



Isomorphism Check for Two-level Multi-Stage Factorial Designs with Randomization Restrictions via an *R* Package: **IsoCheck**

Pratishtha Batra¹, Neil A. Spencer², Pritam Ranjan^{1,*}

¹*OMQT Area, Indian Institute of Management Indore, India*

²*Department of Statistics, University of Connecticut, USA*

Abstract Factorial designs are often used in various industrial and sociological experiments to identify significant factors and factor combinations that may affect the process response. In the statistics literature, several studies have investigated the analysis, construction, and isomorphism of factorial and fractional factorial designs. When there are multiple choices for a design, it is helpful to have an easy-to-use tool for identifying which designs are distinct, and which of those can be efficiently analyzed/has good theoretical properties. For this task, we present an *R* library called **IsoCheck** that checks the isomorphism of multi-stage 2^n factorial experiments with randomization restrictions. Through representing the factors and their combinations as a finite projective geometry, **IsoCheck** recasts the problem of searching over all possible relabeling as a search over collineations, then exploits projective geometric properties of the space to make the search much more efficient. Furthermore, a bitstring representation of the factorial effects is used to characterize all possible rearrangements of designs, thus facilitating quick comparisons after relabeling. This paper presents several detailed examples with *R* codes that illustrate the usage of the main functions in **IsoCheck**. Besides checking equivalence and isomorphism of 2^n multi-stage factorial designs, we demonstrate how the functions of the package can be used to create a catalog of all non-isomorphic designs, and find good designs as per a suitably defined ranking criterion.

Keywords Projective geometry, Spreads, Collineation, Bitstring Mapping, Design catalog

AMS 2010 subject classifications: 62K15, 51A40, 51E14, 51E23, 05-04

DOI: 10.19139/soic-2310-5070-1494

1. Introduction

Factorial experiments are commonly used for significance assessment of factors in a wide spectrum of scientific and industrial applications including agriculture, engineering, and sociological phenomena. In many such experiments, complete randomization of the trials happens to be impractical for a variety of reasons. For instance, changing some factors can be prohibitively expensive, the trials may need to be partitioned into homogeneous batches at each stage, or the experimental units may need to be processed repeatedly in batches. To address these issues, randomization restrictions are imposed on the experimental trials. Classical designs for such factorial experiments include block designs, nested designs, split-plot designs, strip-plot designs, split-lot designs, and combinations thereof. A plethora of research articles have been published till date on the development of theoretical results and efficient algorithms to construct and analyze such designs. Some landmark papers can be traced back to the exploration of completely randomized designs and randomized block designs by Fisher (1942) and Yates (1937).

*Correspondence to: Prof. Pritam Ranjan (Email: pritamr@iimidr.ac.in). Operations Management and Quantitative Techniques Area, Indian Institute of Management Indore, Prabandh Shikhar, Indore, Madhya Pradesh, India (453331).

Later, experimenters investigated several factorial designs with multi-stage randomization restrictions. For instance, [Addelman \(1964\)](#), [Bingham and Sitter \(1999a\)](#) and many others investigated the split-plot designs; [Miller \(1997\)](#) developed the strip-plot designs for measuring wrinkles in a laundry experiment; blocked designs were investigated by [Bisgaard \(1994\)](#); [Mee and Bates \(1998\)](#), [Butler \(2004\)](#) and [Bingham et al. \(2008\)](#) presented some fundamental results on split-plot designs for analyzing the fabrication of integrated circuits using silicon wafers. The following books provide a detailed reference list [Dean and Voss \(1999\)](#), [Mukerjee and Wu \(2006\)](#), [Wu and Hamada \(2009\)](#), [Hedayat et al. \(2012\)](#), and [Cheng \(2016\)](#).

One important aspect in this area of research focuses on finding *distinct* designs that have useful theoretical properties and are easy to analyze. An essential task in such endeavors is to check for the isomorphism between different designs. In a completely randomized setup, two designs d_1 and d_2 are said to be isomorphic if d_1 can be obtained by applying relabeling and rearrangement of the factors and factor combinations on d_2 . [Franklin and Bailey \(1977\)](#) developed theoretical results and algorithms for fractional factorial completely randomized designs. For factorial designs with randomization restrictions, isomorphic designs allow restricted rearrangement of the factorial effects within the subspace that characterizes the randomization defining factors. [Bingham and Sitter \(1999a\)](#) extended the results of [Franklin and Bailey \(1977\)](#) for split-plot designs. In a multi-stage factorial design with randomization restrictions, there are additional restrictions on the within block and between block relabeling and rearrangement (see [Spencer et al. \(2019\)](#)). Several researchers have also focused on proposing innovative design ranking criteria to sort through these non-isomorphic designs and create catalogs of good designs for ready usage by practitioners. Popular design ranking criteria are maximum resolution, maximize the number of clear 2-factor interactions, minimum aberration, etc. ([Wu and Hamada, 2009](#)).

Over the years, a few methodologies have been developed that unify different factorial designs with randomization restrictions. [Nelder \(1965a,b\)](#) developed a unified theory to analyze such experiments through simple block structures. This idea was further generalized to orthogonal block structures through association schemes by [Speed and Bailey \(1982\)](#) and [Tjur \(1984\)](#). More details can be found in [Bailey \(2004\)](#) and [Cheng and Tsai \(2011\)](#). [Bingham et al. \(2008\)](#) introduced the idea of randomization defining factors, which was further taken-up by [Ranjan et al. \(2009\)](#) and [Ranjan et al. \(2010\)](#) to develop Projective Geometry (PG) formulation based on the overlapping pattern of the randomization defining contrast subspaces (referred to as RDCSSs).

The key idea behind this RDCSS-based unified theory is to realize that the set of all factorial effects of a q^n factorial design constitute an $(n - 1)$ -dimensional finite projective geometry $\mathcal{P}_n := PG(n - 1, q)$ over the Galois Field $GF(q)$. The randomization restrictions can be characterized by a projective subspace of \mathcal{P}_n . Such multi-stage factorial designs have been constructed using two geometric structures called “spread” and “star”. The former partitions \mathcal{P}_n into disjoint RDCSSs, whereas the latter is a set of RDCSSs that forms a cover of \mathcal{P}_n with a common overlap. Ranjan et al. have also established that the construction and analysis of classical factorial designs with randomization restrictions like split-plot, strip-plot, split-lot, etc., can be derived from carefully chosen sets of RDCSSs of \mathcal{P}_n . Recently, [Spencer et al. \(2019\)](#) developed isomorphism check algorithms for 2^n multi-stage factorial designs based on spreads and stars. They presented a bitstring representation of \mathcal{P}_n which helps in developing an efficient search algorithm exploiting the geometric structure of RDCSSs to significantly reduce the search space. The results from projective geometry (e.g. [Topaloca and Zhelezova \(2010\)](#); [Mateva and Topalova \(2009\)](#)) are also applied to completely classify the isomorphism properties for several RDCSS-based designs (with small runsizes) that are useful from a practical standpoint.

The key contributions of this paper are highlighted as follows. We present an R ([R Core Team, 2020](#)) package **IsoCheck** which assumes the RDCSS-based structure of the factorial designs and efficiently implements the algorithms of [Spencer et al. \(2019\)](#) to check the isomorphism. The key functions (a)

generate a relabelling and rearrangement of a given spread/star of \mathcal{P}_n via a proper collineation matrix; (b) check equivalence of two spreads (stars); (c) check isomorphism between two spreads (stars); and (d) find a spread embedded in the star-based design. Although, preliminary implementation of some functions can be found on the Github submission (as a part of Spencer et al. paper), **IsoCheck** presents robust and computationally more efficient version of these algorithms with several additional functions which are crucial for isomorphism check. In particular, the new functions are `is.spread()`, `is.star()`, `vectortostring()` and `stringtovector()`. **IsoCheck** is a free software and distributed under the General Public License and available from the Comprehensive R Archive Network. In this paper, we also demonstrate how the functions of **IsoCheck** can be used to construct a catalog of all non-isomorphic designs, and find good designs based on some suitably defined ranking criterion. Of course, it assumes that one can list out all possible designs with a given specification (i.e., number of factors, number of stages, and sizes of each RDCSS).

Section 2 of the paper provides necessary theoretical background on factorial designs, foundations of projective geometry $\mathcal{P}_n = PG(n-1, 2)$, including balanced spreads and covering stars of \mathcal{P}_n , and algorithms for isomorphism check (developed by Spencer et al. (2019)). Section 3 outlines the usage and arguments of important functions of **IsoCheck** including the new functions that were not available in the Github submission. Section 4 provides several examples to present detailed illustration of how isomorphism check can be performed for both spread and star based designs. Section 5 outlines the catalog construction steps using **IsoCheck** for a few designs with small values of n . Section 6 concludes the article with a few remarks.

2. Methodology

In a 2^n factorial experiment, suppose the n basic factors (main effects), F_i , $i = 1, \dots, n$, are expressed as the n canonical vectors, where F_i has $n-1$ zeros and exactly one 1 at the i -th location. These n canonical vectors along with their interactions constitute an n -dimensional vector space V over $GF(2)$. The set of all non-null elements of V form a $(n-1)$ -dimensional projective space over $GF(2)$, denoted by $\mathcal{P}_n := PG(n-1, 2)$ (Bose, 1947). For a given stage of a n -factor multi-stage / multi-stratum factorial design (e.g., split-plot, strip-plot, split-lot, etc.), the randomization restrictions can be characterized by a projective subspace of \mathcal{P}_n . In the context of projective geometry, such a subspace is called a flat. More formally, a $(t-1)$ -flat of \mathcal{P}_n is defined as the set of $2^t - 1$ non-null vectors spanned by t linearly independent effects of \mathcal{P}_n . In the design and analysis of experiments language, we refer to this $(t-1)$ -flat as a *randomization defining contrast subspace* (RDCSS) with t linearly independent factors or factor interactions (fi), which is in the same spirit as *fraction defining contrast subgroup* (FDCS) used to characterize traditional fractional factorial designs (Bingham and Sitter, 1999a).

The multi-stage RDCSS-based designs proposed by Ranjan et al. (2009) and Ranjan et al. (2010) are primarily derived from two geometric structures called spreads and stars of \mathcal{P}_n , which are essentially the set of distinct flats of \mathcal{P}_n that also form a cover of \mathcal{P}_n . In a nutshell, a spread is a collection of disjoint flats, whereas a star is a set of distinct flats that allow a common overlap. Ranjan et al. proposed several multi-stage factorial designs by exploiting the sizes of flats and their overlaps. Recently, Spencer et al. (2019) has developed algorithms for checking isomorphism between a smaller class of balanced spread- and balanced star- based designs. The R library (**IsoCheck**) presented here facilitates easy implementation of these isomorphism check algorithms.

Definition 1: For $1 \leq t \leq n$, a balanced $(t-1)$ -spread ψ of $\mathcal{P}_n := PG(n-1, 2)$ is a set of $(t-1)$ -flats of \mathcal{P}_n which partitions \mathcal{P}_n .

In other words, a *spread* of \mathcal{P}_n is a set of projective subspaces of \mathcal{P}_n that forms a partition and a cover of \mathcal{P}_n i.e., ψ consists of all disjoint flats that includes every element of \mathcal{P}_n . A $(t - 1)$ -spread of \mathcal{P}_n contains $\mu = (2^n - 1)/(2^t - 1)$ distinct $(t - 1)$ -flats that can be used to construct the RDCSSs for different stages of randomization. A necessary and sufficient condition for the existence of a balanced $(t - 1)$ -spread is that t divides n (André, 1954).

If t does not divide n , then either a partial $(t - 1)$ -spread or an overlapping set of RDCSSs have to be used for design construction. Ranjan et al. (2009) presents some results on design construction using partial spreads. However, we restrict to the algorithms on the isomorphism of complete spread based designs. In cases when overlap between two $(t - 1)$ -flats (i.e., RDCSSs) is unavoidable, we focus on balanced star-based designs in \mathcal{P}_n .

Definition 2: For $0 \leq t_0 < t < n$, a *balanced star* of \mathcal{P}_n is a set of μ $(t - 1)$ -flats and a $(t_0 - 1)$ -flat in \mathcal{P}_n , such that the intersection of any two of the μ flats is the $(t_0 - 1)$ -flat.

Such a star, denoted by $\Omega = St(n, \mu, t, t_0)$, consists of μ distinct $(t - 1)$ -flats called rays and a $(t_0 - 1)$ -flat known as the nucleus. The covering star $St(n, \mu, t, t_0)$ provides $\mu = (2^{n-t_0} - 1)/(2^{t-t_0} - 1)$ overlapping RDCSSs of size $2^t - 1$ each.

A balanced spread can be constructed using the cyclic approach of Hirschfeld (1998). The non-zero elements of $GF(2^n)$ can be written as $\{\omega^0, \omega^1, \dots, \omega^{2^n-2}\}$, where ω is a primitive element, and $\omega^i = \alpha_0\omega^0 + \alpha_1\omega^1 + \dots + \alpha_{n-1}\omega^{n-1}$, for $0 \leq i \leq 2^n - 2$, correspond to the vector representation $(\alpha_0, \dots, \alpha_{n-1})$ of elements in \mathcal{P}_n . Let t be an integer where t divides n . If we want to construct a $(t - 1)$ -spread ψ of \mathcal{P}_n , we write the non-zero elements of $GF(2^n)$ in cycles of length μ , where $\mu = (2^n - 1)/(2^t - 1)$. Hirschfeld (1998) showed that the f'_i s are $(t - 1)$ -flats as shown in Table 1 and $\psi = \{f_1, \dots, f_\mu\}$ partitions the set of all non-zero elements of $GF(2^n)$, i.e., ψ is a $(t - 1)$ -spread of \mathcal{P}_n .

Table 1. The elements of $GF(2^n)$ in cycles of length μ

f_1	f_2	\dots	f_μ
ω^0	ω^1	\dots	$\omega^{\mu-1}$
ω^μ	$\omega^{\mu+1}$	\dots	$\omega^{2\mu-1}$
\vdots	\vdots	\ddots	\vdots
$\omega^{2^n-\mu-1}$	$\omega^{2^n-\mu}$	\dots	ω^{2^n-2}

As a quick example, Table 2 shows a cyclic spread of $\mathcal{P}_4 = PG(3, 2)$ using the primitive polynomial $\omega^4 + \omega + 1$. One can use these five 1-flats (subspaces generated using two independent factors or fi's each) for constructing up to five RDCSSs of a multi-stage factorial design with 4 two-level factors.

Table 2. A 1-spread of $PG(3, 2)$ obtained via the primitive polynomial $\omega^4 + \omega + 1$.

f_1	f_2	f_3	f_4	f_5
D	C	B	A	CD
BC	AB	ACD	BD	AC
BCD	ABC	ABCD	ABD	AD

We can also construct a balanced covering star $\Omega = St(n, \mu, t, t_0)$ using such cyclic spreads as shown in Table 1. Let $\{f_1, \dots, f_\mu\}$ denote the flats constituting a $(t - t_0 - 1)$ -spread ψ of \mathcal{P}_{n-t_0} . Then there exists a $(t_0 - 1)$ -flat π in $\mathcal{P}_n \setminus \mathcal{P}_{n-t_0}$ such that $f_i^* = \langle f_i, \pi \rangle$ and $\{f_1^*, \dots, f_\mu^*\}$ form a covering star Ω of \mathcal{P}_n . We denote such stars as $\Omega = \psi \times \pi$ (see [Ranjan et al. \(2010\)](#) for the proof of this result).

We now return to the necessary theoretical details for discussing isomorphism between two designs d_1 and d_2 . Checking isomorphism between two multi-stage factorial designs requires essentially two major checks: (a) rearrangement of factorial effects within each RDCSS and the rearrangement / renaming of RDCSSs themselves, and (b) relabelling of factorial effects. The first step simply amounts to checking the equality of d_1 and d_2 as sets, and if satisfied, we refer to d_1 and d_2 as equivalent.

Definition 3: Let d_1 and d_2 be two 2^n multi-stage factorial designs with μ stages of randomization, and let the respective sets of RDCSSs be denoted by $d_1 = \{f_1, f_2, \dots, f_\mu\}$ and $d_2 = \{g_1, g_2, \dots, g_\mu\}$. Then d_1 is said to be *equivalent* to d_2 (denoted by $d_1 \equiv d_2$) if and only if, for every $f_i \in d_1$, there is a unique $g_j \in d_2$ such that $\{f_i\} = \{g_j\}$ (set equality), for $1 \leq i, j \leq \mu$.

Let $\mathcal{E}(d_1)$ denote the equivalence class of d_1 , and if $|f_i| = 2^t - 1$ for $f_i \in d_1$, then,

$$|\mathcal{E}(d_1)| = \mu![(2^t - 1)!]^\mu.$$

For instance, the size of equivalence class for the design presented in Table 2 is $5!((3!)^5) = 933120$. When n is large, checking the equivalence of two designs by naively iterating through the entire equivalence class is too computationally intensive. However, the computational burden can be reduced through a combination of sorting and *bitstring representation* scheme.

Every element of \mathcal{P}_n can be represented as a unique binary string of $2^n - 1$ bits with exactly one non-zero entry. In this representation, the contents of any RDCSS f can now be identified by the sum of the bitstring representations of its elements. For example, following the Yates Order ([Box et al., 1978](#)) of \mathcal{P}_3 , the bitstring representations of the elements of $\mathcal{P}_3 = \{A, B, AB, C, AC, BC, ABC\}$ are $A \rightarrow 1000000$, $B \rightarrow 0100000$, \dots , $ABC \rightarrow 0000001$. Then, $f = \{AB, AC, BC\}$ can be uniquely represented by the bitstring representation 0010110. As a result, the equivalence check between two designs d_1 and d_2 simplifies to only comparing two sets of μ bitstrings, which is much cheaper than having to compare d_1 to all possible rearrangements of d_2 .

The second major step towards isomorphism check is to go through all possible relabelings of the factors and factor combinations in d_1 and then check for equivalence between the relabeled d_1 and d_2 . In projective geometry literature, relabeling is typically done by applying a collineation.

Definition 4: A collineation of $\mathcal{P}_n = PG(n - 1, 2)$ is a mapping of the points from \mathcal{P}_n to \mathcal{P}_n such that $(t - 1)$ -flats gets mapped to $(t - 1)$ -flats for all $1 \leq t \leq n$.

A collineation of \mathcal{P}_n can be characterized by an $n \times n$ matrix \mathcal{C} over $GF(2)$, referred to as the collineation matrix ([Batten, 1997](#)), where the j -th column of \mathcal{C} is the image of the basic factor F_j (i.e., the effect in \mathcal{P}_n that F_j gets mapped to). For instance, a 3×3 collineation matrix for $PG(2, 2)$ is

$$\mathcal{C} = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 1 \\ 0 & 0 & 1 \end{pmatrix}$$

which relabels the basic factors as $A \rightarrow A$, $B \rightarrow B$ and $C \rightarrow BC$.

Definition 5: Two 2^n RDCSS-based designs $d_1 = \{f_1, f_2, \dots, f_\mu\}$ and $d_2 = \{g_1, g_2, \dots, g_\mu\}$ are said to be *isomorphic* (denoted by $d_1 \cong d_2$) if and only if there exists a collineation \mathcal{C} over \mathcal{P}_n such that $\mathcal{C}(d_1) \equiv d_2$. In this case, we say that \mathcal{C} is an isomorphism establishing collineation (IEC) from d_1 to d_2 .

We now briefly describe the search algorithm for isomorphism check between two spread- (star-) based designs, proposed by [Spencer et al. \(2019\)](#).

2.1. Isomorphism Check for Spread-based Designs

For checking the isomorphism between two $(t - 1)$ -spread based multi-stage factorial designs characterized by $d_1 = \{f_1, f_2, \dots, f_\mu\}$ and $d_2 = \{g_1, g_2, \dots, g_\mu\}$ in \mathcal{P}_n , we follow a systematic approach to search for the IEC by iterating through the candidate collineations. First, choose $l_0 = n/t$ out of μ RDCSSs in d_1 that can generate a basis $\{x_1, \dots, x_n\}$ for \mathcal{P}_n such that each of the l_0 RDCSSs contributed t independent points to the basis. Then, construct a collineation matrix $\mathcal{C}_{x,B}$ to transform the x 's to a canonical basis with basic factors, $\{A, B, \dots\}$. Note that the equivalence of $\mathcal{C}_{x,B}(d_1)$ and d_2 implies the isomorphism between d_1 and d_2 . Now, iterate through all possible sets of l_0 RDCSSs from d_2 to construct the basis set $\{y_1, \dots, y_n\}$ in d_2 and the corresponding collineation matrix $\mathcal{C}_{B,y}$ that maps the canonical basis to y 's. If $\mathcal{C}_{B,y}(\mathcal{C}_{x,B}(d_1))$ is equivalent to d_2 , then we have found the IEC. The step-by-step algorithm from [Spencer et al. \(2019\)](#) is now presented for convenience of the readers.

Algorithm 1 Isomorphism check between two $(t - 1)$ -spread based designs in \mathcal{P}_n

- 1: Choose $l_0 = n/t$ out of μ RDCSSs from $d_1 = \{f_1, f_2, \dots, f_\mu\}$, such that $\langle \cup_{i=1}^{l_0} f_{u_i} \rangle = \mathcal{P}_n$. Let these be $\{f_{u_1}, f_{u_2}, \dots, f_{u_{l_0}}\}$ for $1 \leq u_1, u_2, \dots, u_{l_0} \leq \mu$.
 - 2: For $i = 1, \dots, l_0$, specify $\{x_{i,1}, \dots, x_{i,t}\} \in f_{u_i}$ such that $f_{u_i} = \langle x_{i,1}, \dots, x_{i,t} \rangle$.
 - 3: Construct the collineation matrix $\mathcal{C}_{x,B}$ which maps the x 's in Step 2 to the canonical basis $\{A, B, \dots\}$ such that each $x_{i,j}$ is mapped to $F_{t(i-1)+j}$.
 - 4: (a) Choose l_0 out of μ RDCSSs from $d_2 = \{g_1, g_2, \dots, g_\mu\}$ for mapping f_{u_i} 's (note that ordering is important). Let that be $\{g_{v_1}, g_{v_2}, \dots, g_{v_{l_0}}\}$ for $1 \leq v_1, v_2, \dots, v_{l_0} \leq \mu$. If $|\langle g_{v_1} \cup \dots \cup g_{v_{l_0}} \rangle| < 2^n - 1$, proceed to the next choice for $\{g_{v_1}, g_{v_2}, \dots, g_{v_{l_0}}\}$.
 - (b) For $i = 1, \dots, l_0$, choose a $\{y_{i,1}, \dots, y_{i,t}\} \in g_{v_i}$ such that $g_{v_i} = \langle y_{i,1}, \dots, y_{i,t} \rangle$.
 - (c) Choose one of the $(l_0)!$ permutations of $1, \dots, l_0$, say σ_k , for $k = 1, \dots, (l_0)!$.
 - (d) Construct $\mathcal{C}_{B,y}$ which maps the canonical basis elements to y 's such that $F_{t(i-1)+j}$ is mapped to $y_{\sigma_k(i),j}$.
 - (e) If $\mathcal{C}_{B,y}(\mathcal{C}_{x,B}(d_1))$ is equivalent to d_2 , then $d_1 \cong d_2$, and report $\mathcal{C} = \mathcal{C}_{B,y} \cdot \mathcal{C}_{x,B}$ as an IEC and exit; otherwise, continue.
 - (f) Go to Step 4(c) and choose another ordering σ_k if possible, otherwise, continue.
 - (g) Go to Step 4(b) and choose another basis if possible, otherwise, continue.
 - (h) Go to Step 4(a) and choose another set of RDCSSs if possible, otherwise report that d_1 and d_2 are non-isomorphic.
-

2.2. Isomorphism check for star based design

A balanced star $\Omega = St(n, \mu, t, t_0)$ can be expressed as $\Omega = \psi \times \pi$, where ψ is a $((t - t_0) - 1)$ -spread of \mathcal{P}_{n-t_0} , and π is $(t_0 - 1)$ -dimensional subspace in $\mathcal{P}_n \setminus \mathcal{P}_{n-t_0}$. Thus, the isomorphism check between two star-based designs d_1 and d_2 (with $(t_0 - 1)$ -dimensional nuclei) can be reduced to checking isomorphism between two $(h - 1)$ -spreads of \mathcal{P}_{n-t_0} by iterating through the elements of \mathcal{C}_{n-t_0} instead of \mathcal{C}_n . Algorithm

2 (presented by [Spencer et al. \(2019\)](#)) summarizes the steps of how Algorithm 1 can be used to search for an IEC between ψ_1 and ψ_2 assuming $\Omega_i = \psi_i \times \pi_i$ for $i = 1, 2$.

Algorithm 2 Isomorphism check between two $St(n, \mu, t, t_0)$ -based designs d_1 and d_2 , which correspond to stars $\Omega_1 = \psi_1 \times \pi_1$ and $\Omega_2 = \psi_2 \times \pi_2$, respectively.

- 1: Determine two bases $\{p_{1,1}, \dots, p_{1,t_0}\}$ and $\{p_{2,1}, \dots, p_{2,t_0}\}$ of nuclei π_1 and π_2 , respectively.
 - 2: Construct a collineation matrix $\mathcal{C}_{\pi_1, B}$ mapping $\{p_{1,1}, \dots, p_{1,t_0}\}$ to the t_0 trailing basic factors F_{n-t_0+1}, \dots, F_n . The pre-images of F_1, \dots, F_{n-t_0} can be chosen as an arbitrary linearly independent set from $\mathcal{P}_n \setminus \pi_1$.
 - 3: Similarly, construct a collineation matrix $\mathcal{C}_{\pi_2, B}$ mapping $\{p_{2,1}, \dots, p_{2,t_0}\}$ to the t_0 trailing basic factors F_{n-t_0+1}, \dots, F_n .
 - 4: Extract designs d_1^* and d_2^* on \mathcal{P}_{n-t_0} corresponding to the spreads $\mathcal{C}_{\pi_1, B}(\psi_1)$ and $\mathcal{C}_{\pi_2, B}(\psi_2)$.
 - 5: Run Algorithm 1 on d_1^* and d_2^* . If we come across a \mathcal{C}^* that is an IEC, then an IEC for d_1 and d_2 is given by $\mathcal{C} = \mathcal{C}_{\pi_2, B}^{-1} \cdot \mathcal{C}^* \cdot \mathcal{C}_{\pi_1, B}$. Otherwise, d_1 and d_2 are non-isomorphic.
-

3. IsoCheck package

In this section, we examine the functions in the **IsoCheck** package which checks the isomorphism for RDCSS-based designs through the theoretical results and efficient algorithms proposed by [Spencer et al. \(2019\)](#). We will discuss both spread-based and star-based designs. The most important functions are `checkSpreadIsomorphism()` and `checkStarIsomorphism()` which take two spreads and stars, respectively, as inputs and return a Boolean (TRUE/FALSE) indicating whether or not the inputs are isomorphic. If they are isomorphic, then these two functions also return isomorphism establishing collineations (IECs). We have also packaged a few important additional functions for efficiently checking the equivalence and iterating through different collineations. All of these functions have been summarized as follows:

- `checkSpreadIsomorphism()`: requires two spreads (`spread1` and `spread2`) as inputs whose isomorphism is to be checked. It also takes an argument called `returnfirstIEC` which indicates whether all isomorphism establishing collineations should be returned (default), or terminate only after the first one is found.
- `checkStarIsomorphism()`: works in the similar way as `checkSpreadIsomorphism()`, except it requires two stars (`star1` and `star2`) as inputs, and uses Algorithm 2.
- `checkSpreadEquivalence()`: takes two spreads (`spread1` and `spread2`) as inputs, and compares their sorted bitstring representations. It returns a Boolean- TRUE if the spreads are equivalent, else it returns FALSE.
- `checkStarEquivalence()` : works in the similar way as `checkSpreadEquivalence()`, except it requires two stars (`star1` and `star2`) as inputs.
- `getBitstrings()` : takes a spread (or a star) and returns its bitstring representation. This makes the equivalence check, and subsequently the isomorphism check, significantly more computationally efficient as compared to the naive approach.
- `applyCollineation()` : takes an $n \times n$ collineation matrix and a spread (or a star), and produces the relabeled spread (or the star).

- `star_to_spread()` : takes a star `star` (assumes the structure to be $\Omega = \psi \times \pi$), isolates the nucleus π from this star by using a suitable collineation matrix, and returns the spread ψ embedded in this star along with the collineation matrix.

We have also included two more functions called `stringtovector()` and `vectortoString()` in the *R* package **IsoCheck**, which facilitates the users in inputting the spreads and stars. However, for quick usage and illustration, several spreads and stars have also been hard-coded, e.g., `spreadn4t2a`, `spreadn4t2b`, `starn8t5a`, `starn8t5b` (see the package manual for other builtin spreads and stars). These functions are illustrated in details in Section 4.

The function `star_to_spread()` is called within `checkStarIsomorphism()` which separates the nucleus π_i and $1(= (t - t_0) - 1)$ -spread ψ_i of \mathcal{P}_4 from the star Ω_i where $i = 1, 2$ such that $\Omega_1 = \psi_1 \times \pi_1$ and $\Omega_2 = \psi_2 \times \pi_2$. Then the problem is reduced to checking the isomorphism between the two spreads ψ_1 and ψ_2 and equality of two nuclei π_1 and π_2 . This is Algorithm 2 described in detail by [Spencer et al. \(2019\)](#). See Example 4 for an illustration.

4. Examples using IsoCheck

This section demonstrates the usage of different functions in **IsoCheck** for checking equivalence and isomorphism of multi-stage factorial designs with randomization restrictions. We also show how some of these functions can be used in design ranking and further creating catalogs of good non-isomorphic designs for a practitioner.

Example 1 We know from [André \(1954\)](#) that there exists non-trivial 1-spreads ($t = 2$) of \mathcal{P}_4 and [Soicher \(2000\)](#) has shown that they are isomorphic. Here we illustrate how isomorphism can be established between two 1-spreads of \mathcal{P}_4 . Table 3 shows the two 1-spreads of \mathcal{P}_4 .

Table 3. Two 1-spreads of $\mathcal{P}_4 = PG(3, 2)$

spreadn4t2a					spreadn4t2b				
f_1	f_2	f_3	f_4	f_5	g_1	g_2	g_3	g_4	g_5
D	C	B	A	CD	A	C	D	ABC	AC
BC	AB	ACD	BD	AC	CD	ABCD	B	AD	AB
BCD	ABC	ABCD	ABD	AD	ACD	ABD	BD	BCD	BC

The *R* package **IsoCheck** includes these two 1-spreads of \mathcal{P}_4 that can be called using the `data()` command as follows:

```
R> data("spreadn4t2a", package = "IsoCheck")
R> data("spreadn4t2b", package = "IsoCheck")
```

The users can use `stringtovector()` to manually input the spreads of their choice as a three dimensional array `spr[i, j, k]` which specifies the presence of i -th basic factor in the j -th effect of the k -th flat of `spr`. For instance, `spreadn4t2a` can be coded as follows.

```
R> spr <- array(NA,c(n=4,flatsize=3,mu=5))
R> spr[,1,1] <- stringtovector("D",n=4)
```



```
R> spr[,2,1] <- stringtovector("BC",n=4)
R> spr[,3,1] <- stringtovector("BCD",n=4)
...
R> spr[,3,5] <- stringtovector("AD",n=4)
```

We can check the isomorphism between the two spreads `spreadn4t2a` and `spreadn4t2b` (shown in Table 3) by calling `checkSpreadIsomorphism()`. This function implements Algorithm 1 described in [Spencer et al. \(2019\)](#) to search for the IEC by iterating through all the possible collineations over \mathcal{P}_4 .

```
R> test <- checkSpreadIsomorphism(spreadn4t2a, spreadn4t2b,
+ returnfirstIEC = FALSE, printstatement = TRUE)
```

The output printed on console is shown as follows:

```
[1] "percent done: 0.28"
[1] "percent done: 0.56"
...
[1] "percent done: 99.72"
[1] "percent done: 100"
[1] "The two spreads are isomorphic. For example, one isomorphism establishing
collineation is"
[,1] [,2] [,3] [,4]
[1,] 0 1 0 0
[2,] 1 0 0 0
[3,] 1 1 1 1
[4,] 1 0 0 1
```

The argument `printstatement` when set to `TRUE` declares the isomorphism at the end of the run and returns the first IEC. The output of the function `checkSpreadIsomorphism()` returns a Boolean value `TRUE` and enumerates all the isomorphism establishing collineations. The command `test$IECs[[1]]` shows the first IEC, and `length(test$IECs)` returns the total number of IECs found by the algorithm. The user can instead choose to terminate the search for IEC as soon as the first IEC is found and cut down the run time, by using the argument `returnfirstIEC = TRUE`.

```
R> test$result

[1] TRUE

R> test$IECs[[1]]

[,1] [,2] [,3] [,4]
[1,] 0 1 0 0
[2,] 1 0 0 0
[3,] 1 1 1 1
[4,] 1 0 0 1

R> length(test$IECs)

[1] 360
```

In order to cross-verify that the resultant matrix `test$IEC[[1]]` indeed establishes isomorphism between the two spreads, we first apply the collineation matrix to the first spread `spreadn4t2a` and then check if the resulting spread `Cspreadn4t2a` is equivalent to the second spread `spreadn4t2b`.

```
R> IEC <- test$IECs[[1]]
R> Cspreadn4t2a <- applyCollineation(IEC, spreadn4t2a)
R> vectortostring(Cspreadn4t2a)
```

Table 4 presents the output of `vectortostring(Cspreadn4t2a)`.

Table 4. Equivalent of 1-spread of $PG(3, 2)$

Cspreadn4t2a				
h_1	h_2	h_3	h_4	h_5
CD	C	AC	BCD	D
A	ABD	BC	AD	BD
ACD	ABCD	ABC	ABC	B

By visual inspection it is clear that `spreadn4t2b` is simply a rearrangement of `Cspreadn4t2a`, but for bigger problems it becomes difficult to conclude anything about equivalence by simple visual inspection. Hence we use `checkSpreadEquivalence()` function, which converts the spreads to their bitstring representations and the comparison becomes easy.

```
R> checkSpreadEquivalence(Cspreadn4t2a, spreadn4t2b)
```

[1] TRUE

Example 2 We now consider the isomorphism of 2-spreads ($t = 3$) of $\mathcal{P}_6 = PG(5, 2)$. For illustration, we choose two distinct built-in spreads, `spreadn6t3a` and `spreadn6t3b`, however, the users may input the spreads of their own choice.

```
R> checkSpreadEquivalence(spreadn6t3a, spreadn6t3b)
```

[1] FALSE

The two spreads `spreadn6t3a` and `spreadn6t3b` are presented in Tables 5 and 6 respectively.

Table 5. A 2-spread of $\mathcal{P}_6 = PG(5, 2)$

spreadn6t3a								
f_1	f_2	f_3	f_4	f_5	f_6	f_7	f_8	f_9
A	B	C	D	E	F	BD	AC	AD
EF	AF	AB	BC	CD	DE	BF	CE	BE
AEF	ABF	ABC	BCD	CDE	DEF	DF	AE	ABDE
BCE	CDF	ADE	BEF	ACF	ABD	ACE	BDF	CF
ABCE	BCDF	ACDE	BDEF	ACEF	ABDF	ABCDE	ABCDF	ACDF
BCF	ACD	BDE	CEF	ADF	ABE	ABCEF	BCDEF	BCEF
ABCF	ABCD	BCDE	CDEF	ADEF	ABEF	ACDEF	ABDEF	ABCDEF

We now proceed to check isomorphism between the two spreads.

Table 6. A 2-spread of $\mathcal{P}_6 = PG(5, 2)$

spreadn6t3b								
g_1	g_2	g_3	g_4	g_5	g_6	g_7	g_8	g_9
ABC	E	DF	B	A	EF	BE	ABCDF	AC
AEF	ABCEF	ABCE	DEF	BDF	AB	F	ADF	AE
BCEF	ABCF	ABCDEF	BDEF	ABDF	ABEF	BEF	BC	CE
ADEF	BDE	C	AF	ABCDE	ACE	BCDF	BF	DE
BCDEF	BD	CDF	ABF	BCDE	ACF	CDEF	ACD	ACDE
D	ACDF	ABE	ADE	ACEF	BCE	BCD	ABD	AD
ABCD	ACDEF	ABDEF	ABDE	CEF	BCF	CDE	CF	CD

```
R> test <- checkSpreadIsomorphism(spreadn6t3a, spreadn6t3b,
+   returnfirstIEC = TRUE, printstatement = FALSE)
```

```
R> test$result
```

```
[1] TRUE
```

```
R> test$IECs
```

```
[[1]]
```

```
[,1] [,2] [,3] [,4] [,5] [,6]
[1,] 1 0 0 1 1 0
[2,] 0 1 0 1 0 0
[3,] 1 1 0 0 0 1
[4,] 1 1 1 0 0 1
[5,] 0 1 0 1 0 1
[6,] 1 1 1 1 1 0
```

Similar to Example 1, one can use `applyCollineation()` and `checkSpreadEquivalence()` to cross-check whether the collineation matrix found is indeed an IEC. Since we used `"returnfirstIEC = TRUE"`, the code terminates after the first IEC was found.

Example 3 Mee and Bates (1998) constructed and analyzed split-lot experimental designs for multistage batch processing for fabrication of integrated circuits. Here we illustrate the isomorphism between two designs for a 64-wafer experiment which involves six basic factors and nine disjoint RDCCSs, each of size seven. The two designs are $IC_1 = \{\langle A, EF, BCE \rangle, \langle B, AF, CDF \rangle, \langle C, AB, ADE \rangle, \langle D, BC, BEF \rangle, \langle E, CD, ACF \rangle, \langle F, DE, ABD \rangle, \langle BD, BF, ACE \rangle, \langle AC, CE, BDF \rangle, \langle AD, BE, CF \rangle\}$ and $IC_2 = \{\langle A, BD, CF \rangle, \langle B, AF, CE \rangle, \langle C, BF, DE \rangle, \langle D, AC, BE \rangle, \langle E, AB, DF \rangle, \langle F, AE, CD \rangle, \langle AD, BC, EF \rangle, \langle ACE, ADF, BEF \rangle, \langle ABC, ADE, CEF \rangle\}$. Here, $\langle \cdot, \cdot, \cdot \rangle$ denotes the span of the basis vectors within it. We can construct the full flats using these basis vectors with the following code.

```
R> basistoflat3 <- function(b1,b2,b3, n){
+   base1 <- stringtovector(b1, n)
+   base2 <- stringtovector(b2, n)
+   base3 <- stringtovector(b3, n)
+   v1 <- (base1 + base2) %%2
```

```

+ v2 <- (base1 + base3) %%2
+ v3 <- (base2 + base3) %%2
+ v4 <- (v1 + base3) %%2
+ return(cbind(base1, base2, v1, base3, v2, v3,v4))
+ }

R> n <- 6
R> flatsize <- 2^3-1
R> mu <- 9
R> spread_IC1 <- array(NA, c(n, flatsize, mu))

R> spread_IC1[,,1] <- basistoflat3("A", "EF", "BCE", n)
R> spread_IC1[,,2] <- basistoflat3("B", "AF", "CDF", n)
...
R> spread_IC1[,,9] <- basistoflat3("AD", "BE", "CF", n)

```

The complete spread IC_1 is now constructed and stored in the array `spread_IC1`. Similarly, the second spread IC_2 is constructed and stored as `spread_IC2`. We can now proceed to check the isomorphism between `spread_IC1` and `spread_IC2`.

```

R> test<- checkSpreadIsomorphism(spread_IC1, spread_IC2,
+ returnfirstIEC = T)

R> test$result

[1] TRUE

```

Hence, both the designs IC_1 and IC_2 are isomorphic. As in Example 2, we saved some computational time by terminating the algorithm after the first IEC was found. One can extract the IEC by calling `test$IECs`.

Example 4 We now demonstrate the isomorphism check between two stars `starn5t3a` and `starn5t3b` denoted by Ω_1 and Ω_2 , respectively, (see Table 7). Both of these are balanced covering stars of $\mathcal{P}_5 = PG(4, 2)$ denoted by $St(5, 5, 3, 1)$. The stars consist of $\mu = \frac{2^n - t_0 - 1}{2^t - t_0 - 1} = \frac{2^5 - 1 - 1}{2^3 - 1 - 1} = 5$ rays of 2-flats overlapping with a nucleus which is a 0-flat in \mathcal{P}_5 . A close look at Table 7 shows that the nucleus in Ω_1 is $\pi_1 = \langle A \rangle$ and in Ω_2 it is $\pi_2 = \langle ABC \rangle$.

The following code can be used to quickly verify the equivalence of the two stars.

```

R> checkStarEquivalence(starn5t3a, starn5t3b)

[1] FALSE

```

As discussed in Sections 2, one can check for the isomorphism between two stars either by directly using `checkStarIsomorphism()` or by first decomposing the star to a spread via `star_to_spread()` and then use `checkSpreadIsomorphism()`. The first approach is implemented as follows.

```

R> checkStarIsomorphism(starn5t3a, starn5t3b, returnfirstIEC = TRUE)

$result
[1] TRUE

$IECs[[1]]

```

Table 7. Two stars of $\mathcal{P}_5 = PG(4, 2)$

starn5t3a= Ω_1					starn5t3b= Ω_2				
f_1	f_2	f_3	f_4	f_5	g_1	g_2	g_3	g_4	g_5
A	D	C	B	DE	ABC	AE	D	E	CE
E	BC	BDE	BCE	BD	AC	DE	C	ACDE	A
CDE	BCD	BCDE	CE	BE	CDE	AD	CD	ACD	ACE
AE	AD	AC	AB	A	B	BCE	ABCD	ABCE	ABC
ACD	ABC	ABDE	ACE	ABD	BCDE	ABCDE	AB	BD	BC
ACDE	ABCD	ABCDE	A	ABE	ABDE	BCD	ABD	ABC	BE
CD	A	A	ABCE	ADE	ADE	ABC	ABC	BDE	ABE

```
X1 X2 X3 X4 X5
X1 1 0 1 1 1
X2 1 1 1 0 0
X3 1 0 0 0 0
X4 0 1 0 0 1
X5 0 1 1 1 1
```

For the latter approach, we first assume that $\Omega_i = \psi_i \times \pi_i$, for $i = 1, 2$. Then one can extract ψ_1 and ψ_2 using the function `star_to_spread()` on `starn5t3a` and `starn5t3b`, respectively.

```
R> red_spread_1 <- star_to_spread(starn5t3a)
R> red_spread_2 <- star_to_spread(starn5t3b)
R> psi_1 <- vector_to_string(red_spread_1[[1]])
R> psi_1

[,1] [,2] [,3] [,4] [,5]
[1,] "A"  "B"  "C"  "D"  "AB"
[2,] "ABC" "CD" "ABD" "ACD" "BD"
[3,] "BC"  "BCD" "ABCD" "AC"  "AD"

R> psi_2 <- vector_to_string(red_spread_2[[1]])
R> psi_2

[,1] [,2] [,3] [,4] [,5]
[1,] "C"  "AD" "B"  "A"  "D"
[2,] "ABCD" "AB" "CD" "BC" "AC"
[3,] "ABD"  "BD" "BCD" "ABC" "ACD"
```

The output of `star_to_spread()` is a list containing two values, the reduced spread and a collineation matrix over \mathcal{P}_5 that ensures that the spreads ψ_i spans $\langle A, B, C, D \rangle$ and the nucleus is $\pi_i = \langle E \rangle$. For instance, the collineation matrix for relabelling Ω_2 is obtained as

```
R> red_spread_2$collineation

X1 X2 X3 X4 X5
0 0 0 0 1
0 0 0 1 0
```

```
0 1 1 0 0
1 0 1 0 0
0 0 1 0 0
```

and the corresponding relabelled star can be extracted as follows.

```
R> Cstarn5t3b <- applyCollineation(red_spread_2$collineation, starn5t3b)
R> vectortostring(Cstarn5t3b)
```

```
[,1]    [,2]   [,3]   [,4]   [,5]
[1,] "E"     "AD"   "B"    "A"    "ACDE"
[2,] "CE"     "AB"   "CDE"  "ABCE" "D"
[3,] "ABCDE"  "BD"   "BCDE" "BCE"  "ACE"
[4,] "C"      "ADE"  "BE"   "AE"   "E"
[5,] "ABDE"   "ABE"  "CD"   "BC"   "DE"
[6,] "ABCD"   "BDE"  "BCD"  "E"    "AC"
[7,] "ABD"    "E"    "E"    "ABC"  "ACD"
```

We now check the isomorphism between Ω_1 and Ω_2 by simply checking the isomorphism between `red_spread_1[[1]]` and `red_spread_2[[1]]`.

```
R> checkSpreadIsomorphism(red_spread1[[1]], red_spread2[[1]],
+ returnfirstIEC=TRUE)
```

```
$result
[1] TRUE
```

```
$IECs[[1]]
[,1] [,2] [,3] [,4]
[1,]  1   1   1   1
[2,]  1   0   0   1
[3,]  0   0   1   1
[4,]  1   1   1   0
```

Example 5 [Bingham et al. \(2008\)](#) considered a 2^5 factorial split-lot design for manufacturing plutonium alloy cookies which involved five basic factors with three processing stages. They suggested a design $PA_1 = \{\langle A, B, CDE \rangle, \langle C, AD, BE \rangle, \langle D, E, ABC \rangle\}$. This design is derived from a balanced covering star $St(5, 5, 3, 1)$ of \mathcal{P}_5 . Later on, [Ranjan et al. \(2010\)](#) recommended another design $PA_2 = \{\langle A, B, DE, ACD \rangle, \langle C, AB, DE, ACD \rangle, \langle D, E, AB, ACD \rangle\}$, which represents a balanced covering star $St(5, 3, 4, 3)$ of \mathcal{P}_5 .

We can define the two stars as shown in the following code. For defining PA_1 , `basistoflat3()` was presented in Example 3. We similarly write a function called `basistoflat4()` for constructing the $(4 - 1)$ -flats, and then define PA_2 as follows.

```
R> n <- 5
R> flatsize <- 2^3-1
R> mu <- 3

R> star_PA1 <- array(NA, c(n, flatsize, mu))
R> star_PA1[, ,1] <- basistoflat3("A", "B", "CDE", n)
R> star_PA1[, ,2] <- basistoflat3("C", "AD", "BE", n)
R> star_PA1[, ,3] <- basistoflat3("D", "E", "ABC", n)
```



```
R> n <- 5
R> flatsize <- 2^4-1
R> mu <- 3

R> star_PA2 <- array(NA, c(n, flatsize, mu))
R> star_PA2[,,1] <- basistoflat4("A", "B", "DE", "ACD", n)
R> star_PA2[,,2] <- basistoflat4("C", "AB", "DE", "ACD", n)
R> star_PA2[,,3] <- basistoflat4("D", "E", "AB", "ACD", n)
```

The isomorphism between the two stars can be checked by using the following code.

```
R> checkStarIsomorphism(star_PA1, star_PA2)
```

Stars are not of same dimension.

```
[1] FALSE
```

The output is certainly expected as the `flatsize` in PA_1 and PA_2 are different. One can also verify that the sizes of nucleus in these two stars are different.

```
R> nucleus_PA1 <- suppressMessages(plyr::match_df(data.frame(t(star_PA1[, ,1])),
+ data.frame(t(star_PA1[, ,2])))
R> vectortostring(as.numeric(nucleus_PA1))
```

```
[,1]
[1,] "ABCDE"
```

```
R> nucleus_PA2 <- suppressMessages(plyr::match_df(data.frame(t(star_PA2[, ,1])),
+ data.frame(t(star_PA2[, ,2])))
R> vectortostring(t(as.matrix(nucleus_PA2)))
```

```
[,1]
[1,] "DE"
[2,] "ACD"
[3,] "AB"
[4,] "ACE"
[5,] "ABDE"
[6,] "BCD"
[7,] "BCE"
```

5. Catalog of Multi-Stage Factorial Designs

In this section, we illustrate the usage of `IsoCheck` functions in catalog construction for balanced spread- and balanced covering star- based designs. We do not claim to propose any new designs, new ranking criterion, or new catalogs. In general, the construction of such a catalog requires iterating through all possible candidate designs and then checking isomorphism among them (Bingham and Sitter, 1999b; Lin and Sitter, 2008). Unfortunately, we are unaware of any computationally efficient methodologies that can construct all possible balanced $(t - 1)$ - spreads or balanced covering stars of $PG(n - 1, 2)$. As a result, we follow an exhaustive search approach for constructing all possible spreads.

Researchers and practitioners often combine such catalogs with a carefully chosen design ranking criteria to sort through different designs and select the most optimal candidate for their experiments.

For classical fractional factorial designs, popular design ranking criteria include maximum resolution, generalized minimum aberration, maximum number of clear two-factor interactions (2-fi’s), etc. (Xu et al., 2001; Butler, 2003; Cheng and Tsai, 2011). Let d be a factorial design with randomization restrictions characterized by S_1, \dots, S_k , then, Bingham et al. (2008) proposed a V -criterion defined by

$$V(d) = \sum_{i=1}^k (p_i - \bar{p})^2,$$

where $\bar{p} = \sum_{i=1}^k p_i/k$ and p_i is proportion of main effects and 2-fi’s in S_i . If we have a $(t - 1)$ -spread based design then S_i would be an RDCSS, or equivalently, a $(t - 1)$ -flat in the $(t - 1)$ -spread, whereas, if the design is obtained from a star $St(n, \mu, t, t_0)$, then S_i would be the flat minus the nucleus (i.e., $|S_i| = 2^t - 2^{t_0}$). From an analysis standpoint, if we use half-normal plots for assessing the significance of factorial effects, then S_i represents the set of factorial effects that would be used for the i -th half-normal plot. Thus minimizing this V -criterion encourages homogeneous distribution of main effects and two-factor interactions among the S_i ’s.

We now discuss building a catalog of designs characterized by a $(t - 1)$ -spread of \mathcal{P}_n , for fixed $t < n$. Suppose we wish to build a catalog of 1-spreads of $\mathcal{P}_4 = PG(3, 2)$ (Table 3 presents an example `spreadn4t2a`). This structure contains $2^4 - 1 = 15$ elements (factorial effects) distributed in 5 subspaces of size 3 each. One possible (although computationally inefficient) approach is to exhaustively search all possible permutations/arrangements of these 15 elements, and then check whether or not they form a 1-spread. If yes, then we can check the isomorphism between this spread and the original `spreadn4t2a`. We can also compute the design ranking criterion value for all these spreads. The steps of catalog construction are summarized in Algorithm 3.

Algorithm 3 for constructing a catalog of non-isomorphic spreads (or stars).

- 1: Pick an initial $(t - 1)$ -spread (say, d_1) of $\mathcal{P}_n := PG(n - 1, 2)$.
 - 2: Compute the design ranking criterion value of d_1 .
 - 3: Pick a random permutation (say ρ) of the set of $2^n - 1$ elements of d_1 .
 - 4: Use `is.spread()` to check if $\rho(d_1)$ is a proper $(t - 1)$ -spread of \mathcal{P}_n . If “TRUE”, go to the next step, otherwise go back to Step 3 (if all possible permutations of d_1 have not been exhausted yet).
 - 5: Compute the design ranking criterion value of $\rho(d_1)$.
 - 6: Use `checkSpreadIsomorphism()` to check whether or not $\rho(d_1)$ is isomorphic to d_1 .
 - 7: Go to Step 3 if all possible permutations of d_1 have not been exhausted yet.
-

Note that $15! = 1.307674 \times 10^{12}$ is a big number and one would have to iterate through these many possible rearrangements to ensure the construction of all possible 1-spreads of \mathcal{P}_4 . Admittedly, one can come up with innovative ideas to save some computational cost, but that is not the main objective here. For this example, we ran this algorithm for over 5 million random permutations, and found almost 110 isomorphic spreads. Note that we did not expect to find any non-isomorphic spreads, because Spencer et al. (2019) have already mentioned that all 1-spreads of $PG(3, 2)$ are isomorphic. Nonetheless, we used this spread for illustration because it is a computationally inexpensive small example to follow through. Interestingly, we found designs with two criterion value $V(d) = 0.44$ and 0.22 , which indicates preference of one design over the other. The initial design `spreadn4t2a` gave $V(d) = 0.22$ (with $p_1 = 2/3, p_2 = 2/3, p_3 = 1/3, p_4 = 2/3$ and $p_5 = 1$), whereas, the following design, found through Algorithm 3, corresponds to $V(d) = 0.44$ (with $p_1 = 1/3, p_2 = 2/3, p_3 = 1, p_4 = 1/3$ and $p_5 = 1$).

```
[,1] [,2] [,3] [,4] [,5]
[1,] "ABC" "CD" "AD" "ABD" "B"
```

```
[2,] "D"      "ACD" "AB" "BCD" "C"
[3,] "ABCD" "A"   "BD" "AC"  "BC"
```

Since the objective is to find designs with lower $V(d)$ criterion value, although isomorphic, designs with $V(d) = 0.22$ is better than the one with $V(d) = 0.44$.

If the underlying design is based on a star (say Ω), then one can use `star_to_spread(Ω)` function to extract the spread ψ after removing the nucleus π (assuming $\Omega = \psi \times \pi$) from the star. Subsequently, the designs from the catalog of the underlying spreads can be combined with the nucleus to construct the desired catalog of stars. For instance, `star_to_spread(starn5t3a)` gives a 1-spread of $PG(3, 2)$ (discussed in details).

6. Concluding Remarks

This paper presents an R package **IsoCheck** to check the isomorphism of balanced $(t - 1)$ -spreads and balanced covering stars of $\mathcal{P}_n = PG(n - 1, 2)$, which corresponds to the isomorphism check of two-level multi-stage factorial designs with randomization restrictions (Ranjan et al., 2009, 2010). The main ideas behind the algorithms are to apply the relabellings via collineation matrices and rearrangements or the factorial effects within the RDCSSs through bitstring representation of the elements of \mathcal{P}_n . In this paper, we have presented several worked out examples which illustrate the usage of **IsoCheck** functions and their arguments for the isomorphism check. More importantly, we also outline how **IsoCheck** functions can be used to build catalog of good designs in this class of spread/star-based factorial designs.

A few important remarks are in order. 1. In practice, whenever we have more than one possible design options for conducting an experiment, the ranking of design becomes important. This has traditionally been done in the context of “fractional” factorial designs, as we have several options for choosing the fraction defining contrast subgroups (FDCS). For multi-stage factorial designs with randomization restrictions (i.e., spread/star -based designs), we have to choose even randomization defining contrast subspaces (RDCSSs), which are in some sense similar to FDCS. Therefore, we can also talk about the isomorphism and ranking of the full factorial unreplicated spread/star-based multi-stage factorial designs with randomization restrictions. 2. One can use **IsoCheck** functions to check for the isomorphism of multi-stage fractional factorial designs as well. 3. The generalization of these isomorphism check algorithms for $q(\geq 3)$ -level factorial designs appears to be non-trivial.

Acknowledgement

The authors would like to thank the Editor and the reviewers for their helpful comments which led to substantial improvement in the manuscript.

REFERENCES

- Addelman, S. (1964). Some two-level fractional plans with split-plot confounding. *Technometrics*, 30:253–258.
- André, J. (1954). Über nicht-desarguessche ebenen mit transitiver translationsgruppe. *Mathematische Zeitschrift*, 60(1):156–186.
- Bailey, R. A. (2004). *Association schemes: Designed experiments, algebra and combinatorics*, volume 84. Cambridge University Press.

- Batten, L. M. (1997). *Combinatorics of finite geometries*. Cambridge University Press.
- Bingham, D. and Sitter, R. (1999a). Minimum-aberration two-level fractional factorial split-plot designs. *Technometrics*, 41:62–70.
- Bingham, D., Sitter, R., Kelly, E., Moore, L., and Olivas, J. D. (2008). Factorial designs with multiple levels of randomization. *Statistica Sinica*, pages 493–513.
- Bingham, D. and Sitter, R. R. (1999b). Minimum-aberration two-level fractional factorial split-plot designs. *Technometrics*, 41(1):62–70.
- Bisgaard, S. (1994). Blocking generators for small 2^{k-p} designs. *Journal of Quality Technology*, 26:288–296.
- Bose, R. C. (1947). Mathematical theory of the symmetrical factorial design. *Sankhyā: The Indian Journal of Statistics*, pages 107–166.
- Box, G. E., Hunter, W. G., Hunter, J. S., et al. (1978). *Statistics for experimenters*.
- Butler, N. A. (2003). Some theory for constructing minimum aberration fractional factorial designs. *Biometrika*, 90(1):233–238.
- Butler NA (2004) Construction of two-level split-lot fractional factorial designs for multistage processes. *Technometrics* 46:445–451
- Cheng, C.-S. and Tsai, P.-W. (2011). Multistratum fractional factorial designs. *Statistica Sinica*, 21:1001–1021.
- Cheng C.S. (2016). *Theory of factorial design: Single-and multi-stratum experiments*. Chapman and Hall/CRC
- Dean A. and Voss D. (1999). *Design and Analysis of Experiments*. Springer-Verlag New York/
- Fisher, R. A. (1942). The theory of confounding in factorial experiments in relation to the theory of groups. *Annals of Eugenics*, 11:290–299.
- Franklin, M. and Bailey, R. (1977). Selection of defining contrasts and confounded effects in two-level experiments. *Applied Statistics*, 26:321–326.
- Hedayat AS, Sloane NJA, Stufken J (2012) *Orthogonal arrays: theory and applications*. Springer Science & Business Media
- Hirschfeld, J. (1998). *Projective Geometries Over Finite Fields*. *Oxford Mathematical Monographs*. Oxford University Press New York.
- Lin, C. and Sitter, R. (2008). An isomorphism check for two-level fractional factorial designs. *Journal of Statistical Planning and Inference*, 134:1085–1101.
- Mateva Z.T. and Topalova S.T. (2009). Line spreads of PG (5, 2). *Journal of Combinatorial Designs* 17(1):90–102
- Mee, R. and Bates, R. (1998). Split-lot designs: Experiments for multistage batch processes. *Technometrics*, 40:127–140.
- Miller, A. (1997). Strip-plot configurations of fractional factorials. *Technometrics*, 39:153–161.
- Mukerjee R. and Wu C.F.J. (2006) *A Modern Theory of Factorial Design*. Springer-Verlag New York

- Nelder, J. (1965a). The analysis of randomized experiments with orthogonal block structure. i. block structure and the null analysis of variance. *Proc. R. Soc. Lond. A*, 283:147–162.
- Nelder, J. (1965b). The analysis of randomized experiments with orthogonal block structure. ii. treatment structure and the general analysis of variance. *Proc. R. Soc. Lond. A*, 283:163–178.
- R Core Team (2020). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria.
- Ranjan, P., Bingham, D., and Mukerjee, R. (2010). Stars and regular fractional factorial designs with randomization restrictions. *Statistica Sinica*, pages 1637–1653.
- Ranjan, P., Bingham, D. R., and Dean, A. M. (2009). Existence and construction of randomization defining contrast subspaces for regular factorial designs. *The Annals of Statistics*, pages 3580–3599.
- Soicher, L. (2000). Computation of partial spreads, web preprint.
- Speed, T. P. and Bailey, R. A. (1982). On a class of association schemes derived from lattices of equivalence relations. *Algebraic Structures and Applications*, Marcel Dekker, New York, pages 55–74.
- Spencer, N., Ranjan, P., and Mendivil, F. (2019). Isomorphism check for 2^n factorial designs with randomization restriction. *Journal of Statistical Theory and Practice*, 13(60):1–24.
- Topalova S. and Zhelezova S. (2010). 2-spreads and transitive and orthogonal 2-parallelisms of PG(5, 2). *Graphs and Combinatorics* 26(5):727–735.
- Tjur, T. (1984). Analysis of variance models in orthogonal designs. *Int. Statist. Rev.*, 52:33–81.
- Wu C.F.J. and Hamada M. (2009) *Experiments: Planning, Analysis and Optimization*. Wiley; 2nd edition
- Xu, H., Wu, C. J., et al. (2001). Generalized minimum aberration for asymmetrical fractional factorial designs. *The Annals of Statistics*, 29(4):1066–1077.
- Yates, F. (1937). *Design and Analysis of Factorial Experiments*. Technical Communication 35, Harpenden, United Kingdom: Imperial Bureau of Soil Science.