# Matrices with a given number of violations of Regular Minimality

Ehtibar N. Dzhafarov\* Department of Psychological Sciences, Purdue University

Ali Ünlü, Matthias Trendtel, Faculty of Statistics, Dortmund Technical University, Germany

and Hans Colonius

Department of Psychology, Oldenburg University, Germany

## Abstract

A row (or column) of an  $n \times n$  matrix complies with Regular Minimality (RM) if it has a unique minimum entry which is also a unique minimum entry in its column (respectively, row). The number of violations of RM in a matrix is defined as the number of rows (equivalently, columns) that do not comply with RM. We derive a formula for the proportion of  $n \times n$  matrices with a given number of violations of RM among all  $n \times n$  matrices with no tied entries. The proportion of matrices with no more than a given number of violations can be treated as the *p*-value of a permutation test whose null hypothesis states that all permutations of the entries of a matrix without ties are equiprobable, and the alternative hypothesis states that RM violations occur with lower probability than predicted by the null hypothesis. A matrix with ties is treated as being represented by all matrices without ties that have the same set of strict inequalities among their entries.

KEYWORDS: discriminability, rank order matrices; permutation test, regular minimality, tied ranks.

### 1. PRELIMINARIES

Let  $m: X \times Y \to \mathbb{R}^+$  be some discriminability measure, mapping pairs of stimuli  $x \in X$  and  $y \in Y$  into the set of nonnegative reals. The sets X and Y represent two distinct observation areas (Dzhafarov, 2002b; Dzhafarov & Colonius, 2006a): in a pairwise presentation paradigm, even if x and yhave the same value (say, they are two colors with identical color coordinates), they must occupy different spatial and/or temporal positions to be perceived as two distinct stimuli. So xand y should be designated as, say,  $x = ((x^1, x^2, x^3), \text{ left})$  and  $y = ((y^1, y^2, y^3), \text{ right})$ . Strictly speaking, they can never be equal. The values of m(x,y) may be probabilities with which stimuli x and y (when presented as an ordered pair, say, x on the left and y on the right) are judged to be different; or they can be average numerical estimates of the "dissimilarity" between x and y. The values of m(x, y), however, can also be computed from responses to individual presentations of x and y, one at a time. Thus, they can be computed as some version of the Kullback-Leibler divergence between the probabilities with which x and y are classified into a fixed set of several categories (Dzhafarov, 2010). In a case like this, the difference between the two observation areas reduces to distinguishing Xas the set of stimuli "considered (written) first" and Y as the set of stimuli "considered (written) second" when x and y are compared (theoretically, within the computational procedure).

In this paper we are only concerned with the case when *X* and *Y* consist of *n* elements each. Then the function m(x,y) can be presented as an  $n \times n$  matrix with entries  $m_{ij}$   $(i, j \in \{1, ..., n\})$ . The rows i = 1, ..., n represent stimuli in one observation area (e.g., presented first in time or on the left), the columns j = 1, ..., n represent stimuli in another observation area (presented second or on the right). The cells (i, j) of the matrix represent ordered pairs of stimuli (e.g., first-second, left-right, or even "written first"-"written second"). In the present context only ordinal properties of  $m_{ij}$  matter rather

than the values themselves. With no loss of generality, therefore, we will adopt henceforth the following

**Convention 1.1.** Unless otherwise specified, all entries  $m_{ij}$  in any matrix M mentioned in this paper are assumed to be represented (replaced) by their ranks (ordinal positions).

Thus, the matrix

	3	1	15	20	23	1
	2	5	6	13	9	
$M_1 =$	16	17	4	11	8	l
	18	19	24	12	7	I
$M_1 =$	14	22	25	10	21	

represents (replaces) any matrix in which  $m_{12}$  is the smallest value,  $m_{21}$  is the next smallest value, etc., and  $m_{53}$  is the largest value. This rank order matrix has no ties among its entries. In the case of ties the ranks of the tied entries are averaged in the conventional manner. Thus, in the matrix

$M_2 =$	- 1	2.5	15	23	20 -
	5	2.5	6	8.5	13
$M_2 =$	17	16	4	8.5	11
	19	18	23	7	10
	23	14	23	23	12

we have  $m_{12} = m_{22} = (2+3)/2$ ,  $m_{24} = m_{34} = (8+9)/2$ , and  $m_{14} = m_{43} = m_{51} = m_{53} = m_{54} = (21 + \ldots + 25)/5$ .

An  $n \times n$  matrix *M* is said to comply with *Regular Minimality* (RM) if

(A) every row and every column of *M* contains a unique minimum entry, and

(B) an entry which is minimal in its row is also minimal in its column (hence also vice versa).

The interpretation of this principle is simple. If  $m_{ij}$  is a unique minimum entry in the *i*th row, then in the second observation area (set *Y*, represented by columns) the *j*th stimulus is less discriminable than any other stimulus in *Y* from the *i*th stimulus in the first observation area (set *X*, represented by rows). So, the *j*th stimulus in *Y* can be considered *the best match* for the *i*th stimulus in *X*. Symmetrically, if  $m_{ij}$  is a unique

<sup>\*</sup>Corresponding author: Ehtibar Dzhafarov, Purdue University, Department of Psychological Sciences, 703 Third Street West Lafayette, IN 47907, USA. Email: ehtibar@purdue.edu

minimum entry in the *j*th column, then the *i*th stimulus is less discriminable than any other stimulus in *X* from the *j*th stimulus in *Y*: the *i*th stimulus in *X* therefore can be considered the best match for the *j*th stimulus in *Y*. With this interpretation, RM states that every stimulus, in either observation area, has a unique best match in the other observation area, and the relation "is the best match for" is symmetric.<sup>1</sup>

In our examples above,  $M_1$  is RM-compliant: for instance, 1 is the unique minimum entry in the first row, and it is also the unique minimum entry in the column in which it occurs, the second one, so that the first row and the second column are each other's best matches; and analogously for the rowcolumn pairs (2,1), (3,3), (4,5), (5,4). By contrast,  $M_2$  does not satisfy RM, because, e.g., 12 is the unique minimum entry in the fifth row but not in the fifth column in which it occurs; another violation occurs in the second row, where 2.5 is the unique minimum value without being the unique minimum in its (second) column.

The notion of RM has been proposed in Dzhafarov (2002b) and elaborated in Dzhafarov (2003), Dzhafarov and Colonius (2006a), and Kujala and Dzhafarov (2008, 2009). It was shown to have nontrivial consequences for a variety of issues of traditional importance, ranging from Thurstonian-type modeling of discrimination probabilities (see, e.g., Dzhafarov, 2006, in response to Ennis, 2006) to the "probability-distance" hypothesis (Dzhafarov, 2002a) to Fechnerian Scaling (see, e.g., Dzhafarov & Colonius, 2007) to matching-by-adjustment procedures (Dzhafarov & Perry, 2010) to the comparative version of the ancient "sorites" paradox (Dzhafarov & Dzhafarov, 2010).

In an earlier paper (Trendtel, Ünlü, & Dzhafarov, 2010) a formula was derived for the proportion of RM-compliant matrices among all rank order matrices of a given size and with no ties among their entries. This proportion was given the following "meta-probabilistic" interpretation. Let the initial  $n^2$ entries of an  $n \times n$  matrix (before converting them into ranks) be theoretical values of a discriminability measure (e.g., discrimination probabilities), and let the set of all such values be a subset R of reals of a positive Lebesgue measure (e.g., the interval [0,1] in the case of probabilities). Impose on all  $n^2$  entries one and the same probability measure  $\mu$  absolutely continuous with respect to the Lebesgue measure. It can be loosely interpreted as a "random generator" of the theoretical discriminability values. Then in the space  $\Re^{n^2}$  the RMcompliant matrices occupy a certain subset, and the product measure  $\mu \times \ldots \times \mu$  (n<sup>2</sup> times) of this subset is interpreted as "the probability of obtaining an RM-compliant matrix by chance." Since the absolute continuity of  $\mu$  makes the product measure of matrices with tied values zero, and since the use of one and the same  $\mu$  for all entries makes all permutations of any given set of entries equiprobable, the product measure in question equals the proportion of RM-compliant matrices

among all  $n \times n$  rank order matrices with no ties.

In this paper the work done in Trendtel et al. (2010) is expanded in three directions. First, we propose a way of counting the number of violations of RM in a matrix, and we derive a formula for the proportion  $p_n^r$  of matrices with r violations of RM among all  $n \times n$  rank order matrices with no ties. The formula derived in Trendtel et al. (2010) corresponds to r = 0. Second, in addition to the "meta-probabilistic" interpretation mentioned above we propose a statistical interpretation of  $p_n^r$ in which  $p_n^{\leq r} = \sum_{i=0}^r p_n^i$  (the proportion of matrices with no more than r violations of RM) becomes the p-value of a permutation test. The null hypothesis of this test essentially says that "there is no order among the ranks," while the alternative hypothesis states that "few or no violations of RM occur more frequently than stated in the null hypothesis." Third, we propose a way of representing rank order matrices with ties by classes of rank order matrices without ties. If a matrix M (with ties allowed) is represented by a set  $\{M'_1, \ldots, M'_k\}$  of rank order matrices without ties, and if  $r_i$  denotes the number of violations of RM in  $M'_i$  (i = 1, ..., k), then the violations of RM in *M* are characterized by the vector of violations  $(r_1, \ldots, r_k)$ . In the permutation test a "surrogate *p*-value" (as explained in Section 6) for such a matrix may be computed as an unknown value within the interval  $\left[p_n^{\leq \min\{r_1,\ldots,r_k\}}, p_n^{\leq \max\{r_1,\ldots,r_k\}}\right]$ .

### 2. NUMBER OF VIOLATIONS OF RM

Recall Convention 1.1. In this section the matrices *are allowed to have ties*. The rows and columns of a matrix are identified by their ordinal positions: row 1, column 6, etc.

**Definition 2.1.** A column *j* of a matrix *M* is said to *match* (to be a match for) a row *i* if  $m_{ij}$  is the unique minimum entry in the row *i* (i.e.,  $j' \neq j \Rightarrow m_{ij'} > m_{ij}$ ). A row *i* is said to match (to be a match for) a column *j* if  $m_{ij}$  is the unique minimum entry in the column *j* (i.e.,  $i' \neq i \Rightarrow m_{i'j} > m_{ij}$ ). If a row *i* and a column *j* match each other, (i, j) is referred to as a *matching pair*.

**Lemma 2.2.** A match, if it exists, is unique: no row (column) can have more than one column (respectively, row) matching it. The set of all matching pairs in an  $n \times n$  matrix is a bijection  $\{i_1, \ldots, i_k\} \rightarrow \{j_1, \ldots, j_k\}, k \in \{0, \ldots, n\}.$ 

*Proof.* The uniqueness statement follows from the uniqueness of the minimum requirement in the definition of matching. In the set of matching pairs therefore, if  $(i, j) \neq (i', j')$ , then both  $i \neq i'$  and  $j \neq j'$ . The second statement of the lemma follows.

**Definition 2.3.** A row *i* (column *j*) of a matrix is said to be *RM-compliant* if it forms a matching pair with some column *j* (respectively, row *i*); if additionally i = j, we say that row *i* (column *j*) is RM-compliant in a *canonical form*. A row *i* (column *j*) which is not RM-compliant is called *RM-contravening*.

**Lemma 2.4.** Any RM-compliant row forms a matching pair with an RM-compliant column, and vice versa. The number of the RM-compliant rows equals the number of the RMcompliant columns. The number of the RM-contravening rows equals the number of the RM-contravening columns.

*Proof.* If  $\mathfrak{m}$  is the set of all matching pairs (i, j) then the set of all RM-compliant rows is the first projection of  $\mathfrak{m}$ , and the

<sup>&</sup>lt;sup>1</sup> The property (A) of RM should be qualified as follows. Two rows (or two columns) of a matrix are considered *equivalent* if they have identical entries. The uniqueness requirement (A) should be taken to hold up to this equivalence relation: in some initial (not even necessarily square) matrix the set of matching columns for any given row is nonempty and consists of pairwise equivalent columns, and the same holds for the set of rows matching a given column. Another way of stating this is to say that (A) holds after any two equivalent rows (or columns) in an initial matrix have been merged into a single one. See Dzhafarov and Colonius (2006a) for a more detailed discussion.

set of all RM-compliant columns is the second projection of m. The first two statements of the lemma follow. Since every row (column) is either RM-compliant or RM-contravening, the numbers of the RM-contravening rows and columns are also equal.

*Remark* 2.5. There is, obviously, no natural pairing of RM-contravening rows with RM-contravening columns.

*Remark* 2.6. A matrix satisfies the property of RM (Section 1) if and only if all of its rows (or columns) are RM-compliant. This paper, however, is also consistent with a "gradualized" view, in which the "degree" of the RM-compliance of an  $n \times n$  matrix with *r* RM-contravening rows (columns) is understood as 1 - r/n.

The number of violations of RM can be defined in more than one way. For instance, in each row *i* one could find the minimum  $d_i$  of its entries, determine the columns  $\{j_1, \ldots, j_{k_i}\}$  in which this minimum value occurs, and compute

$$\sum_{i=1}^{n} \left\{ k_i - 1 + \sum_{j \in \left\{ j_1, \dots, j_{k_i} \right\}} \sum_{i' \neq i} \operatorname{Truth} \left( m_{i'j} \leq d_i \right) \right\},\$$

where Truth is 1 or 0 according as the inequality holds or fails. This quantity equals 0 if and only if every row is RM-compliant (i.e., the matrix satisfies RM). If we exchange columns and rows in the formulation of this measure we will get another, generally different measure. We adopt, however, the following, arguably the simplest way of counting the violations.

**Definition 2.7.** The number of violations of RM in a matrix is the number of RM-contravening rows (or columns) it contains.

So the number of violations of RM in an  $n \times n$  matrix is a number between 0 (in which case the matrix is RM-compliant) and n.

**Lemma 2.8.** The number of violations of RM in a matrix is invariant with respect to arbitrary permutations of its rows and columns.

*Proof.* Let the number of violations of RM in an  $n \times n$  matrix M be  $r \in \{0, ..., n\}$ , whence the number of the matching pairs (i, j) in M is n - r. By arbitrary permutations  $\alpha$  and  $\beta$  of the rows and columns, respectively, we transform M into a matrix M'. Its entries  $m'_{ij}$  are related to the entries  $m_{ij}$  of M as

$$m'_{\alpha(i),\beta(j)} = m_{ij}.$$

If  $m_{ij}$  in M is the unique minimum entry in the row i, then  $m'_{\alpha(i),\beta(j)}$  in M' is the unique minimum entry in the row  $\alpha(i)$ , as the latter is merely the  $\beta$ -permutation of the row i of M; and if  $m_{ij}$  in M is the unique minimum entry in the column j, then  $m'_{\alpha(i),\beta(j)}$  in M' is the unique minimum entry in the column  $\beta(j)$ , as the latter is merely the  $\alpha$ -permutation of the column  $\beta(j)$ , as the latter is merely the  $\alpha$ -permutation of the column  $\beta(j)$ , as the latter is merely the  $\alpha$ -permutation of the column  $\beta(j)$ , as the latter is merely the  $\alpha$ -permutation of the column  $\beta(j)$  is a matching pair in M. It follows that if (i, j) is a matching pair in M, then  $(\alpha(i), \beta(j))$  is a matching pair in M'. Since permutations are injective, the number of the matching pairs in M' cannot be less than n - r. By obvious symmetry, if (i', j') is a matching pair in M, whence the number of the matching pairs in M' cannot be greater than n - r. The statement of the lemma follows.

# 3. MATRICES WITHOUT TIES

**Convention 3.1.** In this section the word "matrix" means a (rank order) matrix *without ties*. This convention will remain in force until Section 6.

**Lemma 3.2.** Let  $M_{\alpha\beta}$  be a matrix obtained from a matrix M by permutations  $\alpha$  and  $\beta$  of its rows and columns, respectively. Then  $M_{\alpha\beta} = M_{\alpha'\beta'}$  implies  $(\alpha, \beta) = (\alpha', \beta')$ .

*Proof.* Denoting  $M_{\alpha\beta} = M_{\alpha'\beta'} = M'$ , the entries of *M* and *M'* are related to each other as

and

$$m_{ij} = m'_{\alpha(i),\beta(j)}$$

$$m_{ij} = m'_{\alpha'(i),\beta'(j)}.$$

If  $(\alpha, \beta) \neq (\alpha', \beta')$  then for some (i, j),  $m'_{\alpha(i), \beta(j)}$  and  $m'_{\alpha'(i), \beta'(j)}$ would have to be two identical entries in different cells, which is excluded by Convention 3.1.

**Lemma 3.3.** The number of violations of RM in an  $n \times n$  matrix cannot exceed n - 1.

*Proof.* The row and the column containing the smallest entry, 1, are a matching pair.  $\Box$ 

**Lemma 3.4.** Let an  $n \times n$  matrix M contain n - r RMcompliant rows (and columns) with minima  $d_1, \ldots, d_{n-r}$  (and possibly some other RM-compliant rows and columns). By appropriately chosen permutations of rows and columns one can always (and uniquely) bring such an M to a special form M', in which

(a) the RM-compliant rows with minima  $d_1, \ldots, d_{n-r}$  are arranged in the increasing order of the row minima in the last n-r positions;

(b) the RM-compliant columns are placed so that these minima are on the main diagonal (in the increasing order);

(c) the remaining (upper left)  $r \times r$  submatrix of M' equals the  $r \times r$  submatrix of M formed by the remaining rows and columns.

*Remark* 3.5. A submatrix A' formed by rows and columns  $\{i_1^A < \ldots < i_r^A\} \times \{j_1^A < \ldots < j_r^A\}$  of a matrix A is considered equal to a submatrix B' formed by rows and columns  $\{i_1^B < \ldots < i_r^B\} \times \{j_1^B < \ldots < j_r^B\}$  of a matrix B if any entry  $a'_{i_k^A j_l^A}$  of A' equals the entry  $b'_{i_k^B j_l^B}$  of B', for  $k, l \in \{1, \ldots, r\}$ .

*Proof.* Let  $i_1, \ldots, i_{n-r}$  be the RM-compliant rows in M with minima  $d_1, \ldots, d_{n-r}$ , listed in the increasing order,

$$\min(d_1, \dots, d_{n-r}) = \min(m_{i_11}, \dots, m_{i_{1n}}) < \dots < \min(m_{i_{n-r}1}, \dots, m_{i_{n-r}n}) = \max(d_1, \dots, d_{n-r}),$$

and let these rows be matched by the (RM-compliant) columns  $j_1, \ldots, j_{n-r}$ , respectively. Let  $i_1^* < \ldots < i_r^*$  and  $j_1^* < \ldots < j_r^*$  be the remaining rows and columns (listed in their order of appearance in *M*). Then the permutations

are easily checked to yield the properties (a), (b), and (c). The uniqueness of this special form follows from the uniqueness of the sequences  $i_1^*, \ldots, i_r^*, i_1, \ldots, i_{n-r}$  and  $j_1^*, \ldots, j_r^*, j_1, \ldots, j_{n-r}$ .

**Definition 3.6.** We will call a matrix M' in the form satisfying (a), (b), and (c) of Lemma 3.4 a *special* matrix containing RM-compliant rows (and columns) with minima  $d_1, \ldots, d_{n-r}$  (possibly in addition to other RM-compliant rows and columns).

**Lemma 3.7.** Denoting by  $t_n^{\{d_1,...,d_{n-r}\}}$  the number of  $n \times n$  special matrices containing RM-compliant rows (and columns) with minima  $d_1,...,d_{n-r}$ , and denoting by  $T_n^{\{d_1,...,d_{n-r}\}}$  the number of all  $n \times n$  matrices with the same property,

$$T_n^{\{d_1,\dots,d_{n-r}\}} = [\operatorname{cmb}(n,n-r)]^2 t_n^{\{d_1,\dots,d_{n-r}\}}$$

where cmb is defined as

$$\operatorname{cmb}(x,y) = \begin{bmatrix} \frac{x!}{(x-y)!} & \text{if } x \ge y \ge 0, \\ 0 & \text{otherwise.} \end{bmatrix}$$

*Remark* 3.8. The combinatorial meaning of cmb(x, y) is the number of permutations of *x* objects taken *y* at a time (equivalently, the number of ways *y* distinct objects can be placed in *x* placeholders).

*Proof.* Any matrix M that can be transformed (in the sense of Lemma 3.4) to a given special matrix M' can be obtained from this M' by means of permutations

and

Since the positions  $i_1^* < ... < i_r^*$  are uniquely determined by the choice of  $(i_1, ..., i_{n-r})$ , the number of all distinct permutations  $\alpha^{-1}$  applicable to M' is the number of ways vectors  $(i_1, ..., i_{n-r})$  can be chosen among n rows, which is cmb(n, n-r). Analogously, the number of all distinct permutations  $\beta^{-1}$  applicable to M' is the number of ways vectors  $(j_1, ..., j_{n-r})$  can be chosen among n columns, again cmb(n, n-r). Since, by Lemma 3.2, every combination of  $\alpha^{-1}$  and  $\beta^{-1}$  yields a unique matrix M, the number of such matrices for a given M' is  $[\operatorname{cmb}(n, n-r)]^2$ . Two distinct special matrices M' and M'' cannot be transformed into one and the same M due to the uniqueness statement in Lemma 3.4. The statement of the lemma follows.

Recall that all the matrices mentioned are assumed to be without ties. This convention continues to hold in the next section.

## 4. MAIN THEOREM

We need the following two auxiliary results.

**Lemma 4.1.** Let  $T_n^{\{d_1,\ldots,d_{n-r}\}}$  be as in Lemma 3.7, and let  $U_n^{\{d_1,\ldots,d_{n-r}\}}$  denote the number of all  $n \times n$  matrices containing RM-compliant rows with minima  $d_1,\ldots,d_{n-r}$  and no other RM-compliant rows. Then, if r > 0,

$$U_n^{\{d_1,\dots,d_{n-r}\}} = T_n^{\{d_1,\dots,d_{n-r}\}} - \sum_{q=0}^{r-1} \sum_{d_{n-r+1} < \dots < d_{n-q}} U_n^{\{d_1,\dots,d_{n-r}\} \cup \{d_{n-r+1},\dots,d_{n-q}\}},$$

and if r = 0,

$$U_n^{\{d_1,\ldots,d_n\}} = T_n^{\{d_1,\ldots,d_n\}}$$

*Remark* 4.2. Note that presenting the superscripts in  $T_n^{\{...\}}$  and  $U_n^{\{...\}}$  as sets indicates that the elements of the sets can be written in any order without changing these numbers.

*Proof.* The sets of matrices included in the numbers  $U_n^{\{d_1,\ldots,d_{n-r}\}\cup\{d_{n-r+1},\ldots,d_{n-q}\}}$  and  $U_n^{\{d_1,\ldots,d_{n-r}\}\cup\{d'_{n-r+1},\ldots,d'_{n-q'}\}}$  are clearly disjoint, for any fixed  $\{d_1,\ldots,d_{n-r}\}$  and any distinct sets  $\{d_{n-r+1},\ldots,d_{n-q}\}$  and  $\{d'_{n-r+1},\ldots,d'_{n-q'}\}$   $(q,q' \in \{0,\ldots,r-1\})$ . The quantity

$$\sum_{q=0}^{r-1} \sum_{d_{n-r+1} < \ldots < d_{n-q}} U_n^{\{d_1, \ldots, d_{n-r}\} \cup \{d_{n-r+1}, \ldots, d_{n-q}\}}$$

therefore is the number of all matrices containing RM-compliant rows with the row minima  $d_1, \ldots, d_{n-r}$  and from 1 to *r* additional RM-compliant rows. The statement for r = 0 is obvious.

**Lemma 4.3.** Denoting by  $S_n^r$  the number of  $n \times n$  matrices with exactly  $r \in \{0, ..., n-1\}$  violations of RM,

$$S_n^r = \sum_{d_1 < \dots < d_{n-r}} U_n^{\{d_1, \dots, d_{n-r}\}}$$

and if r > 0, then for any  $q \in \{0, ..., r-1\}$ ,

$$\sum_{d_1 < \dots < d_{n-r}} \sum_{d_n - r+1 < \dots < d_{n-q}} U_n^{\{d_1, \dots, d_{n-r}\} \cup \{d_{n-r+1}, \dots, d_{n-q}\}} = \binom{n-q}{r-q} S_n^q.$$

*Proof.* The first equality follows from the definitions of  $S_n^r$  and  $U_n^{\{d_1,\ldots,d_{n-r}\}}$ , on observing that the sets of matrices counted in the number  $U_n^{\{d_1,\ldots,d_{n-r}\}}$  for different choices of  $\{d_1,\ldots,d_{n-r}\}$  are disjoint. The second equality then follows from presenting

$$S_n^q = \sum_{d_1 < \dots < d_{n-q}} U_n^{\{d_1, \dots, d_{n-q}\}}$$
  
=  $\sum_{d_1 < \dots < d_{n-q}} U_n^{\{d_1, \dots, d_{n-r}\} \cup \{d_{n-r+1}, \dots, d_{n-q}\}}$ 

and observing that in the double-sum

$$\sum_{d_1 < \ldots < d_{n-r}} \sum_{d_n - r < d_n - r+1 < \ldots < d_{n-q}} U_n^{\{d_1, \ldots, d_{n-r}\} \cup \{d_{n-r+1}, \ldots, d_{n-q}\}}$$

each vector  $d_1 < \ldots < d_{n-q}$  occurs  $\binom{n-q}{n-r} = \binom{n-q}{r-q}$  times.

In the proof of our main result below we use the following notion. In an  $n \times n$  matrix M the *kth frame*, k = 1, ..., n, is defined as the set of cells

$$\{(k,j): j < k\} \cup \{(i,k): i < k\}.$$

The number of cells in the *k*th frame is 2(k-1).

**Theorem 4.4.** The number  $S_n^r$  of  $n \times n$  matrices with exactly  $r \in \{0, ..., n-1\}$  violations of RM is given by the recursive formula

$$S_n^0 = (n!)^2 \sum_{d_1 < \dots < d_n} \prod_{k=1}^n \operatorname{cmb}\left(k^2 - d_k, 2(k-1)\right)$$

$$\begin{split} S_n^r &= [\operatorname{cmb}(n, n-r)]^2 r^2! \\ &\times \sum_{d_{r+1} < \dots < d_n} \prod_{k=r+1}^n \operatorname{cmb}\left(k^2 - d_k, 2(k-1)\right) \\ &- \sum_{q=0}^{r-1} \binom{n-q}{r-q} S_n^q, \end{split}$$

where  $d_i \in \{1, ..., n^2\}$ , i = 1, ..., n.

*Proof.* Let  $r \in \{0, ..., n-1\}$  be chosen, and let the n-r bottom-right diagonal entries in the matrix M be chosen and arranged as

$$d_{r+1} = m_{r+1,r+1} < \ldots < d_n = m_{nn}.$$

We begin by computing the number of ways in which we can fill the last n - r frames of M so that the last n - r rows and columns of M are RM-compliant in a canonical form (this will be referred to below as "RM requirements").

The *n*th frame should be filled by 2(n-1) ranks chosen from the set of  $n^2 - d_n$  ranks exceeding  $d_n$ . The number of such choices is

$$\operatorname{cmb}\left(n^{2}-d_{n},2\left(n-1\right)\right).$$
 (1)

Any of these choices complies with the RM requirements, because any rank exceeding  $d_n$  will also exceed any  $d_k$  for k < n.

For  $k \in \{r+1, ..., n-1\}$ , let now all the frames from the (k+1)st to the *n*th have been filled in compliance with the RM requirements. The *k*th frame then should be filled by 2(k-1) numbers chosen from the set of  $n^2 - d_k$  numbers exceeding  $d_k$ , from which however we should remove all the  $n^2 - k^2$  numbers used up in the previously filled frames and higher-up diagonal elements. That is, the *k*th frame can be filled in by

$$(n^2 - d_k) - (n^2 - k^2) = k^2 - d_k$$

numbers taken 2(k-1) at a time. The number of such choices is

$$\operatorname{cmb}(k^2 - d_k, 2(k-1))$$

Any of these choices complies with the RM requirements, because any rank exceeding  $d_k$  also exceeds any  $d_{k'}$  for k' < k, and if k' > k then the choice above is irrelevant. Since the quantity cmb  $(k^2 - d_k, 2(k-1))$  does not depend on the fillings of any of the frames k' > k, the number of ways of filling all the n - r last frames of M is

$$\prod_{k=r+1}^{n} \operatorname{cmb}\left(k^{2}-d_{k},2\left(k-1\right)\right)$$

If r = 0, the formula above shows the number of possible fillings of the entire matrix for a given choice of the diagonal elements  $d_1 < ... < d_n$ , i.e., the number  $t_n^{\{d_1,...,d_n\}}$  of special matrices in accordance with Definition 3.6. By Lemmas 3.7, 4.1, and 4.3 then

$$S_n^0 = \sum_{d_1 < \dots < d_n} (n!)^2 \prod_{k=1}^n \operatorname{cmb} \left( k^2 - d_k, 2(k-1) \right) = (n!)^2 \sum_{d_1 < \dots < d_n} \prod_{k=1}^n \operatorname{cmb} \left( k^2 - d_k, 2(k-1) \right).$$

This result (known from Trendtel et al., 2010) forms the basis of the recursive formula in the formulation of the theorem.

Assuming now that r > 0, the remaining  $r \times r$  submatrix can be filled in  $r^2$ ! ways, given any filling of the last n - r frames and diagonal elements, and it is easy to see that no filling of this submatrix would violate the RM requirements (for the last n - r rows and columns). The quantity

$$r^{2}!\prod_{k=r+1}^{n}\operatorname{cmb}\left(k^{2}-d_{k},2\left(k-1\right)\right)$$

is the number  $t_n^{\{d_{r+1},\dots,d_n\}}$  of special matrices in accordance with Definition 3.6, whence

$$T_n^{\{d_{r+1},\dots,d_n\}} = \left[\operatorname{cmb}\left(n,n-r\right)\right]^2 r^2! \prod_{k=r+1}^n \operatorname{cmb}\left(k^2 - d_k, 2\left(k-1\right)\right)$$

by Lemma 3.7. Applying to this result Lemma 4.1 and Lemma 4.3 (having noted the change in the enumeration of the d's),

$$\begin{split} S_n^r &= \sum_{d_{r+1} < \ldots < d_n} U_n^{\{d_{r+1},\ldots,d_n\}} = \sum_{d_{r+1} < \ldots < d_n} T_n^{\{d_{r+1},\ldots,d_n\}} \\ &- \sum_{d_{r+1} < \ldots < d_n} \sum_{\substack{q=0 \ T_q = 0}} \sum_{d_1 < \ldots < d_{r-q}} U_n^{\{d_1,\ldots,d_{r-q}\} \cup \{d_{r+1},\ldots,d_n\}} \\ &= \sum_{d_{r+1} < \ldots < d_n} T_n^{\{d_{r+1},\ldots,d_n\}} \\ &- \sum_{\substack{q=0 \ T_q = 0}} \sum_{d_1 < \ldots < d_{r-q}} \sum_{d_{r+1} < \ldots < d_n} U_n^{\{d_1,\ldots,d_{r-q}\} \cup \{d_{r+1},\ldots,d_n\}} \\ &= [\operatorname{cmb}(n,n-r)]^2 r^2! \\ &\times \sum_{d_{r+1} < \ldots < d_n} \prod_{\substack{k=r+1 \ \text{cmb}}}^n (k^2 - d_k, 2(k-1)) \\ &- \sum_{\substack{q=0 \ r-q}}^{r-1} \binom{n-q}{r-q} S_n^q. \end{split}$$

The recursive formula for  $S_n^r$  in the formulation of the theorem follows.

**Corollary 4.5.** Assuming all  $n \times n$  matrices are equiprobable, the probability  $p_n^r$  that a randomly chosen matrix has r violations of RM is

$$p_n^r = \frac{S_n^r}{n^2!}$$

where  $S_n^r$  is as in Theorem 4.4.

#### 5. PERMUTATION TEST

We will now use the above combinatorial results to construct a *permutation test* (Good, 2005; Pitman, 1937a-b; Welch, 1990) for the number of violations of RM. Let M now be a rank order matrix representing a data matrix. In the beginning, let us continue to assume that the matrix contains no ties (those will be dealt with in the next section). Intuitively, it is compelling to think that if the size n of M is sufficiently large and the number r of RM violations is sufficiently small, then we have evidence in favor of RM: it seems unlikely that a large amount of structure (here, many RM-compliant rows and columns) occurs "by chance alone." The idea of the "chance" can be formalized by adopting the following proposition as our null hypothesis: *all rank order matrices (i.e., all permutations of the ranks*  $1, ..., n^2$ ) *are equiprobable*. This is the assumption of "no structure." If it is correct, then an  $n \times n$  matrix with r violations of RM occurs with the probability  $p_n^r$  derived in the previous section.

Now, any structure discernible in *M* speaks against this null hypothesis (e.g., larger numbers prevailing above the main diagonal, or even numbers alternating with the odd ones as one reads the matrix row by row), but we are interested in an alternative hypothesis that would make a matrix with smaller number of violations of RM less consistent with the null hypothesis than a matrix with larger number of violations of RM. The least committed formulation of this alternative hypothesis is: for any  $r \in \{0, ..., n-2\}$ , the probability of obtaining a matrix with no more than r violations of RM is greater than follows from the null hypothesis. (The value r = n - 1 is not included because the probability of no more than n - 1 violations is 1.) This assumption can be dubbed "nature favors matching row-column pairs," or "nature favors RM," for short.

It is clear now, that if our matrix M contains r violations, then the probability, under the null hypothesis, of obtaining a matrix with as many or fewer violations of RM will serve as the p-value of our test. In other words, given r violations,

$$p$$
-value =  $p_n^{\leq r} = \sum_{i=0}^r p_n^i$ .

The numerical tables in Appendix show  $p_n^r$  and  $p_n^{\leq r}$  for values of *n* ranging from 2 to 25. Thus, if one obtains a 7 × 7 matrix with just one violation of RM, at the significance level 0.05 one should reject the null hypothesis (of "no structure") in favor of the alternative hypothesis (that "nature favors RM"). In a 20 × 20 matrix, if the number of violations exceeds 6, the hypothesis of "no structure" at the same level of significance cannot be rejected.<sup>2</sup>

It is always possible, of course, that our test will reject the null hypothesis ("in favor of RM") and at the same time the RM-compliance of the entire matrix (or the "complete" RM-compliance, in the gradualized view mentioned in Remark 2.6) will be rejected by another test.<sup>3</sup> Thus, if the entries of the data matrix are probability estimates for responses "different," it is conceivable that, by treating a theoretical matrix as a set of independent binomial variables, a confidence region consisting of the theoretical matrices that agree with the data matrix will not contain matrices without RM violations, even if the permutation test *p*-value is very small. The issue of what one's decisions in such cases should be has complex ramifications, ranging from those applicable to all resampling tests to those more specific to RM. A detailed discussion is outside the scope of this paper.

## 6. HOW TO DEAL WITH TIES

The definition for the number of violations of RM given in Section 2 applies to matrices with ties, but the probability  $p_n^r$ derived in Section 4 does not. There are two ways of dealing with ties. A direct one is to consider a set V of possible values for cells of a matrix (before the latter has been converted into the rank order form), formulate the null hypothesis in terms of chances for each element of V to fall within each cell, and to derive the distribution of the number of RM violations under this hypothesis. Such a theory, if it were applicable to any set V, would have included the one developed in this paper as a special case. Another approach is to stay with rank order matrices, find a way of approximating a matrix containing ties by its several "untied versions," and to gauge how small the numbers of RM violations are in these untied matrices under the null hypothesis of equiprobable permutations. This is the approach we adopt in this paper.

Henceforth we drop Convention 3.1. Convention 1.1 remains in force: all matrices are rank order ones, *unless otherwise specified* (as will be the case with the "*G*-untied versions" in the next section).

**Definition 6.1.** A matrix M' without ties is said to be *an un*tied version of a matrix M (with possible ties) if  $m'_{ij} < m'_{i'j'}$  in M' whenever  $m_{ij} < m_{i'j'}$  in M. If  $\{M'_1, \ldots, M'_k\}$  is the set of all untied versions of M, then, denoting by  $r_i$  the number of violations of RM in  $M'_i$ , the vector  $(r_1, \ldots, r_k)$  is said to *char*acterize violations of RM in M.

Clearly,  $(r_1, \ldots, r_k)$  is determined by a matrix M uniquely up to arbitrary permutations, and k lies between 1 and  $n^2$ !  $(k = 1 \text{ indicating a matrix without ties}, k = n^2!$  a matrix with the value  $(1+n^2)/2$  in all cells). One cannot associate any pvalue with  $(r_1, \ldots, r_k)$  because we have formulated no null hypothesis for the distribution of matrices with possible ties. We resort therefore to the computation of a "surrogate p-value,"  $P_n(r_1,\ldots,r_k)$ , whose meaning is established as follows.<sup>4</sup> Let *R* be a random variable representing the number of RM violations in matrices without ties, distributed as specified by the null hypothesis. If we are told that the observed value of R is r, then the *p*-value is  $p_n^{\leq r}$ . A matrix with possible ties, however, is characterized by a vector  $(r_1, \ldots, r_k)$ . We treat this situation "as if" we were told that the observed number of RM violations in a matrix without ties (i.e., a value of R) belonged to the vector  $(r_1, \ldots, r_k)$ . With this interpretation in mind, the surrogate *p*-value  $P_n(r_1, \ldots, r_k)$  is the answer to the question: what is the probability that R does not exceed a number randomly chosen from the vector  $(r_1, \ldots, r_k)$ ?

Adopting the natural convention that "randomly chosen" here means chosen with probability 1/k, the rigorous procedure is to "roll a fair *k*-sided die," choose  $r_i$  and put  $P_n(r_1,...,r_k) = p_n^{\leq r_i}$ . If this value is very small we reject the null hypothesis that all matrices without ties are equiprobable. To justify calling  $P_n(r_1,...,r_k)$  a *p*-value, even if "surrogate," note that when considered a random variable this probability has a discrete uniform distribution over its attainable values.

<sup>&</sup>lt;sup>2</sup> It is worth mentioning that  $1 - p_n^{\leq r}$  may also be looked at as a "metaprobabilistic" quantification of one's "surprise" at observing n - r matching row-column pairs in the absence of prior knowledge of any structural regularities in the matrix, even if its entities are deterministic, such as theoretical probabilities or theoretical means, with no sampling error involved (see the penultimate paragraph of Section 1).

<sup>&</sup>lt;sup>3</sup> We are grateful to Janne Kujala for bringing up this issue.

<sup>&</sup>lt;sup>4</sup> We are grateful to Matt Jones for pointing out a mistake in the initial version of the proposed computation.

Indeed, with obvious notation,

$$P_n(R_1,\ldots,R_k) = \begin{cases} p_n^{\leq R_1} & \text{with probability } 1/k \\ \vdots & \vdots & \vdots \\ p_n^{\leq R_k} & \text{with probability } 1/k \end{cases},$$

and since each  $R_i$  is distributed as R, we have

$$\Pr[P_n(R_1,...,R_k) \le p] = \sum_{i=1}^k \Pr\left[p_n^{\le R_i} \le p\right] \frac{1}{k} = p \sum_{i=1}^k \frac{1}{k} = p.$$

for any attainable value *p* and any given *k*.

In practice, it may be sufficient to estimate the unknown value of  $P_n(r_1, ..., r_k)$  by the interval

$$\begin{bmatrix} \min\left\{p_n^{\leq r_1}, \dots, p_n^{\leq r_k}\right\}, \max\left\{p_n^{\leq r_1}, \dots, p_n^{\leq r_k}\right\} \end{bmatrix}$$
$$= \begin{bmatrix} p_n^{\leq \min\{r_1, \dots, r_k\}}, p_n^{\leq \max\{r_1, \dots, r_k\}} \end{bmatrix}.$$

With this approach one should be prepared in some cases to abstain from choosing between retention and rejection of the null hypothesis at a given significance level.

As the next lemma shows, the factual number r of violations of RM in M in accordance with Definition 2.7 is not related in any simple way to the vector of violations  $(r_1, \ldots, r_k)$ , except that r cannot be lower than any of the  $r_i$ 's.

**Lemma 6.2.** Any matching row-column pair (i, j) in a matrix M is also a matching pair in any untied version of M. If the violations of RM in M are characterized by a vector  $(r_1, \ldots, r_k)$ , and the number of violations of RM in M is r, then  $r \ge \max{r_1, \ldots, r_k}$ , with both equality and strict inequality possible.

*Proof.* If (i, j) is a matching row-column pair in M, then  $m_{ij} < m_{i'j}$  for all  $i' \neq i$  and  $m_{ij} < m_{ij'}$  for all  $j' \neq j$ . By definition, the same inequalities hold between the corresponding entries of any untied version M' of M. Hence (i, j) is a matching pair in M', and no M' can have fewer matching pairs (equivalently, more violations of RM) than M. That the equality  $r = \max{r_1, \ldots, r_k}$  is possible is shown by an example: the matrix

$$M = \left[ \begin{array}{rrr} 1 & 7 & 3 \\ 5 & 5 & 5 \\ 2 & 8 & 9 \end{array} \right]$$

has r = 2 violations, and its untied versions are

$$M_{1}' = \begin{bmatrix} 1 & 7 & 3 \\ 4 & 5 & 6 \\ 2 & 8 & 9 \end{bmatrix}, M_{2}' = \begin{bmatrix} 1 & 7 & 3 \\ 4 & 6 & 5 \\ 2 & 8 & 9 \end{bmatrix}, M_{3}' = \begin{bmatrix} 1 & 7 & 3 \\ 5 & 4 & 6 \\ 2 & 8 & 9 \end{bmatrix},$$
$$M_{4}' = \begin{bmatrix} 1 & 7 & 3 \\ 5 & 6 & 4 \\ 2 & 8 & 9 \end{bmatrix}, M_{5}' = \begin{bmatrix} 1 & 7 & 3 \\ 6 & 4 & 5 \\ 2 & 8 & 9 \end{bmatrix}, M_{6}' = \begin{bmatrix} 1 & 7 & 3 \\ 6 & 5 & 4 \\ 2 & 8 & 9 \end{bmatrix},$$

yielding the vector of violations (2, 2, 1, 2, 1, 2). The strict inequality  $r > \max\{r_1, \ldots, r_k\}$  will hold whenever r = n (because, by Lemma 3.3,  $r_i \le n - 1$ ). To show that this is not the only case, consider

$$M = \left[ \begin{array}{rrrr} 1 & 6 & 7 \\ 4 & 2.5 & 2.5 \\ 8.5 & 8.5 & 5 \end{array} \right]$$

with r = 2 violations of RM. Its untied versions are

$$M_1' = \begin{bmatrix} 1 & 6 & 7 \\ 4 & 2 & 3 \\ 8 & 9 & 5 \end{bmatrix}, M_2' = \begin{bmatrix} 1 & 6 & 7 \\ 4 & 2 & 3 \\ 9 & 8 & 5 \end{bmatrix},$$
$$M_3' = \begin{bmatrix} 1 & 6 & 7 \\ 4 & 3 & 2 \\ 8 & 9 & 5 \end{bmatrix}, M_4' = \begin{bmatrix} 1 & 6 & 7 \\ 4 & 3 & 2 \\ 9 & 8 & 5 \end{bmatrix},$$

with the vector of violations (1, 1, 1, 1).

A large data matrix may contain several groups of cells with many tied entries in each group, making the number of the untied versions of the data matrix very large. The analysis can be simplified by using only *reduced vectors of RM violations*, as explained below.

## 7. REDUCED VECTORS OF RM VIOLATIONS

Let us denote by  $\mathcal{R}_{\mathcal{M}}(i, j)$ , the following statement about a cell (i, j) of a matrix M: the entry  $m_{ij}$  is the minimal value in this row, and for some  $j' \neq j$ ,  $m_{ij'} = m_{ij}$ . The "transposed" version of this statement is denoted  $C_M(i, j)$ : the entry  $m_{ij}$  is the minimal value in this column, and for some  $i' \neq i$ ,  $m_{i'j} = m_{ij}$ . Clearly,  $\mathcal{R}_M(i, j)$  and  $C_M(i, j)$  imply that the row *i* (respectively, column *j*) are RM-contravening. We define a set of cells *G* as

$$G = \{(i, j) : \mathcal{R}_{\mathcal{M}}(i, j) \text{ or } \mathcal{C}_{\mathcal{M}}(i, j)\}.$$

This set is either empty or it contains at least two cells.

Given an *M* and its untied version *M'*, let an entry *a* occur  $g \ge 0$  times within *G* in *M* and  $t \ge g$  times overall in *M* (t > 0). The following table illustrates the procedure of creating a matrix  $M^*$  called the *G*-untied version of *M* corresponding to M':

cells:	$(i, j)_1$	 $(i,j)_g$	$  (i, j)_{g+1}$	 $(i, j)_t$	
value in $M$ :	а	 a	a	 а	
value in $M'$ :					
value in $M^*$ :	$a - \frac{g-1}{2}$	 $a + \frac{g-1}{2}$	a	 а	

The sequence of cells  $(i, j)_1 \dots (i, j)_g$  within *G* is arranged so that  $a_1 < \dots < a_g$ , and the rest of the cells containing *a* in *M* are arranged so that  $a_{g+1} < \dots < a_t$ .

**Convention 7.1.** We will refer to such a table as the *table of arrangements* for a certain value (in this case, *a*) in *M*.

Note that by the definition of tied ranks (Section 1), *a* is the mean of  $\{a_1, \ldots, a_t\}$ , and that this set consists of all integers ranging from  $a - \frac{t-1}{2}$  to  $a + \frac{t-1}{2}$ . We compute the corresponding values in  $M^*$  by replacing every  $a_k$  outside *G* with  $a \ (k = g + 1, \ldots, t)$ , and replacing every  $a_k$  within *G* by a - (g-1)/2 + k - 1 ( $k = 1, \ldots, g$ ). These numbers form the arithmetic progression with difference 1 of which *a* is the mean. The correspondence of  $M^*$  to M' is in that these numbers are sorted in the same way as  $a_1 < \ldots < a_g$ . We create the matrix  $M^*$  by performing this procedure for all distinct values *a* in *M*.

If g = t in the table of arrangements for every value *a* in *M*, the procedure results in  $M^* = M'$ . Note, however, that if g < t for some *a*, the resulting matrix  $M^*$  is not, generally,

a rank-order matrix, as illustrated by the following table of arrangements:

cells:	$(i, j)_1$	$(i, j)_2$	$(i, j)_{3}$	$  (i, j)_4$
value in M :	4.5	4.5	4.5	4.5
value in $M'$ :	3	4	5	6 .
value in $M^*$ :	3.5	4.5	5.5	4.5

No rank-order matrix can have entries 3.5, 4.5, 4.5, 5.5.

**Lemma 7.2.** Let  $M^*$  be the *G*-untied version of *M* corresponding to an untied version M' of *M*. Then  $M^*$  and M' have the same set of matching row-column pairs, hence the same number of *RM* violations.

*Proof.* If (i, j) is a matching row-column pair in M', then  $m'_{ij} < m'_{i'j}$  for all  $i' \neq i$  and  $m'_{ij} < m'_{ij'}$  for all  $j' \neq j$ . Consider the former inequalities first. By Definition 6.1, they imply that in the matrix M, for any  $i' \neq i$ , either  $a = m_{ij} < m_{i'j} = b$  or  $m_{ij} = m_{i'j} = a$ . In the former case, let the counts of a and b in M be  $t_a$  and  $t_b$ , respectively. Then

$$a + \frac{t_a - 1}{2} < b - \frac{t_b - 1}{2}$$

so the ranges of values in M' corresponding to a and b do not overlap. From the tables of arrangements for a and for b it is clear then that the same is true for the ranges of values in  $M^*$  corresponding to a and b. In particular,  $m_{ij}^* < m_{i'j}^*$ . In the case  $m_{ij} = m_{i'j} = a$ , the cells (i, j) and (i, j') fall within G, and the table of arrangements for a then shows that  $m_{ij}^* < m_{i'j}^*$ . The proof that  $m'_{ij} < m'_{ij'}$  implies  $m_{ij}^* < m_{i'j}^*$  being analogous, we have established that if (i, j) is a matching row-column pair in M' then so is it also in  $M^*$ . The reverse is demonstrated in a similar way, departing from the observation, apparent from the tables of arrangements, that if  $m_{ij}^* < m_{i'j}^*$  then either a = $m_{ij} < m_{i'j} = b$  or  $m_{ij} = m_{i'j} = a$ .

**Lemma 7.3.** Each *G*-untied version  $M^*$  of *M* corresponds to the same number of untied versions M' of *M*.

*Proof.* Consider the table of arrangements for an arbitrary value *a* in *M*. A given  $M^*$  corresponding to an untied version  $M'_1$  also corresponds to another untied version,  $M'_2$ , if and only if, for any *a*, either the matrices  $M'_1$  and  $M'_2$  contain different selections of t - g entries (for the cells outside *G*) from the set of all integers ranging from  $a - \frac{t-1}{2}$  to  $a + \frac{t-1}{2}$ , or they contain different permutations of such a selection. Let  $(m_1, g_1, t_1), \ldots, (m_N, g_N, t_N)$  be the set of all triads containing distinct entries  $m_i$  in *M* with their counts  $g_i$  within *G* and overall counts,  $t_i$ . Then the number of the matrices M' to which a given  $M^*$  corresponds is

$$\prod_{i=1}^{N} \operatorname{cmb}(t_{i}, t_{i} - g_{i}) = \prod_{i=1}^{N} \frac{t_{i}!}{g_{i}!}.$$

This number does not depend on the matrix  $M^*$ .

It follows that it is always sufficient to characterize the RM violations in a matrix M by the vector  $(r_1, \ldots, r_l)$  of the numbers of RM violations in all G-untied versions  $M_1^*, \ldots, M_l^*$  of M. We will call this vector of RM violations *reduced*. Since in the full vector of RM violations all the  $r_i$ 's of the reduced vector are merely replicated a constant number of times, the computation of surrogate p-values remains unchanged.

## 8. TWO ILLUSTRATIONS

Let us illustrate both the permutation test and our method of dealing with ties on real data. In Dzhafarov and Colonius (2006b) a certain procedure (Fechnerian Scaling) which is predicated on RM was applied to data matrices taken from Rothkopf (1957) and Wish (1967). The two data matrices, however, contain violations of RM, so their use in Dzhafarov and Colonius (2006b) was justified by deeming the matrices to provide compelling evidence for RM in spite of these violations. We now can quantify this judgment.

Rothkopf's (1957) data set can be arranged in a  $36 \times 36$  matrix of pairwise discrimination frequencies (among 36 auditory Morse codes). 35 of the rows and columns of this matrix are RM-compliant in the canonical form, but the second row contains two identical minimal values:

		j = 2		j = 24	
÷	·	:	۰.		·
i = 2	• • •	0.16		0.16	
÷	·	:	·	••••	·
i = 24		·		0.09	
÷	·	:	·		·

All other entries in column 2 are greater than 0.16. So there is one violation of RM in this matrix in accordance with Definition 2.7, and the set *G* consists of the cells (2,2) and (2,24). Depending on how one breaks the tie between them, the number of RM violations in the *G*-untied version of Rothkopf's matrix will be 0 or 1. In other words, the RM violations in the data matrix are characterized by the reduced vector (0, 1). The surrogate *p*-value of the permutation test therefore ranges between  $p_{36}^0 \approx 5 \cdot 10^{-21}$  and  $p_{36}^{\leq 10} \approx 6 \cdot 10^{-18}$ , definitely rejecting the null hypothesis at any conventional significance level.

Wish's (1967) data consist of pairwise discrimination frequencies among 32 auditory Morse-code-like signals. They are arranged in a  $32 \times 32$  matrix in which 30 rows and columns are RM-compliant in the canonical form. The two RMcontravening rows and columns exhibit the following pattern:

$\dots j = 20 \dots j = 22 \dots$						
÷	۰.	•••	·	•••	۰.	
i = 20		0.06		0.03		
÷	·	••••	·	••••	۰.	
<i>i</i> = 22		•••		0.03		
÷	·.	•	·	•	•••	

All other entries in rows 20, 22 and column 22 are greater than 0.03 and all other entries in column 20 are greater than 0.06. The set *G* here is {(20,22),(22,22)}. It is easy to see that irrespective of how one breaks the tie in column 22, we end up with just one violation of RM: if the rank of the entry in (20,22) precedes that of the entry in (22,22) then *i* = 20 and *j* = 22 form a matching pair; and if the order of the ranks reverses, a matching pair is formed by *i* = 22 and *j* = 22. This means that the RM violations in the data matrix are characterized by the reduced vector (1,1). The surrogate *p*-value of the test is then  $p_{32}^{\leq 1} \approx 10^{-15}$ , again well below any conventional significance level.

# 9. COMPUTATIONAL ALGORITHM

In formula

$$S_{n}^{r} = [\operatorname{cmb}(n, n-r)]^{2}r^{2}! \times \sum_{d_{r+1} < \dots < d_{n}} \prod_{k=r+1}^{n} \operatorname{cmb}(k^{2} - d_{k}, 2(k-1)) - \sum_{q=0}^{r-1} {n-q \choose r-q} S_{n}^{q},$$

the expression

$$v_n^r = \sum_{d_{r+1} < \dots < d_n} \prod_{k=r+1}^n \operatorname{cmb}\left(k^2 - d_k, 2(k-1)\right)$$

can be rewritten in a computationally more economic way, using the inequalities  $d_{r+1} \ge 1$ ,  $d_k \ge d_{k-1} + 1$  for k > r+1, and  $d_k \le k^2 - 2(k-1)$  for k = r+1, ..., n:

$$v_n^r = \sum_{\substack{d_{r+1}=1\\ \dots \sum_{\substack{j=2\\d_i=d_{j-1}+1\\ \dots \sum_{\substack{d_i=d_{n-1}+1\\d_n=d_{n-1}+1}}}^{(r+1)^{2-2r}} \frac{1}{(k^2-d_i)!} \prod_{\substack{k=1\\k=r+1}}^{n} \frac{(k^2-d_k)!}{(k^2-d_k-2k+2)!}$$

This expression can be made still more economic computationally if we rewrite it as

$$v_n^r = \sum_{d_{r+1}=1}^{(r+1)^2 - 2r} \frac{((r+1)^2 - d_{r+1})!}{((r+1)^2 - d_{r+1} - 2r)!}$$
$$\cdots \sum_{d_j=d_{j-1}+1}^{j^2 - 2(j-1)} \frac{(j^2 - d_j)!}{(j^2 - d_j - 2j + 2)!}$$
$$\cdots \sum_{d_n=d_{n-1}+1}^{n^2 - 2(n-1)} \frac{(n^2 - d_n)!}{(n^2 - d_n - 2n + 2)!}$$

**Algorithm 9.1.** The following is a Mathematica<sup>TM</sup> program for computing precise vectors  $(p_n^0, p_n^1, ..., p_n^{n-1})$  and  $(p_n^0, p_n^{\leq 1}, ..., p_n^{\leq n-1})$  for arbitrary values of n:

A variant of this code was used to compute the tables in Appendix, as well as the surrogate *p*-values in Section 8.

# 10. OTHER MEANINGS OF "BY CHANCE"

Our notion of a matrix being obtained "by chance" is based on the null hypothesis adopted in our permutation test. This hypothesis states that all rank order matrices (equivalently, all permutations of a given set of entries, without ties) are equiprobable. One might object against this choice of the null hypothesis on the grounds that it is "obviously false," perhaps even too easy to reject. As a matter of logic of statistical testing this objection can be countered by pointing out that most if not all null hypotheses do not aim at describing a realistic population scenario. Rather they depict some intuitive notion of "no change," "no relation," or "no structure." One can also point out that the rejection of our null hypothesis is not based on finding just any kind of structure in a matrix, but a particular kind of structure only, the "degree of adherence" to RM. The probabilities shown in the tables in Appendix do not seem to support the expectation that with this kind of structure the null hypothesis should be too easy to reject (although the expectation being unquantifiable it cannot be definitively refuted either). Thus, a  $15 \times 15$  matrix with 5 violations of RM can be thought of as revealing a considerable amount of structure "of the right kind," 2/3 of its rows and columns being RMcompliant. Nevertheless, at conventional significance levels it should be deemed to be consistent with the hypothesis that all permutations are equiprobable, as  $p_{15}^{\leq 5} = 0.097$ .

With all this said, however, it is always possible and perfectly reasonable to modify the null hypothesis in light of additional knowledge. Thus, all rank order matrices without ties have the property of every row and every column in them possessing a single minimum. Suppose that we know, in addition, that the discriminability values (hence also the ranks representing them) monotonically increase as one moves within any row or any column away from its minimum entry. In other words, if  $m_{ij}$  is the minimum entry in the row *i*, then  $m_{ik_1} < m_{ik_2}$  whenever  $j < k_1 < k_2$  and  $m_{ik_1} > m_{ik_2}$  whenever  $k_1 < k_2 < j$  (and analogously for columns). The matrices with this property form a proper subset of the set of all rank order matrices without ties, and it is reasonable then to take for the null hypothesis that all matrices within this subset are equiprobable. The alternative hypothesis is modified accordingly: for any  $r \in \{0, ..., n-2\}$ , the probability of obtaining a matrix within the subset in question with no more than r violations of RM is greater than follows from the null hypothesis.

Another example:<sup>5</sup> suppose we somehow know that, with a certain arrangement of rows and columns of a matrix, the match of the match for a row *i* or a column *j* in the matrix cannot deviate from *i* (respectively, *j*) by more than a certain value  $\Delta$ . Recall that the (best) match for a row *i* is the column h(i) such that  $m_{i,h(i)}$  is the smallest value in the *i*th row; and the (best) match for a column *j* is the row g(j) such that  $m_{g(j),j}$  is the smallest value in the *j*th column (matches are uniquely determined in a matrix without ties). So our hypothetical knowledge is that  $|g(h(i)) - i| \leq \Delta$  and  $|h(g(j)) - j| \leq \Delta$  for all *i* and *j*. Then the null hypothesis can be formulated as the assumption that all matrices satisfying these inequalities occur equiprobably, with the alternative hypothesis reformulated accordingly. Clearly, the smaller the value of  $\Delta$ , the smaller the number of RM violations at which the null hypothesis is reformance.

<sup>&</sup>lt;sup>5</sup> This example is prompted by a comment by Matt Jones.

jected at a given significance level.

Generalizing, given any nonempty subset  $\mathfrak{M}$  of the set of all rank order matrices (without tied entries), one can test the null hypothesis that all matrices within  $\mathfrak{M}$  are equiprobable against the alternative hypothesis that within  $\mathfrak{M}$  "nature favors RM." The *p*-value in this test is computed as the ratio of the number of matrices in  $\mathfrak{M}$  with *r* or fewer violations of RM to the total number of matrices in  $\mathfrak{M}$ .

# APPENDIX

The tables below present numerical values of  $p_n^r$  and  $p_n^{\leq r}$  for n = 2, ..., 25, rounded to the sixth decimal place.

			r	$p_3^r$	$p_3^{{\scriptscriptstyle \leq} {\tt r}}$
r	$p_2^r$	$p_2^{\leq r}$	0	0.1	0.1
0	0.333333	0.333333	1	0.6	0.7
1	0.666667	1.	2	0.3	1.

 $p_5^r$ 

0 0.007937

1 0.15873

2 0.47619

3 0.31746

4 0.039683

r

r	$p_4^r$	$p_4^{\leq r}$
0	0.028571	0.028571
1	0.342857	0.371429
2	0.514286	0.885714
3	0.114286	1.

r	$p_6^r$	$p_6^{\leq r}$
0	0.002165	0.002165
1	0.064935	0.0671
2	0.324675	0.391775
3	0.4329	0.824675
4	0.162338	0.987013
5	0.012987	1.

r	$p_7^r$	$p_7^{\leq r}$
0	0.000583	0.000583
1	0.024476	0.025058
2	0.183566	0.208625
3	0.407925	0.61655
4	0.305944	0.922494
5	0.073427	0.995921
6	0.004079	1.

 $p_5^{\leq r}$ 

1.

0.007937

0.166667

0.642857

0.960317

r	$p_8^r$	$p_8^{\leq r}$
0	0.000155	0.000155
1	0.008702	0.008858
2	0.091375	0.100233
3	0.304584	0.404817
4	0.38073	0.785548
5	0.182751	0.968298
6	0.030458	0.998757
7	0.001243	1.

r	$p_{10}^r$	$p_{10}^{\leq r}$
0	0.000011	0.000011
1	0.000974	0.000985
2	0.017537	0.018522
3	0.109117	0.127639
4	0.286432	0.41407
5	0.343718	0.757789
6	0.190955	0.948743
7	0.046764	0.995508
8	0.004384	0.999892
9	0.000108	1.

r	$p_9^r$	$p_9^{\leq r}$		
0	0.000041	0.000041		
1	0.002962	0.003003		
2	0.041464	0.044467		
3	0.193501	0.237968		
4	0.362814	0.600782		
5	0.290251	0.891032		
6	0.09675	0.987783		
7	0.011847	0.99963		
8	0.00037	1.		
r	$p_{11}^r$	$p_{11}^{\leq r}$		
0	$3.  imes 10^{-6}$	$3.  imes 10^{-6}$		
1	0.000312	0.000315		
2	0.007017	0.007332		
3	0 056136	0 063467		

0	$3.  imes 10^{-6}$	$3.  imes 10^{-6}$
1	0.000312	0.000315
2	0.007017	0.007332
3	0.056136	0.063467
4	0.196475	0.259943
5	0.330079	0.590021
6	0.275065	0.865087
7	0.112272	0.977359
8	0.021051	0.998409
9	0.001559	0.999969
10	0.000031	1.

r	$p_{12}^{r}$	$p_{12}^{\leq r}$
0	$1.  imes 10^{-6}$	$1.  imes 10^{-6}$
1	0.000098	0.000098
2	0.002685	0.002783
3	0.026848	0.029631
4	0.120814	0.150445
5	0.270623	0.421068
6	0.315727	0.736796
7	0.193302	0.930098
8	0.060407	0.990505
9	0.008949	0.999454
10	0.000537	0.999991
11	$9.  imes 10^{-6}$	1.

r	$p_{13}^{r}$	$p_{13}^{\leq r}$
0	0.	0.
1	0.00003	0.00003
2	0.00099	0.00102
3	0.012099	0.013119
4	0.068059	0.081178
5	0.196009	0.277187
6	0.304902	0.582089
7	0.261345	0.843434
8	0.122505	0.965939
9	0.030248	0.996188
10	0.00363	0.999818
11	0.00018	0.999998
12	$2.  imes 10^{-6}$	1.

r	$p_{14}^r$	$p_{14}^{\leq r}$
0	0.	0.
1	$9.  imes 10^{-6}$	$9.  imes 10^{-6}$
2	0.000354	0.000363
3	0.00519	0.005553
4	0.035682	0.041235
5	0.128454	0.169689
6	0.256909	0.426598
7	0.29361	0.720207
8	0.192681	0.912889
9	0.071363	0.984252
10	0.014273	0.998525
11	0.001415	0.99994
12	0.000059	0.999999
13	$1. imes 10^{-6}$	1.

r	$p_{15}^{r}$	$p_{15}^{\leq r}$
0	0.	0.
1	$3.  imes 10^{-6}$	$3.  imes 10^{-6}$
2	0.000123	0.000126
3	0.002135	0.002261
4	0.017617	0.019878
5	0.077515	0.097394
6	0.193789	0.291183
7	0.284751	0.575934
8	0.249157	0.825091
9	0.129192	0.954283
10	0.038758	0.993041
11	0.006406	0.999447
12	0.000534	0.999981
13	0.000019	1.
14	0.	1.

r	$p_{16}^r$	$p_{16}^{\leq r}$
0	0.	0.
1	$1.  imes 10^{-6}$	$1.  imes 10^{-6}$
2	0.000042	0.000043
3	0.000848	0.000891
4	0.008266	0.009157
5	0.043645	0.052802
6	0.13336	0.186162
7	0.244947	0.431109
8	0.275565	0.706674
9	0.190514	0.897188
10	0.080016	0.977204
11	0.019839	0.997043
12	0.002755	0.999798
13	0.000196	0.999994
14	$6.  imes 10^{-6}$	1.
15	0.	1.

r	$p_{17}^{r}$	$p_{17}^{\leq r}$
0	0.	0.
1	0.	0.
2	0.000014	0.000014
3	0.000326	0.000341
4	0.003712	0.004053
5	0.023165	0.027218
6	0.084939	0.112157
7	0.190679	0.302836
8	0.268143	0.570979
9	0.238349	0.809328
10	0.133475	0.942803
11	0.04633	0.989134
12	0.009652	0.998786
13	0.001142	0.999928
14	0.00007	0.999998
15	$2.  imes 10^{-6}$	1.
16	0.	1.

# Number of Violations of Regular Minimality

r	$p_{18}^r$	$p_{18}^{ m sr}$
0	0.	0.
1	0.	0.
2	$5.  imes 10^{-6}$	$5.  imes 10^{-6}$
3	0.000122	0.000127
4	0.001605	0.001732
5	0.011684	0.013416
6	0.050632	0.064049
7	0.136398	0.200446
8	0.234433	0.43488
9	0.260481	0.695361
10	0.187547	0.882908
11	0.086798	0.969706
12	0.025316	0.995022
13	0.004494	0.999516
14	0.000459	0.999975
15	0.000024	0.999999
16	$1. imes 10^{-6}$	1.
17	0.	1.

r	$p_{19}^r$	$p_{19}^{\leq r}$
0	0.	0.
1	0.	0.
2	$1.  imes 10^{-6}$	$1.  imes 10^{-6}$
3	0.000045	0.000046
4	0.000671	0.000717
5	0.005637	0.006355
6	0.0285	0.034855
7	0.090736	0.125592
8	0.187143	0.312735
9	0.254145	0.56688
10	0.228731	0.795611
11	0.136104	0.931716
12	0.052929	0.984645
13	0.013154	0.997799
14	0.002013	0.999812
15	0.000179	0.999991
16	$8.  imes 10^{-6}$	1.
17	0.	1.
18	0.	1.

r	$p_{22}^{r}$	$p_{22}^{\leq r}$
0	0.	0.
1	0.	0.
2	0.	0.
3	$2.  imes 10^{-6}$	$2. \times 10^{-6}$
4	0.000042	0.000044
5	0.000509	0.000553
6	0.003848	0.004401
7	0.01885	0.023251
8	0.061851	0.085102
9	0.138973	0.224075
10	0.216798	0.440873
11	0.236507	0.67738
12	0.180665	0.858045
13	0.096212	0.954258
14	0.035343	0.989601
15	0.008797	0.998397
16	0.001443	0.999841
17	0.00015	0.99999
18	$9.  imes 10^{-6}$	1.
19	0.	1.
20	0.	1.
21	0.	1.

r	$p_{23}^{r}$	$p_{23}^{\leq r}$
0	0.	0.
1	0.	0.
2	0.	0.
3	$1.  imes 10^{-6}$	$1.  imes 10^{-6}$
4	0.000016	0.000016
5	0.000215	0.000232
6	0.00183	0.002061
7	0.010156	0.012217
8	0.038086	0.050303
9	0.098741	0.149044
10	0.179708	0.328751
11	0.231689	0.560441
12	0.212382	0.772823
13	0.138237	0.911059
14	0.063476	0.974535
15	0.020312	0.994848
16	0.004443	0.999291
17	0.000646	0.999937
18	0.00006	0.999997
19	$3.  imes 10^{-6}$	1.
20	0.	1.
21	0.	1.
22	0.	1.

r	$p_{24}^r$	$p_{24}^{\leq r}$
0	0.	0.
1	0.	0.
2	0.	0.
3	0.	0.
4	$6.  imes 10^{-6}$	$6.  imes 10^{-6}$
5	0.000089	0.000095
6	0.000843	0.000937
7	0.005262	0.0062
8	0.022365	0.028565
9	0.066267	0.094832
10	0.139161	0.233993
11	0.209317	0.44331
12	0.22676	0.67007
13	0.177114	0.847184
14	0.099401	0.946585
15	0.03976	0.986345
16	0.011183	0.997528
17	0.002167	0.999695
18	0.000281	0.999975
19	0.000023	0.999999
20	$1.  imes 10^{-6}$	1.
21	0.	1.
22	0.	1.
23	0.	1.

r	$p_{25}^{r}$	$p_{25}^{\leq r}$
0	0.	0.
1	0.	0.
2	0.	0.
3	0.	0.
4	$2.  imes 10^{-6}$	$2.  imes 10^{-6}$
5	0.000036	0.00038
6	0.000377	0.000415
7	0.002632	0.003047
8	0.012585	0.015633
9	0.042262	0.057895
10	0.101429	0.159324
11	0.176034	0.335359
12	0.222488	0.557847
13	0.205374	0.76322
14	0.138313	0.901533
15	0.06762	0.969153
16	0.023773	0.992925
17	0.005923	0.998848
18	0.001024	0.999872
19	0.000119	0.999991
20	$9.  imes 10^{-6}$	1.
21	0.	1.
22	0.	1.
23	0.	1.
24	0.	1.

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-		
r	$p_{20}^r$	$p_{20}^{\leq r}$
0	0.	0.
1	0.	0.
2	0.	0.
3	0.000016	0.000017
4	0.000272	0.000289
5	0.002616	0.002905
6	0.015258	0.018163
7	0.056673	0.074836
8	0.13814	0.212976
9	0.225117	0.438093
10	0.247629	0.685722
11	0.184187	0.869908
12	0.092093	0.962002
13	0.030516	0.992518
14	0.006539	0.999057
15	0.000872	0.999929
16	0.000068	0.999997
17	$3.  imes 10^{-6}$	1.
18	0.	1.
19	0.	1.

	mr	m≤r
r	$p_{21}^{r}$	$p_{21}^{\leq r}$
0	0.	0.
1	0.	0.
2	0.	0.
3	$6.  imes 10^{-6}$	$6.  imes 10^{-6}$
4	0.000108	0.000114
5	0.001172	0.001286
6	0.007815	0.009101
7	0.033493	0.042594
8	0.095247	0.137841
9	0.183438	0.321279
10	0.242138	0.563417
11	0.220126	0.783543
12	0.137579	0.921121
13	0.058613	0.979735
14	0.016747	0.996481
15	0.003126	0.999607
16	0.000366	0.999974
17	0.000025	0.999999
18	$1.  imes 10^{-6}$	1.
19	0.	1.
20	0.	1.

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