Structure of single-peaked preferences

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Abstract

The paper studies a variety of domains of preference orders that are closely related to single-peaked preferences. We develop recursive formulas for the number of single-peaked preference profiles and the number of preference profiles that are single-peaked on a circle. The number of Arrow's single-peaked preference profiles is found for three, four, and five alternatives. Random sampling applications are discussed. For restricted tier preference profiles, a forbidden subprofiles characterization and an exact enumeration formula are obtained. It is also shown that each Fishburn's preference profile is also single-peaked on a circle preference profile, and Fishburn's preference profiles cannot be characterized by forbidden subprofiles.

1 Introduction

Unidimensional unfoldoing is a classical problem in mathematical psychology [15, 16]. It is a problem of converting the qualitative scale to a numerical one. There is a set of individuals. Each agent has a preference order (a qualitative scale) represented by a linear order. Representing dissimilarities as distances we locate both agents' ideal points and alternatives on a numerical scale. This numerical scale represents agents preferences if each agent always prefers an alternative which is nearer to his/her ideal point according to the numerical scale. A necessary and sufficient condition for unidimensional unfolding was obtained by [47]. Doignon [21] proposed an algorithm for testing unidimensionality and for constructing numerical scale representing given preferences, when it exists.

If we weaken requirement of existence of a numerical scale to existence of a qualitative scale, we get *single-peaked consistency problem* [26]. Qualitative scale is represented by a linear order of alternatives that is commonly called *axis*. Each agent has an ideal point on this axis. The axis represents agents' preferences if, for each agent and for each pair of alternatives that lay on the same side of the axis with respect to the agent's ideal point, the agent always prefers an alternative which is nearer to his/her ideal point. Preferences over alternatives from the different sides from the ideal point are not derived from the axis. Agents with the same ideal point may have different preferences over pairs of alternatives from different sides from the ideal point. This preference model is called the single-peaked preferences. All upper contour sets of single-peaked preference orders are connected with respect to the given axis. This fact is utilized in solution of the single-peaked consistency problem [26].

The structured preferences approach is based on a similarity assumption. All agents share a common representation of alternatives space. The idea that similarity among agents is the basis for constructing a solution of aggregation problem comes from Arrow (see [4]).

Structured alternatives space leads to structured preferences. We analyze several structures of alternatives space and connect them with the structures of preference profiles. Preference profile is a tuple of preference orders. We are interested in counting and characterizing some classes of structured preference profiles. Finding the number of structured preference profiles is aimed to estimate the relative frequency of different structures. By finding the number of single-peaked preference profiles we find the probability that there exists a solution for the single-peaked consistency problem.

By forbidden subprofiles characterization we get a detection algorithm. By detecting structured preference profiles one can exploit the properties of a structured set of alterna-

tives. Structured preferences have wide applications in computational social choice [25, 38].

Single-peaked preferences imply median voter theorem [7], have vast computational applications [9, 27, 18], axiomatic justification [52], and forbidden subprofiles characterization [3]. Single-peaked preferences are consistent with attribute-based choice rules [17, 2]. Due to Fishburn's book [31] single-peaked preferences are sometimes called in computer science literature "preferences derived from a psychological model" [5]. Simplicity and clear properties predetermine wide applications of single-peaked preferences in economics, political science, psychology and computer science.

There were several attempts to find the number of single-peaked preference profiles. Durand [23] found them for three and four alternatives. Lackner and Lackner [42] found the number of single-peaked preference profiles with two agents. Karpov [37] solved the problem for five alternatives. The problem of finding the precise number of single-peaked preference profiles faces a high combinatorial complexity, because of the exponential number of different axes (there are $m!/2$ different axes). Many combinatorial problems are computationally intractable (see [56, 55] for the definition of #P-complete problems and corresponding examples). Up to now no computationally efficient method was known for counting single-peaked preference profiles.

This paper solves the general problem of counting single-peaked preference profiles by finding a recursive formula.

Single-peaked on a circle preferences were introduced by [50] and by [48] as a particular case of the generalized single-peaked domain. This preference model has several computational applications. Utilizing our result for the single-peaked preference profiles, we obtain a recursive formula for the number of preference profiles that are single-peaked on a circle.

Arrow's single-peaked preferences are single-peaked on each triple of alternatives. The number of Arrow's single-peaked preference profiles is found for three, four, and five alternatives.

Narcissistic preference profiles consist of m preference orders over m alternatives such that all agents have different top choice alternatives. Narcissistic single-peaked preferences are applied to some matching problems [5, 11]. We obtain some results about the number of single-peaked narcissistic preference profiles and single-peaked on a circle narcissistic preference profiles.

Some important restrictions of single-peaked and single-peaked on a circle preferences are considered. Restricted tier preferences share common relation over groups of alternatives, each of them contains one or two alternatives. Liu and Zeng [44] applied this preference model to the probabilistic assignment problem. We prove that the restricted tier preference profiles are single-peaked, and provide a forbidden subprofiles characterization.

Condorcet domains are sets of linear orders with the property that, whenever the preferences of all agents belong to this set, the majority relation, induced by the preference profile with an odd number of agents, has no cycles. Fishburn's domain [32] is a nicely structured Condorcet domain in which some triples of alternatives are single-peaked and some are single-dipped. It is the largest Condorcet domain in case of a small number of alternatives. Galambos and Reiner [35] showed that it is true up to seven alternatives, for a higher number of alternatives it is still an open problem. Fishburn's domain is a basis for constructing large Condorcet domains [20, 40]. We proved that Fishburn's domain is single-peaked on a circle.

The related literature consists of counting results for the number of single-peaked for a given axis narcissistic and single-crossing narcissistic preference profiles [12], group-separable and group-separable narcissistic preference profiles [36], and enriched group-separable preference profiles [30]. Forbidden configurations characterization is known for single-peaked preference profiles [3], group-separable preference profiles [3], single-crossing preference profiles [10], single-peaked single-crossing preference profiles [24], small one-dimensional Eu-

clidean preference profiles [13], and structured dichotomous preference profiles [54]. There are polynomial time recognition algorithms for top-monotonic preference profiles [46], and 2-axes single-peaked preference profiles [58].

The structure of the paper is as follows. Section 2 contains the main result concerning the number of single-peaked preference profiles. Section 3 counts single-peaked on a circle preference profiles. Section 4 presents the calculation of the number of Arrow's single-peaked preference profiles. Section 5 contains the enumeration and characterization results for the restricted tier preference profiles. Section 6 introduces Fishburn's domain and proves that it is a subset of single-peaked on a circle domain. Section 7 concludes and discusses an application of combinatorial results to random sampling algorithms.

2   Single-Peaked Preferences

Let a finite set $X = \{1, \ldots, m\}$ be the set of alternatives, and a finite set $N = \{1, \ldots, n\}$ be the set of agents. Each agent $i \in N$ has a preference order P_i over X (each preference order is a linear order). Let $L(X)$ be the set of all linear orders over X. An n-tuple of preference orders is a preference profile $\mathcal{P} = (P_1, \ldots, P_n) \in L(X)^n$. For brevity, we will write the preference order as a string, e.g. $12 \ldots m$, which means $1P2P3 \ldots Pm$.

A subset of preference orders $D = \{P_1, \ldots, P_k\} \in L(X)^k$ is called a *domain* of preference orders. Each domain of single-peaked preferences is defined by an axis. An axis is a linear order over X. A preference profile $\mathcal{P}$ is *single-peaked* with respect to an axis A, if, for all $i \in N$, agent i's upper-contour sets $U(P_i, x) = \{y \in X | yP_ix\}$ are connected according to the axis (this means that for any two elements from this set all elements between them according to the axis belong to this set). A preference profile $\mathcal{P}$ is *single-dipped* with respect to an axis A, if for all $i \in N$ agent i's lower-contour sets $L(P_i, x) = \{y \in X | xP_iy\}$ are connected according to the axis.

A domain is called *normal single-peaked* if it contains preference order $12 \ldots m$ and it is a maximal single-peaked domain, i.e. there is no possibility to add a preference order outside without violating single-peakedness. Each maximal single-peaked domain contains 2^{m-1} preference orders [41].

A domain D is called *isomorphic* to domain D' if there is a permutation σ, which renames alternatives, such that $D^\sigma = D'$, where D^σ is an image of domain D under renaming permutation σ. For a given m, all maximal single-peaked domains are isomorphic to each other (see, e.g., the work of [28]).

Let $NSP(m, n)$ be the number of single-peaked preference profiles with m alternatives and n agents, such that the first agent has preference order $12 \ldots m$ (these preference profiles are called *normal single-peaked preference profiles*). The number of single-peaked preference profiles equals $SP(m, n) = m! NSP(m, n)$.

Proposition 1. *For $m \geq 3$, we have*

$$NSP(m, n) = 2^{m-2} 2^{(m-1)(n-1)} - \sum_{k=2}^{m-1} \sum_{i=0}^{m-k-1} \binom{m-k-1}{i} \binom{m-k}{i}^{n-1} NSP(k, n),$$

with $NSP(2, n) = 2^{n-1}$.

Proof. Each maximal single-peaked domain is associated with two axes that have reversed order of alternatives. We consider such axes as equivalent. This means that axes 123 and 321 and corresponding domains are the same. An axis is *normal* if it associated with a normal single-peaked domain and has m at the right end. For $m = 3$, axes 123, 213 are normal.

$$
\left.
\begin{array}{l}
12345 - 000 \left.\rule{0pt}{10pt}\right\} \\
21345 - 001 \left.\rule{0pt}{10pt}\right\} \\
32145 - 010 \left.\rule{0pt}{10pt}\right\} \\
31245 - 011 \left.\rule{0pt}{10pt}\right\} \\
43215 - 100 \left.\rule{0pt}{10pt}\right\} \\
43125 - 101 \left.\rule{0pt}{10pt}\right\} \\
41235 - 110 \left.\rule{0pt}{10pt}\right\} \\
42135 - 111 \left.\rule{0pt}{10pt}\right\}
\end{array}
\right\}.
$$

Figure 1: Binary representation and partitions of normal axes for $m = 5$.

We first count naively summing the number of preference profiles that are associated with all normal axes. This result leads to over-counting, as one profile can be single-peaked with respect to multiple axes. Dealing with over-counting problem, we consider a series of partitions of the normal axes that are based on a bijection between normal axes and binary strings of length $m - 2$, and use it to count the number of profiles that are single-peaked with respect to two or more axes.

In each normal axis, sets of alternatives $\{1, 2, \ldots, k\}$, $k \in \{2, \ldots, m - 1\}$ form intervals according to the axis. For each pair of alternatives $k, k + 1$, there are two possibilities for mutual arrangement: consecutive k and $k + 1$ (in any order) and separated k and $k + 1$ (in any order). There are $m - 2$ pairs, and for each of them consecutive/separated positions are independent. Hence, the number of normal axes is 2^{m-2}. Defining a correspondence: consecutive $k, k + 1$ is 0, separated $k, k + 1$ is 1, we get a binary representation of normal axes. The position of alternatives 2 and 3 defines the lowest-order bit, and the position of alternatives $m - 1$ and m defines the highest-order bit. Numbers from 0 to $2^{m-2} - 1$, which are expressed in the base-2 numeral system, define the order of axes. Let A_m be the set of normal axes with m alternatives. A_5 is presented in Figure 1.

Each set of normal axes A_m can be obtained from the previous set A_{m-1} by the following operation. The first 2^{m-3} axes are obtained from the previous set by adding the alternative m to the right end. The second 2^{m-3} axes are obtained from the previous set by reversing them and adding the alternative m to the right end. The first subset consists of axes where m and $m - 1$ appear consecutively; the high-order bit in their binary representation is 0. The second subset consists of axes where m and $m - 1$ are separated; the high-order bit in their binary representation is 1.

We define $m - 2$ partitions of A_m. There are 2^{k-1} axes in each part. Each part consists of consecutive axes according to the order of the binary representation. Each part contains axes, which have common $m - k - 1$ highest order bits in the binary representation. For $m = 5$, these partitions are presented in Figure 1. Each part contains all possible normal axes on alternatives $1, \ldots, k$ and identical remainder (suborder on alternatives $\{k + 1, \ldots, m\}$). Consecutive and separating positions of pair $k, k + 1$ define two possibilities for connecting $1, \ldots, k$ and the remainder. Because of identical remainder all possible normal subaxes on alternatives $1, \ldots, k$ of the part start from the same position. For $m = 5$, subaxes 12, 21 start from position 0 in the first part, and from position 1 in the second part, etc. Each normal subaxis on alternatives $1, \ldots, k$ occurs exactly two times (in reversed versions).

We will find the number of normal single-peaked preference profiles that are associated with each part starting from the smallest one.

Each normal single-peaked preference profile in which sets $\{1, \ldots, k\}$, $\{k+1, \ldots, m\}$ form intervals in each preference order from the profile, and set $\{1, \ldots, k\}$ is an upper-contour set in each preference order from the profile, is associated with two axes in which subaxes on alternatives $1, \ldots, k$ are reversed. Thus, each such a preference profile is associated with

$$
\left.
\begin{array}{l}
\left.\begin{array}{l}
\left.\begin{array}{l}
\left.\begin{array}{l}
12345 \\
21345 \\
32145 \\
31245
\end{array}\right\} \quad
\begin{array}{l}
-NSP(2,n) \\[4pt]
-3^{n-1}NSP(2,n)
\end{array}
\end{array}\right\} - NSP(3,n) \\[20pt]
\left.\begin{array}{l}
\left.\begin{array}{l}
43215 \\
43125
\end{array}\right\} -3^{n-1}NSP(2,n) \\
\left.\begin{array}{l}
41235 \\
42135
\end{array}\right\} -3^{n-1}NSP(2,n)
\end{array}\right\} - 2^{n-1}NSP(3,n)
\end{array}\right\} - NSP(4,n).
$$

Figure 2: Structure of intersections for $m = 5$.

two axes from different parts of the previous partition (for the finest partition we simply have two different axes).

Suppose, that there exists a preference profile that associated with to two axes: one from the first part of the smaller size, and one from the second part of the smaller size; and this preference profile contains a preference order $\tilde{P}$, which does not have upper contour set $\{1,\ldots,k\}$. If $\tilde{P}$ starts from an alternative from set $\{k+1,\ldots,m\}$, then consecutive and separated positions of $k, k+1$ lead to different position of k in order $\tilde{P}$ (it is the worst from alternatives $\{1,\ldots,k\}$ in one case, and is the best from alternatives $\{1,\ldots,k\}$ in another case). If $\tilde{P}$ starts from an alternative from set $\{1,\ldots,k\}$ and $\{1,\ldots,k\}$ is not an upper contour set, then consecutive and separated positions of $k, k+1$ lead to different best alternatives from set $\{k+1,\ldots,m\}$. We get a contradiction.

Thus, preference profiles that are associated with two parts of the smaller size have the the following structure. Top k alternatives of each order form a normal single-peaked subprofile, bottom $m-k$ alternatives of each order form a normal single-peaked with given axis and one or two given top alternatives subprofile (these two alternatives are neighbouring to alternatives $\{1,\ldots,k\}$ in all axes of the part).

The number of normal single-peaked subprofiles on set $\{1,\ldots,k\}$ is $NSP(k,n)$.

The number of normal single-peaked subprofiles on set $\{k+1,\ldots,m\}$ depends on starting position of subaxis on alternatives $1,\ldots,k$. The number of single-peaked preference orders starting from position i on the axis with $m-k+1$ alternatives equals $\binom{m-k}{i}$ [6].

Thus, the number of normal single-peaked preference profiles that are associated with two parts of the smaller size is $\binom{m-k}{i}^{n-1} NSP(k,n)$, where i is the starting position of alternatives $\{1,\ldots,k\}$ in all axes from the part.

The structure of partitions leads to the structure of intersections (for $m = 5$, it is presented in Figure 2). The first column of numbers starting from $-NSP(2,n)$ represents numbers of normal single-peaked preference profiles that are associated with both axes from the part. The second column of numbers represents numbers of normal single-peaked preference profiles that are associated with at least one axis from the first part of the finer partition and at least one axis from the second part of the finer partition. The same interpretation for the last column.

For m alternatives, the number of parts of the kth partition with axes that have alternatives $\{1,\ldots,k\}$ starting from position $i \in \{0,\ldots,m-k-1\}$ is the number of ways to put the alternatives $\{k+1,\ldots,m\}$ to the left and to the right from alternatives $\{1,\ldots,k\}$, knowing that m must be on the extreme right, and exactly i elements must be on the left. For each combination of alternatives there is exactly one way to order them (in descending order before alternatives $\{1,\ldots,k\}$ and in ascending order after alternatives $\{1,\ldots,k\}$). Thus,

$\binom{m-k-1}{i}$ is the number of parts of the kth partition with axes that have alternatives $\{1, \ldots, k\}$ starting from position $i \in \{0, \ldots, m-k-1\}$.

Since there are $\binom{m-k-1}{i}$ parts with $\binom{m-k}{i}^{n-1} NSP(k,n)$ preference profiles that are associated with two parts of the smaller size we subtract

$$\sum_{i=0}^{m-k-1} \binom{m-k-1}{i} \binom{m-k}{i}^{n-1} NSP(k,n)$$

to get the number of normal single-peaked preference profiles associated with axes from the next level partition. Starting from $2^{m-2}2^{(m-1)(n-1)}$ normal single-peaked preference profiles associated with 2^{m-2} normal axes and consequently deducting cardinality of intersections we get the final answer

$$NSP(m,n) = 2^{m-2}2^{(m-1)(n-1)} - \sum_{k=2}^{m-1} \sum_{i=0}^{m-k-1} \binom{m-k-1}{i} \binom{m-k}{i}^{n-1} NSP(k,n),$$

with $NSP(2,n) = 2^{n-1}$.

$\square$

For a small number of alternatives, we have

$$SP(3,n) = 3!(2 \cdot 4^{n-1} - 2^{n-1}),$$

$$SP(4,n) = 4!(4 \cdot 8^{n-1} - 3 \cdot 4^{n-1}),$$

$$SP(5,n) = 5!(8 \cdot 16^{n-1} - 6 \cdot 8^{n-1} - 3 \cdot 6^{n-1} + 2 \cdot 4^{n-1}),$$

$$SP(6,n) = 6!(16 \cdot 32^{n-1} - 12 \cdot 16^{n-1} - 9 \cdot 12^{n-1} + 8^{n-1} + 6 \cdot 6^{n-1} - 4^{n-1}).$$

The first three formulas were already presented in the literature, the last one is novel. The probability of occurrence of a single-peaked preference profile under the Impartial Culture assumption equals $SP(m,n)/(m!)^n$. If we reverse each preference order in a single-peaked preference profile then we obtain a single-dipped preference profile. Thus, we have also found the number of single-dipped preference profiles.

A narcissistic preference profile is a preference profile with m alternatives and m agents such that alternative j is the most preferred alternative for agent j. There are $(m-1)!^m$ narcissistic preference profiles [12]. There are $\prod_{i=2}^{m-1} \binom{m-1}{i-1}$ single-peaked for a given axis narcissistic preference profiles [12], where $\binom{m-1}{i-1}$ is the number of single-peaked preference profiles starting from position i on the axis [6].

In each *normal narcissistic* preference profile agent 1 has preference order $1 \ldots m$.

Proposition 2. *For $m \geq 3$, the number of normal single-peaked narcissistic preference profiles equals*

$$NSPN(m) = \frac{m}{2} \prod_{i=2}^{m-1} \binom{m-1}{i-1},$$

the number of single-peaked narcissistic preference profiles equals

$$SPN(m) = \frac{m!}{2} \prod_{i=2}^{m-1} \binom{m-1}{i-1}.$$

Proof. Each maximal single-peaked domain contains only one preference order that starts from the first alternative of the axis and only one preference order that starts from the last alternative of the axis. Each single-peaked narcissistic preference profile contains two totally reversed preference orders, which coincide with axis and reversed axis. There is no single-peaked narcissistic preference profile that is associated with two axes. Having $m!/2$ axes we multiply the number of single-peaked for a given axis narcissistic preference profiles by $m!/2$ and get the number of single-peaked narcissistic preference profiles.

All single-peaked narcissistic preference profiles can be partitioned on sets with different first preference orders. Since there are $(m-1)!$ distinct first preference orders, we have $NSPN(m) = SPN(m)/(m-1)!$. $\square$

Proofs of the subsequent theorems are moved to the appendix.

Since single-dipped preference profiles have at most two distinct top alternatives, there are no single-dipped narcissistic preference profiles for $m \geq 3$.

3   Preferences Single-Peaked on a Circle

A preference profile $\mathcal{P}$ is *single-peaked on a circle* (SPOC) with respect to a circular permutation of alternatives C if, for all $i \in N$, agent i's upper-contour sets $U(P_i, x) = \{y \in X | y P_i x\}$ are intervals according to the circular permutation. Lower contour sets also form intervals according to the circular permutation. Therefore, SPOC preferences and preferences single-dipped on a circle are equivalent.

For a given circular permutation of alternatives, the number of preference orders that start from alternative 1 equals 2^{m-2}. Each other alternative leads to the same number of preference orders that start from this alternative. Thus, the number of preference orders in each maximal SPOC domain equals $m2^{m-2}$. Each maximal SPOC domain is symmetric, i.e. for each order, its reverse also belongs to the domain (see [19, 39] for studies of symmetric Condorcet domains).

Because each maximal SPOC domain is invariant to rotating and flipping a circle, there are at most $(m-1)!/2$ maximal SPOC domains. The corresponding circular permutations are free circular permutations (*free* means that circular permutations are invariant to flipping). Let us prove, that we have $(m-1)!/2$ distinct maximal SPOC domains. For $m = 3$, we have only one maximal SPOC domain. Suppose that for $m - 1$ alternatives we have $(m-2)!/2$ different maximal SPOC domains. For each maximal SPOC domain on $m - 1$ alternatives we construct $m - 1$ different maximal SPOC domains on m alternatives by inserting alternative m in one of $m - 1$ possible positions of free circular permutation on $m - 1$ alternatives. Thus, there are $(m-1)!/2$ different maximal SPOC domains.

All maximal SPOC domains of equal size are isomorphic to each other.

Maximal SPOC domains are neither Condorcet domains nor subcyclic domains (domains that contain at most five suborders in each restriction to triple of alternatives, see [34]). SPOC domains contain all six suborders in each restriction to triple of alternatives. Therefore, SPOC domains are a dictatorial [49].

A domain is called *normal SPOC* if it contains preference order $12 \ldots m$ and it is a maximal SPOC domain. Let $NSPOC(m, n)$ be the number of SPOC preference profiles with m alternatives and n agents such that the first agent has preference order $12 \ldots m$. These preference profiles are normal SPOC. The corresponding free circular permutations are called normal. We represent normal free circular permutations as a string, with $m - 1$ m at the right end.

Proposition 3. *For $m \geq 4$, we have*

$$NSPOC(m, n) = 2^{m-3}(m2^{m-2})^{n-1} - \sum_{k=2}^{m-2} 2^{m-k-2}2^{(m-k)(n-1)}NSP(k, n),$$

with $NSPOC(2, n) = 2^{n-1}$, $NSPOC(3, n) = 6^{n-1}$, $SPOC(m, n) = m!NSPOC(m, n)$.

For a small number of alternatives, we have

$$SPOC(3, n) = 3! \cdot 6^{n-1};$$

$$SPOC(4, n) = 4!(2 \cdot 16^{n-1} - 8^{n-1});$$

$$SPOC(5, n) = 5!(4 \cdot 40^{n-1} - 4 \cdot 16^{n-1} + 8^{n-1});$$

$$SPOC(6, n) = 6!(8 \cdot 96^{n-1} - 12 \cdot 32^{n-1} + 5 \cdot 16^{n-1}).$$

There are $2^{m(m-2)}$ narcissistic preference profiles that are SPOC for a given free circular permutation.

Proposition 4. *[50] A preference profile is SPOC if and only if it avoids three configurations ($\{x, y\}$ means, that alternatives are situated in any order)*
(i) there are two agents $i, j \in N$ and five alternatives $x, y, z, t, r \in X$ such that

$$\{x, y\}P_i z P_i\{t, r\},$$

$$\{x, t\}P_j z P_j\{y, r\};$$

(ii) there are three agents $i, j, k \in N$ and four alternatives $x, y, z, t \in X$ such that

$$\{x, y\}P_i\{z, t\},$$

$$\{x, z\}P_j\{y, t\},$$

$$\{x, t\}P_k\{y, z\};$$

(ii) there are three agents $i, j, k \in N$ and four alternatives $x, y, z, t \in X$ such that

$$\{y, z\}P_i\{x, t\},$$

$$\{x, z\}P_j\{y, t\},$$

$$\{x, y\}P_k\{z, t\}.$$

Condition (i) of proposition 4 is a condition on pairs of preference orders. It can be rewritten in terms of permutation patterns. A permutation $\sigma \in S_n$ contains pattern $\tau \in S_k$ if there is a tuple $(x_1, \ldots, x_k) \in \{1, \ldots, n\}^k$ such that $1 \leq x_1 \leq x_2 \leq \ldots \leq x_k \leq n$ and for all $i, j \in \{1, \ldots, k\}$ we have $\sigma(x_i) < \sigma(x_j)$ if and only if $\tau(i) < \tau(j)$. For each pair of preference orders $(P, P') \in L(X)$ there is a permutation $\sigma \in S_n$, which renames alternatives, such that $P^\sigma = P'$. From Condition (i) of Proposition 4 we have pair of preference orders (P, P') that is not SPOC, then σ avoids permutation patterns 14325, 14352, 15324, 15342, 24315, 24351, 25314, 25341, 41325, 41352, 42315, 42351, 51324, 51342, 52314, 52341. This permutation pattern is called square permutations, and their number (it is found in [22]) is equal to the number of two-agents normal SPOC preference profiles

$$NSPOC(m, 2) = (m + 2)2^{2m-5} - 4(2m - 5)\binom{2m - 6}{m - 3}.$$

4   Arrow's Single-Peaked Preferences

Arrow [1] used a local single-peakedness condition, requiring only the single-peakedness on each triple of alternatives. Slinko [53] discovered the structure of Arrow's single-peaked domains for three, four, and five alternatives. Karpov and Slinko [40] discovered a recursive structure of Arrow's single-peaked domains. Each maximal Arrow's single-peaked domain contains 2^{m-1} preference orders [53].

Let $ASP(m, n)$ be the number of Arrow's single-peaked preference profiles with m alternatives and n agents. For $m =$, single-peakedness coincides with Arrow's single-peakedness, therefore, $ASP(3, n) = 3!(2 \cdot 4^{n-1} - 2^{n-1})$.

Up to isomorphism, there are two types of maximal Arrow's single-peaked domains with four alternatives. The first type is the single-peaked domain. The second type is the following:

$$D_{4,2} = \{1234, 2134, 2314, 3214, 2341, 3241, 2431, 4231\}.$$

From Section 2 we know that there are four single-peaked domains that contain order 1234. For the second type, there are eight renaming permutations that lead to a domain with order 1234 (one permutation for each order from $D_{4,2}$). Four permutations in which we have $\sigma(4) = 4$ lead to different domains. Four permutations in which we have $\sigma(4) = 1$ lead to the same set of domains. Thus there are only four maximal Arrow's single-peaked domains that contain order 1234.

Computing all intersections of the eight normal domains, we obtain

$$ASP(4, n) = 4!(8 \cdot 8^{n-1} - 6 \cdot 6^{n-1} - 4^{n-1}).$$

$ASP(4, n)$ is also calculated in ([23] p. 586).

Durand [23] on p. 590 claimed that there are

$$\frac{m(m-1)}{2} 2^{(m-2)(m-3)} 3^{(m-2)(m-3)(m-4)/6}$$

maximal Arrow's single-peaked domains. Because all domains have equal cardinality, and all preference orders have equal frequency, there are

$$\frac{m(m-1)}{2} 2^{(m-2)(m-3)} 3^{(m-2)(m-3)(m-4)/6} 2^{m-1}/m!$$

maximal normal Arrow's single-peaked domains. For $m \geq 7$, it is not an integer that is impossible. This result shows that the asymptotic formula for the number of maximal Arrow's single-peaked preference profiles from [23] is erroneous. For a small number of alternatives, the number of maximal Arrow's single-peaked domains was found by Liversidge [45].

For $m = 5$, we computationally found all intersections of maximal normal Arrow's single-peaked domains, and obtain the number of Arrow's single-peaked preference profiles

$$ASP(5, n) = 5!(64 \cdot 16^{n-1} - 56 \cdot 14^{n-1} - 24 \cdot 12^{n-1} + 20 \cdot 10^{n-1}$$

$$-8 \cdot 8^{n-1} + 6 \cdot 6^{n-1} - 4^{n-1}).$$

Because Arrow's single-peaked preferences have no restrictions to pairs of preference orders (see [53]), we get $ASP(m, 2) = m!^2$.

5 Restricted tier preferences

A preference profile $\mathcal{P}$ is *restricted tier* if there is an weak order of alternatives (ordered partition) such that the cardinality of each equivalence class (part) does not exceed two, and each preference order inherits the weak order. For $m = 3$, domains $\{123, 213\}$ and $\{123, 132\}$ are maximal restricted tier domains. In the first domain we have weak order with equivalence classes $\{1, 2\}$, $\{3\}$, and the first one is preferable. Restricted tier domains are applied in random assignment problem (the problem of assignment of n indivisible items among n agents). Liu and Zeng [44] proved that under restricted tier preferences the probabilistic serial rule [8] is uniquely characterized by strategy-proofness, efficiency and equal treatment of equals. For $m \geq 3$, each maximal restricted tier domain is not a maximal Condorcet domain, but Condorcet consistency does not matter in random assignment problem.

A preference profile $\mathcal{P}$ is *group-separable* if for each subset of X of cardinality of at least two there is a partition of the subset on two nonempty sets such that, for each agent, we have either the agent prefers each alternative from the first set of the partition to each alternative from the second set of the partition or the agent prefers each alternative from the second set of the partition to each alternative from the first set of the partition. $\{123,213,312,321\}$ is an example of maximal group-separable domain. $\{1, 2\}$ and $\{3\}$ is partition of the general set. Each group-separable domain is a Condorcet domain, and it has an application in matching theory [43].

Proposition 5 links group-separable and single-peaked domains by showing that restricted tier domain is simultaneously group-separable and single-peaked.

Proposition 5. *Restricted tier domain is simultaneously group-separable and single-peaked.*

There exists group-separable and single-peaked domain that is not restricted tier (e.g. $\{1234, 2314, 3214, 4321\}$).

Proposition 6. *The number of restricted tier preference profiles equals*

$$RT(m,n) = m! \sum_{k=0}^{\lfloor \frac{m}{2} \rfloor} \binom{m-k}{k} (2^{n-1} - 1)^k.$$

Proposition 6 provides the exact number of restricted tier preference profiles, and gives a lower bound for the number of single-peaked group-separable preference profiles. The following proposition provides a characterization of restricted tier preference profiles via forbidden subprofiles (configurations).

Proposition 7. *A preference profile is restricted tier if and only if there is no two distinct agents $i, j \in N$ and three distinct alternatives $a, b, c \in X$ such that*

$$aP_i bP_i c \text{ and}$$

$$cP_j bP_j a, \text{ or } cP_j aP_j b, \text{ or } bP_j cP_j a.$$

Configuration from proposition 7 corresponds to a permutation pattern that avoids patterns 231, 321, 312. Such permutations are called free permutations and are counted in the Fibonacci sequence [51].

For $m \geq 3$, there are no narcissistic restricted tier preference profiles.

6 Fishburn's preferences

A domain is called Fishburn's domain if it satisfies an *alternating scheme* [32, 33]: there exists a linear ordering of alternatives $a_1 \ldots a_m$ such that for all i, j, k with $1 \le i < j < k \le m$ the restriction of the domain to set $\{a_i, a_j, a_k\}$ is single-peaked with never-bottom alternative a_j if j is even, and it is single-dipped with never-top alternative a_j if j is odd, or it is single-peaked with never-bottom alternative a_j if j is odd, and it is single-dipped with never-top alternative a_j if j is even.

Having the natural ordering of alternatives we obtain the following maximal Fishburn's domains:

$F_3 = \{123, 213, 231, 321\}$,

$F_4 = \{1234, 1243, 2134, 2143, 2413, 2431, 4213, 4231, 4321\}$,

$F_5 = \{12345, 12354, 13245, 13254, 13524, 13542, 31245, 31254, 31524, 31542,$
$35142, 35412, 35421, 53124, 53142, 53412, 53421, 54312, 54321\}$.

The reversed domains are also Fishburn's domains. [35] gave the exact formula for the cardinality of F_m:

$$|F_m| = (m+3)2^{m-3} - \begin{cases} (m - \frac{3}{2})\binom{m-2}{\frac{m}{2}-1} & \text{for even } m; \\ (\frac{m-1}{2})\binom{m-1}{\frac{m-1}{2}} & \text{for odd } m. \end{cases}$$

For a big m, it is approximately two times smaller than the cardinality of maximal SPOC domain, which equals $m2^{m-2}$. The union of F_4 and its reverse constitute a maximal SPOC domain with free circular permutation 2134. The union of F_5 and its reverse has strictly less preference orders than maximal five-alternatives SPOC domain. For $m = 5$, orders 21354 and 45312 belong to the maximal SPOC domain with free circular permutation 31245, but do not belong to the Fishburn's domains.

A domain D satisfies *maximal width* if it contains a pair of completely reversed preference orders [52]. A domain D is *semi-connected* if it satisfies maximal width and it contains a sequence of preference orders such that the first and the last preference orders in this sequence are completely reversed and each pair of consecutive preference orders differs by only one swap of consecutive alternatives.

Proposition 8. *[20] Each maximal Fishburn's domain is semi-connected.*

A Condorcet domain D is *copious* if for each triple of alternatives the restriction of domain D to this triple has four distinct orders [53]. Because of semi-connectedness, each restriction of a maximal Fishburn's domain to three alternatives is connected, and contains a pair of reversed orders (each restriction is a maximal single-peaked domain or a maximal single-dipped domain). Thus, each maximal Fishburn's domain is copious.

Proposition 9. *Each maximal Fishburn's domain is a subset of a maximal SPOC domain.*

Fishburn's domains receive clear SPOC interpretation and inherits all algorithmic applications of SPOC domains from Peters and Lackner [50]. The following proposition describes the structure of corresponding free circular permutation.

Proposition 10. *For a maximal Fishburn's domain with ordering $a_1 \ldots a_m$, the corresponding free circular permutation of alternatives of a SPOC domain that contains this Fishburn's domain equals, for odd m, $a_1 a_2 \ldots a_{m-1} a_m a_{m-2} \ldots a_3$, and, for even m, $a_1 a_2 \ldots a_{m-2} a_m a_{m-1} \ldots a_3$.*

Proposition 11. *The set of maximal Fishburn's domains is not closed under removing candidates operation.*

Some restrictions of the Fishburn's domain to a subset of alternatives do not constitute a maximal Fishburn's domain on this subset, or even a subset of a maximal Fishburn's domain. Thus, there is a configuration that is forbidden for a small number of alternatives and is permitted for a higher number of alternatives. It leads to the following proposition.

Proposition 12. *There is no forbidden configurations characterisation for Fishburn's preference profiles.*

In addition to configurations from proposition 4 Fishburn's preference profiles avoid two configurations that guarantees that there are no never-top alternative, and never-bottom alternative.

Proposition 13. *Fishburn's preference profiles avoid two configurations*
(iv) (never-middle pattern) there are four agents $i, j, k, l \in N$, and three alternatives $x, y, z \in X$ such that xP_iyP_iz, xP_jzP_jy, zP_kyP_kx, yP_lzP_lx;
(v) (Condorcet cycle) there are three agents $i, j, k \in N$, and three alternatives $x, y, z \in X$ such that $xP_iyP_iz, yP_jzP_jx, zP_kxP_ky$.

For $m \geq 4$, there are no narcissistic Fishburn's preference profiles. For $m = 3$, there are no narcissistic single-dipped preference profiles, and all narcissistic Fishburn's preference profiles are narcissistic single-peaked preference profiles.

7   Conclusion

We have considered a preference profile as a tuple of preference orders. The obtained numbers of structured preference profiles can be used for counting probabilities under the Impartial Culture assumption.

$SP(m,n)$, $SPOC(m,n)$, $ASP(m,n)$ can be presented as a sum of $b^n s$ with some coefficients, where b is the number of preference orders in an intersection of some domains. The number of multisets of the same preference orders equals $\binom{b+n-1}{n}$. Thus, replacing b^n with $\binom{b+n-1}{n}^n$, we get the number of structured preference profiles under the Impartial Anonymous Culture assumption.

There are several random sampling algorithms for single-peaked preference profiles. Conitzer [14] developed a random sampling algorithm for single-peaked preference profiles with a given axis that preserves the uniform distribution of the first-choice votes (for unrestricted domain this approach is known as the Uniform Plurality Culture assumption introduced by Karpov [37]). Walsh [57] developed a random sampling algorithm for single-peaked preference profiles with a given axis under the Impartial Culture assumption. Uniform sampling of axes and independent sampling of single-peaked preference profiles leads to the over-representation of preference profiles with identical preference orders, because these preference profiles are associated with several axes.

The presented nested structure of the partitions of normal axes can be applied for a random sampling algorithm of single-peaked preference profiles with an unknown axis under the Impartial Culture assumption. We can generate single-peaked preference profiles iteratively starting from the two alternatives case. On each iteration, we find probabilities of the occurrence of a preference profile with a common upper contour set of cardinality k and utilize the single-peaked preference profiles generated in the previous iterations. After finding the conditional probabilities of the subaxis starting position and conditional probabilities of different axes, we can apply an algorithm to generate single-peaked preference profiles with a given axis, which can guarantee the identity/diversity of lower/upper contour sets. A close conditional probabilities approach was applied for random sampling algorithm of group-separable preference profiles [29].

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