A deterministic matching method for exact matchings to compare the outcome of different interventions

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Abstract Statistical matching methods are widely used in the social and health sciences to estimate causal effects using observational data. Often the objective is to find comparable groups with similar covariate distributions in a dataset, with the aim to reduce bias in a random experiment. We aim to develop a foundation for deterministic methods which provide results with low bias, while retaining interpretability. The proposed method matches on the covariates and calculates all possible maximal exact matches for a given dataset without adding numerical errors. Notable advantages of our method over existing matching algorithms are that all available information for exact matches is used, no additional bias is introduced, it can be combined with other matching methods for inexact matching to reduce pruning and that the result is calculated in a fast and deterministic way. For a given dataset the result is therefore provably unique for exact matches in the mathematical sense. We provide proofs, instructions for implementation as well as a numerical example calculated for comparison on a complete survey.

Keywords Statistical exact matching; evaluation of observational studies; matched sampling; weighted matching

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1 Introduction

Statistical matching (SM) is widely used to reduce the effect of confounding \cite{Anderson1980, Kupper1981, Rubin1973} when estimating the causal effects of two different paths of action in an observational study. Such a study consists, e.g., of a dataset containing two therapy groups $A$ and $B$, which in turn contain patients $a_1, \ldots, a_{|A|}$, $b_1, \ldots, b_{|B|}$. Every patient $p \in D$ has an $s$-dimensional covariate vector $cv(p)$, describing the patients\' condition, and an observed value $o(p)$, describing the result of the therapy, for examples see \cite{Abidov2005, Adams2017, Burden2017, Capucci2017, Chen2016, Cho2017, Dou2017, Fukami2017, Gozalo2017, Kishimoto2017, Kong2017, Lau2016, Lee2017, Liu2016, McDonald2017, McEvoy2016, Ray2017, Salati2017, Schermerhorn2008, Seung2008, Shaw2008, Svanstrom2013, Tranchart2016, Zangbar2016, Zhang2016, Zhang2015}.

The goal in regard to SM would then be to find a matching such that patients which are similar according to a chosen similarity measure, e.g., Mahalanobis distance or propensity score, are compared with each other and a reliable conclusion with regards to the preferable therapy under the circumstances defined by the underlying model and hypothesis can be drawn from the matching, while bias potentially introduced through a comparison of dissimilar patients is reduced. If the matching is also maximal in the sense that all possibly matchable patients, i.e., patients which are similar to other patients, are matched, the matching is called a maximal matching.

Regrettably, minimizing bias is not the only key aspect to be considered: maximal matching can lead to the pruning of patients, thus possibly ignoring relevant information contained in the dataset. As these matchings are usually not unique, there can be a high variance in information in between matchings and thus conclusions drawn from them can potentially vary to a high degree. Hence one needs to find a matching optimized in regards to bias and pruning. As the underlying distribution of the dataset and the influence of the therapy is unknown, finding the optimal maximal patient-to-patient matching is difficult. Based on the foundation laid by Rosenbaum and Rubin (1983) for propensity score matching (PSM), many different methods have been proposed to deal with this problem, e.g., nearest neighbour matching \cite{Rubin1973}, stratification matching on propensity scores \cite{Anderson1980}, caliper matching \cite{Stuart2010}, optimal matching \cite{Rosenbaum1989}, coarsened matching \cite{Iacus2012} or full matching \cite{Hansen2004, Hansen2012}. A comprehensive overview can be found for example in the article from Stuart (2010).

The aforementioned methods inspect either one or several matchings and try to cope with the problem of not being able to calculate all possible maximal matchings through numerical or stochastic methods \cite{Stuart2010} and have some limitations which have been investigated lately \cite{Austin2011, King2019, Pearl2000}. Therefore, researchers find themselves sometimes in the difficult position where different matchings, while being statistically sound, can suggest different conclusions.

Due to the aforementioned reasons we investigate a slightly different approach in this article. After showing that considering only one or several patient-to-patient matchings over the whole dataset is inadequate as exponentially many different patient-to-patient matchings exist, implying that high variance in the deduced conclusions is possible, we proceed to propose a method that matches clusters of patients. The goal is to develop a method which uses all information contained in the dataset and considers all possible maximal matchings of a dataset in accordance to a chosen similarity, thus leading to low confounding and low variance. The proposed method has the desirable property of calculating a matching in ac-
cordance to the expectancy value of all possible maximal exact matchings in the dataset, while being fast and deterministic and therefore can support decision making processes as no additional errors are included during the matching process.

A short note on terminology: We use the terms terms therapy group, patient, covariate vector and observed value for clarity and simplicity of presentation and that they can be substituted for any type of group, member of said group, properties of the member and observed result for the member.

1.1 Contribution

We investigate the quantity of possible exact matchings and show that, even under the restriction that only exact matches are considered, many possible matchings exists. For this reason we propose a different approach, which uses all available information in a given dataset for an exact matching and show that the proposed method has desirable properties for SM. We confirm our theoretical contributions by evaluating a complete survey and comparing the proposed method with the de-facto standard for SM in such applications, namely propensity score matching (PSM).

1.2 Structure of the Remainder

We proceed to show that even in an exact matching context multiple possible matchings exist and propose an algorithm to cope with this problem and prove desirable properties of the algorithm. In Section 3, we describe and confirm the findings made in the previous section based on a comparison of the proposed algorithm with an established method for SM on a complete survey. We conclude with Section 4, which is used to summarize our results as well as the algorithm’s benefits and drawbacks and to give an outlook for potential further development.

2 Deterministic exact matching

As stated in the introduction (Section 1), the goal of SM in a general setting is to match as many patients between two groups with regards to a chosen similarity or distance measure as possible. One can immediately distinguish two cases:

- Exact matching (Iacus et al., 2012; Stuart, 2010): Only members of different sets with equal covariate vectors are matched.
- \(\delta\)-matching or caliper/inexact matching (Stuart, 2010): Members of different sets can be matched if their difference with regard to a chosen similarity measure is smaller than \(\delta\).

Thus exact matching is a special case of \(\delta\)-matching for \(\delta = 0\) and one can define potentially matchable patients in the following way.

Definition 1 (Matchable Patients) Let \(p\) and \(q\) be two patients from different therapy groups and let \(d(\cdot, \cdot)\) be an arbitrary similarity measure. Then \(p\) and \(q\) are matchable patients for a \(\delta\)-matching, if \(d(p, q) \leq \delta\).
We will only consider exact matches, $\delta = 0$, for the remainder of this manuscript. We refer to Section 4 for a discussion of a potential extension of this method to $\delta$-matchings with $\delta > 0$.

We first formalize an observation made during statistical matching, which states that the number of all different possible exact matches may be prohibitively large, so that not all matchings can be computed in acceptable time. Based on this we proceed by showing that it is possible to calculate a matching on a dataset in accordance with the expectancy of the observed values, if one uses clusters instead of patients and show that the proposed algorithm has additional desirable properties for statistical matching.

2.1 Preparations

The general idea of the proposed method is to cluster patients with the same covariate vector for each therapy group and generate a matching between both therapy groups for the constructed clusters.

Clustering of patients $p$ and $q$ on their covariate vectors requires a similarity measure. In the remainder, we will use the $L_1$ distance measure (also known as Manhattan metric)

$$d(p, q) := \sum_{i=1}^{s} |cv_i(p) - cv_i(q)|,$$  \hspace{1cm} (2.1)

but other distance measures (possibly defined through similarity measures) are applicable as well as long as they can be calculated for every pair of patients.

**Remark 2** Note that two patients $p$ and $q$ have identical covariate vectors if and only if $d(p, q) = 0$. Thus for exact matching $d(p, q) = 0$ is required for all matchable patients $p$ and $q$.

Together with a distance measure we can define the notion of clusters.

**Definition 3 (Cluster of patients)** In an SM context, a cluster of patients from one therapy group $H$ is a non-empty set $C_H$ of patients with properties:

1. $d(p, q) = 0 \forall p, q \in C_H$.
2. For $p \in C_H$ it holds that $\exists q \in H$ such that $q \notin C_H$ and $d(p, q) = 0$.
3. If $p \in C_H$, then the assigned covariate vector of $C_H$ is $cv(p)$.

Hence, clusters have the following properties:

**Proposition 4** Let $H$ be a therapy group in an SM context, then the following holds for clusters in this therapy group:

1. Every patient in $H$ belongs to exactly one cluster.
2. Every cluster can have exactly one covariate vector assigned to it.
3. Any two clusters in $H$ have different assigned covariate vectors.

**Proof** We prove every characteristic individually:

1. As $d(p, p) = 0, \forall p \in H$, all patients belong to at least one cluster. Thus it remains to show that there exists no patient $p \in H$ belonging to two different clusters $C_{H,1}$ and $C_{H,2}$. Assume that $p \in C_{H,1} \cap C_{H,2}$ and let $q_1 \in C_{H,1}$ and $q_2 \in C_{H,2}$ be two patients in $C_{H,1}$ and $C_{H,2}$ respectively. Then it holds by Definition 3.1 that $d(p, q_1) = 0 = d(p, q_2)$ and therefore $d(q_1, q_2) = 0$. This is a contradiction to Definition 3.2 and therefore every patient belongs to exactly one cluster.
2. As clusters are non-empty sets of patients every cluster has at least one covariate vector assigned to it. Therefore assume that cluster $C$ has two assigned covariate vectors $v_1$ and $v_2$ differing in at least one entry. Then by Definition 3, it holds that there exists patients $p, q \in C$ such that $v_1 = cv(p)$ and $v_2 = cv(q)$. As $v_1 \neq v_2$ holds by assumption it follows that $d(p, q) \neq 0$, contradicting Definition 3 as $p, q \in C$.

3. Assume that different clusters $C_{h,1}$ and $C_{h,2}$ have the same assigned covariate vector. This implies that $d(p, q) = 0, \forall p \in C_{h,1}, q \in C_{h,2}$ and is a contradiction to Definition 3.

Because of Proposition 4, clusters can be assigned unique covariate vectors. Thus the similarity of clusters $C_A$ and $C_B$ – for therapy groups $A$ and $B$ respectively – can be denoted similarly to patients as $d(C_A, C_B)$. This leads to the following observation in regards to exact matching:

For an arbitrary dataset $D = (A, B)$ and a cluster $C_H$ belonging to a therapy group $H \in \{A, B\}$ only the following situations can occur:

1. For $C_A$ there exists one cluster $C_B$ with $d(C_A, C_B) \equiv 0$.
2. For $C_A$ there exists no cluster $C_B$ with $d(C_A, C_B) \equiv 0$.
3. For $C_B$ there exists no cluster $C_A$ with $d(C_A, C_B) \equiv 0$.

Only situation (I) is relevant for exact matching of single patients or clusters, as exact matching can only occur for clusters with a corresponding cluster in the opposite therapy group. Furthermore if situation (I) occurs, then the match is unique in regards to the clusters.

**Proposition 5** Let $C_A$ and $C_B$ be clusters from different therapy groups, then $d(C_A, C_B) \equiv 0$ holds iff the two clusters have the same assigned covariate vector.

**Proof** Let $C_A$ and $C_B$ be clusters from different therapy groups and $d(C_A, C_B) \equiv 0$. As every cluster has exactly one assigned covariate vector it remains to show $cv(C_A) \equiv cv(C_B)$:

$$d(C_A, C_B) \equiv 0 \Leftrightarrow \sum_{i=1}^{s} |cv_i(C_A) - cv_i(C_B)| \equiv 0 \Leftrightarrow cv_i(C_A) \equiv cv_i(C_B), \forall 1 \leq i \leq s. \quad (2.2)$$

Thus both clusters have the same assigned covariate vector. The reverse direction follows as all implications in equation (2.2) are given through equivalence.

Motivated by the previous proposition and by the definition of matchable patients (Definition 3) we can define exact matchable clusters.

**Definition 6** (Matchable Cluster) Two clusters $C_A$ and $C_B$ of $A$ and $B$ respectively are exactly matchable clusters iff $d(C_A, C_B) \equiv 0$.

Equipped with Definitions 3 and 4 as well as Propositions 4 and 5 we can identify the exact cardinality of exact matchable clusters.

Additionally, we can calculate the number of all different possible matchings between two exact matchable clusters (Proposition 7) and for whole datasets (Proposition 8). Note that the necessity to calculate all possible matchings arises as observed results between different maximal matchings can show a large variation, see Section 3 even if the dataset is large and matches are exact (Table 1).

**Proposition 7** Let $C_A$ and $C_B$ be exact matchable clusters of $A$ and $B$ with $|C_A| = a$ and $|C_B| = b$ respectively, then
1. A set of exact matches $M$ between $A$ and $B$ with a maximal number of matches includes 
$$\min(a, b)$$ exact matches from $C_A$ and $C_B$.

2. For $C_A$ and $C_B$ there exists $\binom{\max(a, b)}{\min(a, b)}$ sets with $\min(a, b)$ exact matches, where $\binom{\max(a, b)}{\min(a, b)}$ denotes the binomial coefficient of $\max(a, b)$ and $\min(a, b)$.

Proof We can w.l.o.g. assume that $a \leq b$, as one can simply substitute $a$ for $b$ and $b$ for $a$ in the other case. Thus $\min(a, b) = a$ and as $C_A$ and $C_B$ are exact matchable clusters, a matchable pairs $(p, q)$ with $p \in C_A$, $q \in C_B$ exist. Due to Proposition 5, this is the maximal matchable number of patients between $C_A$ and $C_B$ as $M$ was assumed to be maximal. Assume now that only $a < a$ of these matchable pairs are contained in $M$. This contradicts the maximality of $M$ as the remaining matchable pairs could be added. This proves (1).

As $a \leq b$, it holds that every element from $C_A$ is matched to elements of $C_B$ and these matches constitute a many tuples of matched elements, in short an $a$-tuple. As $|C_B| = b$, one can construct $\binom{b}{a}$ different matchings by selecting different elements of $C_B$ for the matches.

Therefore for two matching clusters $C_A$ and $C_B$ exist $\binom{\max(a, b)}{\min(a, b)}$ sets with $\min(a, b)$ exact matches in general.

Proposition 8 Let $n$ be the number of exact matching clusters in $A$ and $B$ and let $C_{A,j}$ and $C_{B,j}$ with $1 \leq j \leq n$ be exact matching clusters of $A$ and $B$ with $|C_{A,j}| = a_j$ and $|C_{B,j}| = b_j$ respectively. Then the number of different exact matchings that exist on the whole dataset is

$$\prod_{j=1}^{n} \binom{\max(a_j, b_j)}{\min(a_j, b_j)}$$

(2.3)

Proof By Proposition 4 there exist $\binom{\max(a_j, b_j)}{\min(a_j, b_j)}$ exact maximal matchings for every pair of exact matching clusters $1 \leq j \leq n$. Therefore we have

$$\prod_{j=1}^{n} \binom{\max(a_j, b_j)}{\min(a_j, b_j)}$$

maximal exact matchings in total.

Note that the number of different maximal matchings in Proposition 8 is smaller for exact matchings than it is for $\delta$-matchings with $\delta > 0$ or one-to-many matchings.

Proposition 4 shows that even for small datasets the naive way of calculating all possible matchings can be infeasible due to the binomial coefficient. One could now calculate only one or several matchings, but these will possibly neglect important parts of available information in the dataset.

2.2 A deterministic balancing exact matching algorithm

Motivated by the findings of the previous subsection and the use-oriented necessity to use all available information in a given dataset, we investigate the outcomes of an observed value in a dataset regarding clusters. For simplicity of presentation we henceforth assume that $\sigma(x)$ is in $\{0, 1\}$, see Remark 11 for a short discussion of other settings.
Definition 9 (Relative frequency of an observed value in a cluster) Let \( C_H := \{x_1, \ldots, x_{|C_H|}\} \) be a cluster in therapy group \( H \). Then the relative frequency of the observed value \( \sigma(x_a) = 1 \) in \( C_H \) is defined as

\[
F(C_H) := \frac{1}{|C_H|} \sum_{x_a \in C_H} \sigma(x_a). \tag{2.4}
\]

Remark 10 (Different intervals for observational values) Besides simplicity of presentation, the assumption that \( \sigma(x) \) is in \( \{0, 1\} \) has several advantages and can be easily generalized:

1. The relative frequency of the observed value \( \sigma(x_a) = 1 \) in \( C_H \) is \( 1 - F(C_H) \).
2. Any binary setting with \( \sigma \in \{0, K\} \), \( K \in \mathbb{R} \), can be mapped to \( \sigma \in \{0, 1\} \).
3. For non-binary outcomes \( \sigma \in \{K_1, K_2, \ldots\} \), one has to consider the modification

\[
F^{(K)}(C_H) = \frac{1}{|C_H|} \sum_{x_a \in C_H} \chi(\sigma(x_a) = K_i),
\]

where \( \chi(\sigma(x_a) = K_i) \) denotes the indicator function, i.e.

\[
\chi(\sigma(x_a) = K_i) = \begin{cases} 1, & \text{if } \sigma(x_a) = K_i, \\ 0, & \text{otherwise.} \end{cases}
\]

The relative frequency of an observed value in a cluster can be seen as the relative outcome value for the cluster. In the context of statistical matching the observed value data of patients should only contribute to the final conclusion if the whole cluster can be matched. Regrettably this is not the case in general as a cluster \( C_A := \{x_1, \ldots, x_{|A|}\} \) does not necessarily have a matching cluster. Additionally even if a matching cluster \( C_B := \{z_1, \ldots, z_{|B|}\} \) for \( C_A \) exists only an accumulated observed value of \( \min(a, b) \) patients should contribute to the frequency evaluated in the end to prevent a distortion of the end result by large clusters. A first approach, which we will refine subsequently, to prevent this distortion leads to the definition of the relative matching frequency of an observed value.

Definition 11 (Relative matching frequency of an observed value) Let \( C_A := \{x_1, \ldots, x_{|A|}\}, C_B := \{z_1, \ldots, z_{|B|}\} \) be two exact matching clusters. Then the relative matching frequency of an observed value \( \sigma(x_a) = 1 \) for \( C_A \) is defined as

\[
F_M(C_A) := \frac{1}{\min(a, b)} \sum_{x_a \in C_A} \sigma(x_a). \tag{2.5}
\]

Using the relative matching frequency of observed values to evaluate the final outcome of a dataset in terms of an observed value results in incomplete usage of information as only \( \min\{a, b\} \) patients are matched and thus only the observed values of \( \min\{a, b\} \) patients affect the outcome. This problem is independent of the matching method used, if the method does not consider all possible matchings. Note that many commonly used matching methods as described e.g. in [Stuart, 2013] implicitly consider the relative matching frequency \( F_M(C_A) \) as a result after a single matching realization as can be seen by interpreting the used patients as clusters appropriate to the chosen \( \delta \).

We change the perspective to show that usage of the full information available is possible. For this we begin by considering one realization of a maximal matching between clusters as the result of a random experiment. As all patients in a cluster are the same with respect to their covariates, all patients in the same cluster should have the same probability to be chosen in a maximal matching to be matched to patients from a matching cluster. Thus every possible maximal matching has the same probability to appear in a single maximal matching experiment. Repeating the random experiment for maximal matchings between
two clusters results in a sequence of maximal matchings, which we call a uniform sequence of matchings.

**Definition 12 (Uniform sequence of matchings)** Let \( C_A := \{x_1, \ldots, x_a\} \) and \( C_B := \{z_1, \ldots, z_b\} \) be two exact matching clusters. An infinite sequence of matchings \( M = (M_1, M_2, \ldots) \) is called a uniform sequence of matchings if every possible matching between patients of \( C_A \) and \( C_B \) has the same probability to be drawn as a matching \( M_r \) in the sequence.

With these notions we can show that the expectancy of the observed value over all possible maximal matchings is a term, whose value can be directly calculated through a cluster matching. Proposition 13 examines this for the case of two exact matching clusters.

**Proposition 13** Let \( C_A := \{x_1, \ldots, x_a\} \), \( C_B := \{z_1, \ldots, z_b\} \) be two exact matching clusters and let \( M \) be a uniform sequence of maximal matched pairs between \( C_A \) and \( C_B \). Then

1. Every \( M_k \) contains \( \min(a, b) \) matching pairs and
2. The expectancy of the relative matching frequency over the sequence of uniform matchings for \( C_A \) and \( C_B \) can be calculated as

\[
E(C_A) := \lim_{r \to \infty} \frac{1}{r} \left( \sum_{k=1}^{r} F_M(C_A)_k \right) = \frac{\min(a, b)}{a^2} \sum_{i=1}^{a} \sigma(x_i) \quad \text{and} \\
E(C_B) := \lim_{r \to \infty} \frac{1}{r} \left( \sum_{k=1}^{r} F_M(C_B)_k \right) = \frac{\min(a, b)}{b^2} \sum_{i=1}^{b} \sigma(z_i). \tag{2.6}
\]

**Proof** By Proposition 8, every exact match with a maximum number of matches includes \( \min(a, b) \) pairs of \( C_A \) and \( C_B \). Therefore every \( M_k \) contains \( \min(a, b) \) pairs of patients from \( C_A \) and \( C_B \). For the second part we can w.l.o.g. assume that \( a \leq b \), as one can simply substitute in the other case. As \( \alpha = \min(a, b) \) it follows that

\[
F_M(C_A)_k = F_M(C_A) = F(C_A) = \frac{1}{a} \sum_{i=1}^{a} \sigma(x_i) = \frac{\min(a, b)}{a^2} \sum_{i=1}^{a} \sigma(x_i)
\]

for all \( k \).

For \( a = 1 \) it follows that exactly one patient \( \tilde{x}_w, w \in \{1, \ldots, b\} \) of \( C_B \) gets chosen in every maximal matching \( M_k \). As all patients have the same probability to be chosen the probability is \( \frac{1}{b} \) for every patient. Evaluating the limits and referring to the patients of \( C_B \) chosen in one realization of a maximal matching as \( \tilde{x}_w \) leads to:

\[
\lim_{r \to \infty} \frac{1}{r} \left( \sum_{k=1}^{r} F_M(C_B)_k \right) = \lim_{r \to \infty} \frac{1}{r} \left( \sum_{k=1}^{r} \frac{1}{b} \sum_{i=1}^{a} \sigma(\tilde{x}_w) \right) = \frac{1}{b^2} \sum_{i=1}^{b} \sigma(z_i), \tag{2.7}
\]

where the second equation follows by the law of large numbers as all patients have the same probability to be chosen in a maximal matching.

Now let \( a > 1 \). Thus out of \( b \) patients \( a \) patients get matched and every patient has the same probability to be chosen in a maximal matching \( M_k \). Again by the law of large numbers in the second equation it follows that

\[
\lim_{r \to \infty} \frac{1}{r} \left( \sum_{k=1}^{r} F_M(C_B)_k \right) = \lim_{r \to \infty} \frac{1}{r} \left( \sum_{k=1}^{r} \frac{a}{b} \sum_{i=1}^{a} \sigma(\tilde{x}_w) \right) = \frac{a}{b^2} \sum_{i=1}^{b} \sigma(z_i). \tag{2.8}
\]
It is straightforward to generalize Proposition 13 to uniform sequences of matchings over therapy groups containing several clusters, as a single realization of maximal matchings between clusters is independent of maximal matchings between other clusters.

**Proposition 14** Let $n$ be the number of exact matching clusters and let $C_{A,j}$ and $C_{B,j}$ with $1 \leq j \leq n$ be exact matching clusters of $A$ and $B$ with $|C_{A,j}| = a_j$ and $|C_{B,j}| = b_j$ respectively. Let $M$ be the uniform sequence of maximal exact matchings between all clusters. Then

1. Every element $M_k$ of $M$ contains

$$|M_k| = \sum_{j=1}^{n} \min(a_j, b_j)$$

(2.9)

matches.

2. For the expectancy of the relative matching frequencies of observed values for $A$ of any maximum exact matching it holds that

$$E_A := \lim_{r \to \infty} \frac{1}{r} \sum_{k=1}^{r} \left( \sum_{j=1}^{n} F_M(C_{A,j})_k \right) = \sum_{j=1}^{n} E(C_{A,j}),$$

(2.10)

with $x_{j,k,v}, \ v \in \{1, \ldots, a_j\}$ as the patients from cluster $C_{A,j}$ chosen in the $k$-th matching $M_k$. Analogously it holds that

$$E_B := \lim_{r \to \infty} \frac{1}{r} \sum_{k=1}^{r} \left( \sum_{j=1}^{n} F_M(C_{B,j})_k \right) = \sum_{j=1}^{n} E(C_{B,j}).$$

**Proof** Equation (2.9) holds as it is a summation over the equation from Proposition 13. Similarly equation (2.10) holds as a summation over equation (2.6) as a maximal matching between two clusters is independent of a maximal matching between other clusters.

The previous proposition shows that for each therapy group $A$ and $B$ not all possible matches are realized during a single matching and that the relative matching frequency of observed values for uniform sequences of matchings converges to the expectancy of the observed results, which in this case is an easily calculable value. The added benefit being that the term is unique for a dataset and independent of the used matching method.

We are now prepared to propose an algorithm, which calculates the expectancy of the relative matching frequencies of observed values in a deterministic fashion. The full algorithm (Algorithm 4) is divided into three stages.

In its first stage clusters according to Definition 3 are generated (Algorithm 1). In the second stage the algorithm will try to match as many clusters as possible (Algorithm 2), while in the third stage it weights the patients of each cluster in accordance to the size of its matching cluster and its own size according to equation (2.6) (Algorithm 3).
Algorithm 1 Clustering step
1: Set $c = 0$ and $is\_clustered(x_i) = 0$ for all patients in $A$.
2: for each patient $x_v, 1 \leq v \leq |A|$ do
3:  if $is\_clustered(x_v) \equiv 0$ then
4:      Set $c = c + 1, C_{a,c} := \{x_v\}$ and $is\_clustered(x_v) = 1$.
5:  else
6:      continue
7:  end if
8:  for each patient $x_u$ with $v < u \leq |A|$ and $is\_clustered(x_u) \equiv 0$ do
9:     if $d(x_u, C_{a,c}) \equiv 0$ then
10:        Set $C_{a,c} = C_{a,c} \cup x_u$ and $is\_clustered(x_u) = 1$
11:     end if
12:  end for
13: end for
14: Set $n_A = c$.
15: Repeat steps 2 – 13 for $B$ and set $n_B = c$.
16: return $C_{a,1}, \ldots, C_{a,n_A}, C_{b,1}, \ldots, C_{b,n_B}$.

Algorithm 2 Matching step
1: Set $i = 1$.
2: for every cluster $C_{A,g}, 1 \leq g \leq n_A$ do
3:  Search for cluster $C_{B,h}$ with $d(C_{A,g}, C_{B,h}) \equiv 0$.
4:  if a cluster $C_{B,h}$ was found in the previous step then
5:      Create matching set $M_i = \emptyset$.
6:      Set $M_i = \{C_{A,g}, C_{B,h}\}$.
7:  end if
8:  end for
9: return Matching sets $M_1, \ldots, M_s$.

Algorithm 3 Weighing step
1: Set $w(C_{A,g}) = 0 \forall 1 \leq g \leq n_A$ and $w(C_{B,h}) = 0 \forall 1 \leq h \leq n_B$
2: for all $C_{A,g}, 1 \leq g \leq n_A$, with $M_g \neq \emptyset$ do
3:  Search for $C_{B,h}, 1 \leq h \leq n_B$, as the previously calculated matching cluster of $C_{A,g}$.
4:  Calculate $S_{A,g} := S_{B,h} := \min\{|C_{A,g}|, |C_{B,h}|\}$.
5:  Compute $w(C_{A,g}) := S_{A,g}/|C_{A,g}|^2$ and $w(C_{B,h}) := S_{B,h}/|C_{B,h}|^2$.
6:  end for
7: Compute Min-weighted results:

$$R_A := \sum_{g=1}^{n_A} \left[ w(C_{A,g}) \sum_{k=1}^{|C_{A,g}|} \phi(x_{A,k}) \right],$$

$$R_B := \sum_{h=1}^{n_B} \left[ w(C_{B,h}) \sum_{k=1}^{|C_{B,h}|} \phi(x_{B,k}) \right],$$

where $x_{A,k} \in C_{A,g}$ and $x_{B,k} \in C_{B,h}$.
8: return weighted results $R_A, R_B$.

Linked together, Algorithms 1 – 3 form the DeM algorithm.
Algorithm 4 Deterministic balancing score exact matching algorithm (DeM)

1: Cluster the patients with Algorithm 1 for $A$ and $B$ into $C_{A,1}, \ldots, C_{A,n_A}$, $C_{B,1}, \ldots, C_{B,n_B}$.
2: Compute matchings sets $M_1, \ldots, M_n$ through application of the matching Algorithm 2 on the clusters $C_{A,1}, \ldots, C_{A,n_A}, C_{B,1}, \ldots, C_{B,n_B}$.
3: Compute the weighted result with Algorithm 3 for $M_1, \ldots, M_n$.
4: return Weighted results $R_A, R_B$ and the set of matched clusters $M$.

As shown in Proposition 14, the DeM algorithm calculates the expectancy value for the uniform sequence of exact maximal matchings for a given dataset (equations (2.10) and respectively (2.11) or (2.12)), and uses every information contained in the dataset available for an exact matching (equations (2.9) and steps 5 – 8 of Algorithm 2 in conjunction with Algorithm 1). This is summarized in the following theorem.

Theorem 15 (Matching properties of the DeM algorithm)

The DeM algorithm (Algorithm 4) is deterministic and produces exactly one matching result in accordance to the expectancy value of all possible matches in the dataset.

Additionally one can prove that the proposed DeM algorithm (Algorithm 4) is fast and deterministic.

Theorem 16

The DeM algorithm (Algorithm 4) is a deterministic algorithm and has a runtime of $O(|A| \cdot |B| \cdot s + |A|^2 + |B|^2)$, where $s$ is the dimension of the covariate vectors.

Proof

An algorithm is deterministic if given a particular input it will always produce the same output. Algorithm 4 takes a dataset as input and will, in the case of an exact matching, always produce the same clusters during step 1. As the same clusters were produced in step 1, the same clusters are matched in step 2, because of Proposition 5. Step 3 calculates the weight of the respective matched clusters, which is always same since the matched clusters from step 2 are the same. Thus Algorithm 4 is deterministic.

Evaluating the runtime can be achieved by looking at every step separately:

1. In Algorithm 1 the steps 1-14 have a runtime of $|A|^2$, while step 15 has a runtime of $|B|^2$.
2. Algorithm 2 investigates every cluster in $B$ at most $|A|$ times and every comparison between clusters needs $s$ operations to determine the distance. Thus Algorithm 2 has a runtime of $O(|A| \cdot |B| \cdot s)$.
3. As $n_A \leq |A|$ and $n_B \leq |B|$ it follows that Algorithm 3 has a runtime of $O(\max\{|A|, |B|\})$.

Adding all the runtimes together and making no further assumptions in regards to the comparative size of $s$, $|A|$ and $|B|$, one concludes that Algorithm 3 has a runtime of $O(|A| \cdot |B| \cdot s + |A|^2 + |B|^2)$.

The exclusive applicability of the proposed algorithm to exact matches which can be seen as a limitation will be discussed in Section 4.
2.3 Additional properties of the DeM algorithm

As shown in the previous subsection, the DeM algorithm calculates matchings in accordance to the expected value over all possible matchings in the dataset. This section discusses two additional properties of the DeM algorithm.

We first discuss an a posteriori property of the proposed cluster matching. For statistical tests it is often necessary to calculate the variance inherent to the final matching result. For clusters this can be achieved by looking at matchings through the perspective of hypergeometric distributions:

Let \( C_A := \{ x_1, \ldots, x_a \} \) and \( C_B := \{ z_1, \ldots, z_b \} \) be two exact matching clusters, then \( a \) can be interpreted as the population number of which \( \sum_{v=1}^{a} o(x_v) = 1 \) patients have some property and \( \min(a, b) \) of \( a \) patients are chosen in this maximal matching. Thus a realization of a maximal matching in the sense of relative matching frequencies can be interpreted as a sample drawn from a hypergeometrically distributed random variable projected onto the interval \([0, 1]\).

The view of maximal matchings as realization of a drawing from a hypergeometric distribution concurs with the results of Propositions 13 and 14 from the previous subsection as the expectancy of a hypergeometric distribution for two exact matching clusters is \( E(C_A) \) and \( E(C_B) \), respectively, where the terms \( a \) and \( b \) stem from reversing the normalization done in the previous subsection.

Taking this perspective allows to calculate the variance for maximal matchings.

**Proposition 17** Let \( C_A := \{ x_1, \ldots, x_a \} \), \( C_B := \{ z_1, \ldots, z_b \} \) be two exact matching clusters. Then the variance of matchings for \( C_A \) is given by

\[
\text{Var}(C_A) = E(C_A) \left( 1 - \frac{\sum_{v=1}^{a} o(x_v)}{a} \right) \frac{a - \min(a, b)}{a - 1} \tag{2.13}
\]

**Proof** Viewing one realization of a cluster matching as the realization of a hypergeometrically distributed random variable yields the probability of picking one patient with \( o(x_v) = 1 \) as \( \frac{\sum_{v=1}^{a} o(x_v)}{a} \). From Proposition 13 it is know that \( E(C_A) = \frac{\min(a, b)}{a} \sum_{v=1}^{a} o(x_v) \). Thus using the formula for the variance of hypergeometric distributions yields equation (2.13).

As exact matchings of different clusters are independent from each other, the variance for a matching over a therapy group follows immediately from the previous Proposition 17.

**Corollary 18** Let \( n \) be the number of exact matching clusters in \( A \) and \( B \) and let \( C_{A,j} \) and \( C_{B,j} \) with \( 1 \leq j \leq n \) be exact matching clusters of \( A \) and \( B \) with \( |C_{A,j}| = a_j \) and \( |C_{B,j}| = b_j \), respectively. Let \( M \) be the uniform sequence of maximal exact matchings between all clusters. Then the variance of therapy group \( A \) is

\[
\text{Var}(A) = \sum_{j=1}^{n} \text{Var}(C_{A,j}). \tag{2.14}
\]

For therapy group \( B \) equation (2.14) holds similarly.

Note that all values used in Proposition 17 and Corollary 18 are available after matching with the DeM algorithm and that the clusters are matched such that no additional factor is introduced into the variance. Additionally note that the variance of a cluster for which all patients are matched, i.e. for \( C_A \) with \( \min(a, b) = a \), is 0. The same holds for clusters for which all patients have the same observed result, as then either \( F_w(C_A) = 0 \) or \( 1 - \)
\[
\sum_{a=1}^{\min\{a, b\}} \sigma(s_i) = 0. \quad \text{Thus at least half of all matched clusters from } A \text{ and } B \text{ fulfil either the } \\
\min(a, b) = a \text{ or } \min(a, b) = b \text{ condition, and therefore have a variance of 0 in the matching calculated by the DeM algorithm. }
\]

The second property we discuss relates to the calculation of clusters and the initial matching procedure. Rosenbaum and Rubin (1983) defined the balancing score \( b(p) \) of a patient \( p \) as a value assignment such that the conditional distribution of \( \text{cv}(p) \) is the same for patients \( p \) from both treatment groups, \( A \) and \( B \). They have shown that \( \text{cv}(p) \) is the finest balancing score ((Rosenbaum and Rubin, 1983), section 2) and that if treatment assignment is strongly ignorable, then the difference between the two respective treatments is an unbiased estimate of the average treatment effect at that balancing score value ((Rosenbaum and Rubin, 1983), theorem 3). Since we use \( \text{cv}(p) \) in our calculations, the result calculated by Algorithm 4 is an unbiased estimate of the average treatment effect, if the strong ignorability assumption holds, additionally to the properties proven previously.

3 Numerical example

3.1 Description of dataset and setup

We use an official complete survey to illustrate the effect of ignoring different possible matchings as well as the results of the proposed DeM algorithm.

The dataset used is the quality assurance dataset of isolated aortic valve procedures in 2013, which is an official mandatory dataset including all aortic valve surgery cases in German hospitals. It contains patient information (covariates) and mortality information (observed results) for 17,427 patients. For each patient the corresponding record contains \( s = 19 \) covariate variables. The 17,427 patients are divided into two therapy groups. 9,848 SA VR cases (replacement surgery of aortic valves) and 7,579 TF-AVI cases (transcatheter/transfemoral implantation of aortic valves). The cases were documented in accordance with §137 Social Security Code V (SGB V) by hospitals registered under §108 SGB V. The data collection is compulsory for all in-patient isolated aortic valve procedures in German hospitals. The dataset is held by the Federal Joint Committee (Germany) and freely accessible for researchers after application. Given this dataset, it can be safely assumed that the data is independent in a statistical sense as patients were only recorded once.

We proceed to compare the proposed DeM algorithm with two other approaches: the de facto standard for statistical matching, the 1:1 propensity score matching (PSM), as well as a bootstrapped variant of 1:1 PSM by Austin and Small (2014). For the regression based PSM algorithms, relevant regression variables and their values have to be determined. For our example, we consider the \( H_0 \)-hypothesis: \( \text{The mortality-rate does not depend on therapy} \), for which the relevant variables are internationally validated in the Euroscore II (http://www.euroscore.org). The corresponding regression values for this setting are taken from the quality assurance dataset of isolated aortic valve procedures. PSM itself was then calculated using functions provided by IBM SPSS Statistics for Windows, Version 24.0.

The decision to use 1:1 PSM for comparison was made as it has the highest amount of possible matchings for fixed match-sizes and is the most commonly used (Stuart, 2010). Furthermore all possible \( v : w \) matchings, for arbitrary \( v, w \in \mathbb{N} \) are included in the set of possible 1:1 matchings, while the reverse is obviously not true for arbitrary \( v, w \in \mathbb{N} \) and any given dataset.
Table 1 Results for maximal matchings

|                              | SAVR in-hospital death | TF-AVI in-hospital death | $\chi^2$ Test (2-tailed) |
|------------------------------|------------------------|--------------------------|--------------------------|
|                              | count | %    | count | %    | p-value   |
| PSM Set 1                    | 73    | 4.9% | 33    | 2.2% | <0.0001  |
| PSM Set 2                    | 73    | 4.9% | 34    | 2.3% | <0.0001  |
| PSM Set 3                    | 42    | 2.8% | 32    | 2.1% | 0.2398   |
| PSM Set 4                    | 24    | 1.6% | 15    | 1.0% | 0.1470   |
| PSM Set 5                    | 73    | 4.9% | 50    | 3.3% | 0.0342   |
| PSM Set 6                    | 24    | 1.6% | 50    | 3.3% | 0.0021   |
| PSM Set 7                    | 73    | 4.9% | 15    | 1.0% | 0.0001   |
| Uniform Bootstrapping (10,000 samples) | 52.47 | 3.49% | 32.10 | 2.14% | 0.0210 (t-test) |

DeM 

53.01 | 3.5% | 32.32 | 2.1% | 0.0227

We additionally note that a match of two patients with $\delta > 0$ in this dataset would imply a difference of at least 5% between patients in regards to covariates as there are only 19 covariate variables.

We explicitly stress that the purpose of this section is not the recommendation of any kind of treatment, but the illustration of the usage of results presented in Subsections 2.1–2.3.

3.2 Computational results

We computed the exact 1:1 matchings with PSM and the proposed DeM algorithm. For comparison purposes we present seven realizations of the non-deterministic PSM (Set 1 – 7).

Out of the 9,848 SAVR patients 3,361 had at least one exact TF-AVI match, while out of the 7,579 TF-AVI patients, 2,249 patients had at least one exact SAVR match. Thus one third of all patients could be exactly matched. As stated in the previous section, the null hypothesis for calculation of the p-values was $H_0$: The mortality-rate does not depend on therapy. The results of some maximum matchings and the differences between them are indicated in Table 1.

A maximal matching 1:1 comprises 1,502 matching pairs of patients, meaning that 3,004 patients were matched during any exact non-cluster matching. We only considered maximal exact matches, therefore every shown matching matches the maximal number of patients possible and matches two patients if and only if their covariates are equal, meaning that the standardized differences in all presented sets is 0. Still the large discrepancy between the observed results in the shown sets immediately indicates that many maximal matchings exist, as shown in Proposition 8. Calculating all possible maximal matchings would be a futile endeavour and not necessary if the observed results between different maximal matchings would not vary. Unfortunately observed results can vary to a very high degree, as can be seen in Table 1. They vary in such a way that one could even draw different conclusions based on the matching one calculated, see sets 1, 5 and 7 while arguing that the calculated p-value is below a threshold of 1%. For other sets one can see that they are on either side of the spectrum, favouring one, the other, or no therapy. Even the bootstrapping result for 10,000 samples did not exhaust all possible maximal matchings and is only similar to the result of DeM, which gives as a result the expectancy of all possible maximal exact matches in the given dataset, see Theorem 15.

a The t-test values for all sets without replacement are < 0.0001, with replacement 0.0005.
As can be seen from the results, given one dataset and a non-deterministic method one could obtain different results even when regression variables are given, which leads to uncertainty in the evaluation process as fellow researchers cannot reconstruct results obtained through statistical matching based on regression methods. The proposed algorithm tries to resolve this issue for exact matches. Even though this is a limitation in applicability, exact cluster matches obtained through the DeM algorithm can be used at the core of a matching, ascertaining that at least the exact matchable contingent of a dataset is matched deterministically (Theorem 16) and corresponds to the expectancy value of the exact matches (Theorem 15). Additionally, if in large datasets no exact matches can be found, researchers should thoroughly investigate for systematic differences in the therapy groups, as comparisons of therapy-effects are not recommended if systematic differences exist.

4 Conclusion

We proposed an alternative deterministic exact matching method (DeM) for SM in the exact case. The proposed method is based on matching clusters of patients from therapy groups instead of matching patients to patients directly. The presented cluster matching approach computed with the DeM algorithm (Algorithm 3) extracts all possible information from a given dataset as all possibly matchable patients get matched and the constructed matching is in accordance with the expectancy value of the dataset (Theorem 15). The constructed matching also has the desirable property of having low variance while being in accordance to the expectancy of all possible maximal exact matchings in the dataset (Proposition 17 and Corollary 18).

As the proposed algorithm is deterministic and fast (Theorem 16) as well as easy to implement, it can be used to produce exact matchings on datasets and to discuss findings in a reliable way as the results are easily reproducible. This is an important property as it makes a subsequent decision-making process more transparent and not susceptible to random events, such as random draws not in accordance to the expectancy. Thus discussions about conclusions drawn can be done based on the dataset and the method used for data acquisition as uncertainties regarding the matching method are eliminated through a proven guarantee that there are no additional errors introduced by the matching procedure.

The results from the numerical example, calculated on a dataset containing a complete survey, validate the shown theoretical propositions and theorems. The proposed method can furthermore be seen as an extension of state of the art methods as results obtained through their usage would converge in the limit against the result calculated through the proposed algorithm.

The exclusive applicability of the proposed algorithm to exact matches might be seen as a limitation. Then again for small datasets, which are statistically more prone to high variance in regards to two different matchings, the proposed algorithm provides a reliable result for the exact matches. For the case of large datasets, a practitioner should be wary if only few exact matches exist or a matching result varies to a high degree from the result given by the proposed deterministic algorithm as a systematic difference between the two compared therapy groups might exist or measuring inaccuracies for continuous covariates might be too large in the given dataset to draw reliable conclusions.

Finally, we highlight that the algorithm can be used as an a priori method for another matching method to extract all available information contained in exact matchings, therefore ascertaining that at least the exact matchable patients of both therapy groups are matched deterministically and their information is completely used. Further research will be dedicated
to extend the presented model towards $\delta$-matching for $\delta > 0$ while keeping the desirable properties presented in this paper and therefore extend the applicability of the proposed method.

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