisfy the AS model and that all cell probabilities are strictly positive (interior-point condition), so that the maximum likelihood estimators under each sub-model are consistent and asymptotically normal.

Theorem 2. *Under the AS model, the following asymptotic equivalence holds:*

$$G^2(\mathrm{AS}) \simeq G^2(\mathrm{ATRPS}) + G^2(\mathrm{AGSME}). \tag{9}$$

Proof. By Proposition 1, the AS, ATRPS, and AGSME models for the original table correspond, respectively, to the S, TRPS, and GSME models for the transformed table. By Lemma 1,

$$G_P^2(\mathrm{AS}) = G_Q^2(\mathrm{S}), \qquad G_P^2(\mathrm{ATRPS}) = G_Q^2(\mathrm{TRPS}), \qquad G_P^2(\mathrm{AGSME}) = G_Q^2(\mathrm{GSME}),$$

where the subscripts indicate the table to which the statistic is applied. Tahata and Tomizawa [9] proved that, under the S model for the transformed table,

$$G_Q^2(\mathrm{S}) \simeq G_Q^2(\mathrm{TRPS}) + G_Q^2(\mathrm{GSME}),$$

that is, the difference between the two sides is $o_p(1)$. Substituting the three identities above gives

$$G_P^2(\mathrm{AS}) \simeq G_P^2(\mathrm{ATRPS}) + G_P^2(\mathrm{AGSME}),$$

which is exactly (9).

Because the degrees of freedom also satisfy

$$\mathrm{df}(\mathrm{AS}) = \mathrm{df}(\mathrm{ATRPS}) + \mathrm{df}(\mathrm{AGSME}) = (m-2) + 2,$$

Theorem 2 gives a statistically interpretable partition of the lack of fit of the AS model into an ATRPS part and an AGSME part. This partition is especially useful when the ATRPS model fits adequately but the AS model does not, because it shows that the main source of misfit lies in the AGSME component rather than in the structured anti-diagonal asymmetry captured by ATRPS.

5. Example: Grip Strength Test Data

We illustrate the proposed methodology with the grip strength data for 2356 men aged 15–69 years from the National Health and Nutrition Examination Survey (NHANES) 2011–2012, reproduced from Yamamoto, Aizawa and Tomizawa [17]. The row and column variables are the right- and left-hand grip strength categories, respectively, where category 1 denotes the highest level and category 5 the lowest. This dataset is well suited to anti-diagonal modeling because a pair of cells related by anti-diagonal reflection compares opposite directional configurations of right-left dominance at the same anti-diagonal distance. The same table has therefore been used in earlier studies on anti-diagonal symmetry and related models [13–15]. All maximum likelihood estimates reported below were obtained by maximizing the multinomial log-likelihood. For the ATRPS model, under the reparametrization $(\eta, \xi) = (\log\gamma, \log\phi)$, the likelihood reduces to a two-parameter grouped binomial likelihood across anti-diagonal distances, and the reported estimates were obtained by Newton–Raphson iteration with starting values $\eta = 0$ and $\xi = 0$ (corresponding to the AS model); convergence was declared when the maximum absolute change in parameter values fell below 10^{-10}.

Table 2: Grip strength test data for men aged 15–69 years.

	Left hand					
Right hand	(1)	(2)	(3)	(4)	(5)	Total
Highest (1)	215	124	46	14	2	401
(2)	37	143	165	74	16	435
(3)	7	45	156	166	51	425
(4)	2	20	62	226	210	520
Lowest (5)	1	2	16	61	495	575
Total	262	334	445	541	774	2356

Table 3 summarizes the goodness-of-fit statistics for all models considered in the empirical analysis, including the decomposition models AGS, AME, and AGSME, thereby avoiding repeated entries for the AS and ATRPS models. We employ the modified forms $\mathrm{AIC}^\dagger = G^2 - 2\,\mathrm{df}$ and $\mathrm{BIC}^\dagger = G^2 - (\log N)\,\mathrm{df}$, which differ from the standard AIC and BIC only by model-independent constants and thus preserve model rankings; smaller values are preferred. The AS model is strongly rejected, and the ACS model is also inadequate. Hence a constant anti-diagonal odds ratio is too restrictive for these data. By contrast, the ADPS, ALDPS, and ATRPS models all fit satisfactorily, which indicates that the departure from AS is largely explained by a systematic dependence on anti-diagonal distance. The information criteria provide a complementary model-selection perspective. Among the well-fitting models, ALDPS is marginally preferred to ATRPS, with ADPS also competitive. Thus ATRPS should not be viewed as uniformly superior in empirical fit. Rather, the primary value of ATRPS is theoretical: it is the minimal two-parameter anti-diagonal model whose structure supports the orthogonal decomposition $G^2(\mathrm{AS}) \simeq G^2(\mathrm{ATRPS}) + G^2(\mathrm{AGSME})$ established in Theorem 2. The present decomposition framework is not available from the ALDPS model, which has only one asymmetry parameter and does not separate the global and distance components needed for the AGSME partition. In this sense, ATRPS complements ALDPS: the latter may be preferred for pure model selection, while the former is indispensable for diagnostic decomposition of anti-symmetry.

Table 3: Goodness-of-fit statistics and information criteria for anti-diagonal asymmetry and decomposition models applied to Table 2. Here $\mathrm{AIC}^{\dagger} = G^2 - 2\,\mathrm{df}$ and $\mathrm{BIC}^{\dagger} = G^2 - (\log N)\,\mathrm{df}$ with $N = 2356$; these differ from the standard AIC and BIC only by model-independent constants, so the model rankings are unchanged. Smaller values are preferred.

Model	Degrees of freedom	G^2	p-value	$\mathrm{AIC}^{\dagger}$	$\mathrm{BIC}^{\dagger}$
AS	10	167.37	< 0.01	147.37	89.72
ACS	9	43.92	< 0.01	25.92	-25.96
ADPS	6	5.35	0.50	-6.65	-41.24
ALDPS	9	7.65	0.57	-10.35	-62.23
ATRPS	8	6.21	0.62	-9.79	-55.91
AGS	1	123.44	< 0.01	121.44	115.68
AME	1	160.07	< 0.01	158.07	152.31
AGSME	2	161.16	< 0.01	157.16	145.63

Under the ATRPS model, the maximum likelihood estimates are

$$\widehat{\gamma} = 1.142, \qquad \widehat{\phi} = 0.788.$$

Since $\widehat{\gamma} > 1$, the global ratio component alone would favor the upper anti-diagonal half (i.e., $p_{ij} > p_{j^*i^*}$). However, the distance effect $\widehat{\phi} < 1$ acts multiplicatively and, because $\widehat{\phi}^k$ decreases rapidly with k, it dominates the global component over the observed range of distances. Accordingly, the fitted anti-diagonal ratios $\widehat{\gamma}\widehat{\phi}^k$ equal 0.90, 0.71, 0.56, and 0.44 for $k = 1, 2, 3, 4$, respectively—all below one. Thus, while the global parameter $\widehat{\gamma}$ by itself exceeds one, the joint effect $\widehat{\gamma}\widehat{\phi}^k < 1$ for every observed k, meaning that the probability above the anti-diagonal is consistently smaller than the reflected probability below it. This discrepancy is mild near the anti-diagonal ($k = 1$) but substantial for the most distant paired cells ($k = 4$). In particular, the fitted ratio for the pair $(1, 1)$ and $(5, 5)$ is well below one, which reflects a marked imbalance between the strongest-both-hands and weakest-both-hands classifications.

The nested comparisons clarify the role of the two ATRPS parameters. First,

$$G^2(\mathrm{ACS}) - G^2(\mathrm{ATRPS}) = 37.72,$$

with 1 degree of freedom ($p < 0.01$), so the additional distance parameter ϕ is decisively supported. Thus the anti-diagonal pattern cannot be represented adequately by a single global ratio. Second,

$$G^2(\mathrm{ALDPS}) - G^2(\mathrm{ATRPS}) = 1.44,$$

with 1 degree of freedom ($p = 0.23$), showing that the extra global parameter γ in ATRPS produces only a modest improvement beyond ALDPS. Finally,

$$G^2(\mathrm{ATRPS}) - G^2(\mathrm{ADPS}) = 0.86,$$

with 2 degrees of freedom ($p = 0.65$), which indicates that the proposed two-parameter form captures almost all of the anti-diagonal asymmetry accounted for by the more general ADPS model. From a modeling point of view, ATRPS therefore achieves an effective compromise between parsimony and fit.

To examine the decomposition theorem, we use the entries for AS, ATRPS, and AGSME in Table 3. The numerical decomposition predicted by Theorem 2 is very close:

$$167.37 \approx 6.21 + 161.16.$$

Indeed, the displayed rounded values happen to agree at two decimal places: the right-hand side sums to 167.37. This equality should be interpreted at the displayed precision; Theorem 2 is an asymptotic statement, not an exact finite-sample identity. In the present data, however, the approximation is remarkably close. Thus, nearly all of the lack of fit of the AS model is attributable to the AGSME component, whereas the ATRPS component itself fits quite well.

This example therefore illustrates the intended interpretation of the theory. The structured anti-diagonal asymmetry is adequately summarized by ATRPS, but the full AS model fails because the table also exhibits strong imbalance in the combined AGSME constraints. In this sense, the orthogonal decomposition is not only an asymptotic statement about likelihood ratio statistics; it also gives a practically meaningful diagnosis of why anti-symmetry breaks down.

6. Discussion

This paper introduced the anti-two-ratios-parameter symmetry (ATRPS) model for $R \times R$ square contingency tables with ordered categories and established its role in the decomposition theory of the anti-symmetry model. The work belongs to the symmetry-model decomposition tradition for ordered categorical data, which seeks to express complex symmetry hypotheses as conjunctions of simpler, interpretable components and to partition the associated test statistics accordingly [10, 11]. The proposed family provides a natural anti-diagonal counterpart of the TRPS model in ordinary main-diagonal analysis [7, 9]. At the model level, ATRPS sits between ACS and ADPS: it is more flexible than a single-ratio representation, yet substantially more parsimonious than a model with a separate parameter for each anti-diagonal distance. Because its two parameters isolate a global anti-diagonal ratio and a distance effect, the model yields a structurally interpretable description of anti-diagonal departure from symmetry.

The first main result is a characterization of AS in terms of simpler components. We proved that the AS model is equivalent to the simultaneous validity of ATRPS, AGS, and AME, and equivalently to the joint validity of ATRPS and AGSME. This decomposition identifies two distinct ingredients of anti-symmetry: a patterned anti-diagonal component described by the two-ratio mechanism, and a residual balance component described by aggregate anti-global and anti-marginal restrictions. From a mathematical standpoint, this clarifies how the anti-diagonal symmetry condition can be reconstructed from interpretable lower-dimensional constraints. This result is in the spirit of the classical decomposition of Caussinus [8], who showed that the symmetry model is equivalent to the simultaneous validity of quasi-symmetry and marginal homogeneity [18], as well as the more recent developments reviewed in Tomizawa and Tahata [10] and Tahata and Tomizawa [11].

The second main result is the asymptotic orthogonal decomposition

$$G^2(\mathrm{AS}) \simeq G^2(\mathrm{ATRPS}) + G^2(\mathrm{AGSME}).$$

This relation is important because it converts the structural decomposition into a statistical one. When the AS model is rejected, the total likelihood-based lack of fit can be separated into the part attributable to failure of the ATRPS structure and the part attributable to failure of the AGSME constraints. Consequently, the proposed theory has a dual role: it gives a concise representation of anti-diagonal asymmetry and, at the same time, supplies a diagnostic framework for locating the source of departure from AS. Analogous orthogonal decomposition principles have been developed for point-symmetry models [19] and other extended symmetry models [20]; the present paper extends this program to the anti-diagonal setting.

Although our proofs rely on a column-reversal transformation, the resulting theory should not be viewed as a mere reformulation of the ordinary TRPS case. The transformed representation is a technical bridge, but the substantive interpretation remains anti-diagonal throughout. In applications, the quantities of interest are the original paired probabilities p_{ij} and $p_{j^*i^*}$, the anti-diagonal-distance parameter $R + 1 - (i + j)$, and the decomposition of anti-symmetry in the original table. The present formulation is therefore needed to state and interpret the theory in the language appropriate to anti-diagonal problems. Mathematically, the essential point is that the same bijection carries over all ingredients required for the decomposition theorem: the paired cells, the distance index, the global upper/lower balance, the anti-marginal mean, and the likelihood itself. Once this package of correspondences is established, the TRPS orthogonality theory becomes available in a genuinely anti-diagonal form.

We note that when $R = 3$, the ATRPS and ADPS models are equivalent, because there are only two anti-diagonal distance classes and the two distance-specific ratios in the ADPS model can be written as $\delta_1 = \gamma\phi$ and $\delta_2 = \gamma\phi^2$. Hence both models have $\mathrm{df} = m - 2 = 1$. By contrast, the ALDPS model has $\mathrm{df} = m - 1 = 2$ and is more restrictive. The advantage of ATRPS over ADPS becomes more pronounced for larger tables ($R \geq 4$), where the two-parameter structure achieves meaningful parsimony while preserving the separation of a global ratio effect and a distance effect.

The grip strength analysis illustrates these points concretely. The ATRPS model provides an adequate and parsimonious account of the anti-diagonal pattern, whereas the AS model fails because the AGSME component is strongly violated. The orthogonal decomposition reveals that more than 96% of the total $G^2(\mathrm{AS})$ is attributable to the AGSME component, confirming that the structured anti-diagonal trend is well captured by the two-ratio mechanism. This is precisely the type of conclusion for which the orthogonal decomposition is useful: it distinguishes a well-structured anti-diagonal trend from a broader failure of global and marginal balance.

Several extensions appear promising. A systematic simulation study comparing the finite-sample behavior of ATRPS with competing anti-diagonal models across different table dimensions and parameter settings is an important topic for future work. The most immediate one is to develop anti-diagonal analogues of quasi-symmetry and related association models. This seems feasible, but it requires identifying a log-linear interaction structure that remains interpretable after column reversal and that still separates anti-diagonal effects from baseline association. Another direction is to construct numerical measures of departure from ATRPS and AS, parallel to existing measures for ordinary symmetry-type models; here the main technical issue is to normalize the departure in a way that respects anti-diagonal pairing rather than ordinary diagonal pairing. It would also be of interest to examine whether similar decomposition principles can be formulated for multiway tables or for settings in which the anti-diagonal structure is only partially observed. In that case the main obstacle is that there is no unique canonical anti-diagonal indexing once more than two margins are involved. Such developments would deepen the mathematical theory of anti-diagonal models and broaden their applicability in the analysis of ordered categorical data.

7. Concluding Remarks

In summary, the proposed ATRPS model provides a mathematically interpretable anti-diagonal counterpart of the TRPS model and yields an orthogonal decomposition of the anti-symmetry model into structured and residual components. The empirical example shows that this decomposition can offer a useful diagnostic explanation even when a simpler model such as ALDPS is competitive in pure goodness-of-fit terms. We hope that the present formulation will serve as a basis for further methodological developments in anti-diagonal analysis of ordered categorical data.

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