Group-matching algorithms for subjects and items

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Abstract

We consider the problem of constructing matched groups such that the resulting groups are statistically similar with respect to their average values for multiple covariates. This group-matching problem arises in many cases, including quasi-experimental and observational studies in which subjects or items are sampled from pre-existing groups, scenarios in which traditional pair-matching approaches may be inappropriate. We consider the case in which one is provided with an existing sample and iteratively eliminates samples so that the groups “match” according to arbitrary statistically-defined criteria. This problem is NP-hard. However, using artificial and real-world data sets, we show that heuristics implemented by the ldamatch package produce high-quality matches.

1 Introduction

When studying the effect of group differences on target variables, it is essential to control the effects of other confounding variables associated with the dependent and independent variables under consideration. One can deal with potential confounding covariates at various points during a study (Szatmari et al., 2004, p. 55). First, one can design the study to minimize confounds using a randomized controlled trial or stratified sampling. Such designs also minimize the effect of unobserved independent variables. Secondly, one can perform analysis on a subsample chosen so that the groups are statistically similar. We refer to this subsampling technique as matching. Third and finally, covariates can be dealt with in the analysis phase using statistical techniques such as ANCOVA or multivariate regression. In this section, we motivate the use of matching. In subsequent sections, we present methods for selecting matched groups, implemented in the R package ldamatch.

Subject matching is a common strategy in quasi-experimental or observational studies in which subjects’ assignment to group is pre-existing or otherwise not under experimental control. For instance, an experimenter might use post-hoc subject matching to compare diseased or impaired humans to those without a disease or impairment. While less common, matching of items or stimuli grouped into “conditions” or treatments can also be used. For example, an experimenter studying lexical processing might wish to balance different word lists for frequency, length, and so on.

Some researchers have questioned whether experimenters ought to use matching at all, particularly in the study of developmental disorders (e.g., Jarrold and Brock, 2004). Covariate analysis is recommended as an alternative to matching when, due to a large difference between group characteristics, matching would distort the groups so much that they would no longer be faithful representations of the populations from which they were sampled (Seltzer et al., 2004; Tager-Flusberg, 2004). For example, Jarrold and Brock (2004), argue that matching subjects with autism from a wide range of intellectual abilities on IQ could easily reduce the autism group to only those with very high IQ. They also observe (p. 84) that “matching groups on more than one criterion is often extremely difficult and, even if possible, will involve such a degree of selectivity that the generalizability of the findings will be reduced considerably.” Thus Jarrold and Brock conclude that matching on multiple variables is non-trivial, and may produce non-representative subsamples. On the other hand, if there is little
residual variance associated with the covariates targeted, one would suppose that subject matching could be applied, and would likely require few subjects to be removed.

It should be noted that one can combine matching with covariate analysis during statistical inference. The matching framework does not make any specific assumptions about the relationship between variables of interest, and statistical techniques like ANCOVA or multivariate regression can control for any group differences remaining after matching is applied (Tager-Flusberg, 2004). Blackford (2009, p. 349) argue that matching has other advantages, including that “matching produces effect-size estimates with smaller variance than covariate adjustment, analyses on matched data are more robust, and matching can control for more confounders than covariate adjustment, for a given sample size.”

Perhaps the best-known matching technique is pair-matching as proposed by (Rubin, 1973; Rosenbaum and Rubin, 1983). The idea behind this approach is that if we could know the outcome in a person’s life both if they receive or do not receive a certain treatment, then we could easily measure the effect of that treatment. This can be approximated as follows. First we identify pairs of subjects that are similar on all relevant variables before treatment. One of the subjects then receives the treatment, and we measure changes in all outcome variables. One can assume that any difference arising between them later is the effect of the treatment. If this procedure is repeated for many pairs of subjects, one can calculate a quantity known as the Average Treatment Effect for the Treated Subjects (ATT), an estimate of the effect of a treatment on the dependent variable or variables. The goal of pair-matching is thus to pair control and treated subjects such that the pairs are very similar with respect to the variables used for matching before receiving the treatment. One-to-one, one-to-N, and M-to-N pairing can all be used in this setting, since one can just as well compare outcome averages when multiple subjects are selected. As a side effect, the selection of well-matched subject pairs results in a good balance between groups of the selected subjects overall (Gu and Rosenbaum, 1993). The notion of “treatment” is quite general: it might include actual drug treatment, partaking in an intervention or change of habit, or even the prior presence or absence of a disease or disorder. Thus the above approach can be used in experimental, quasi-experimental, and observational studies. Several implementations for pair-matching are available, including the R packages Optmatch (Hansen, 2007), MatchIt (Ho et al., 2011), and Matching (Sekhon, 2011), all of which support two-group pair-matching; the twang R package (Ridgeway et al., 2014) supports pair-matching for two or more groups.

Pair-matching is generally performed based on propensity scores, the estimated probability of a subject being assigned to the treatment group. The use of propensity scores results in an unbiased estimate of the treatment effect so long as outcomes are independent of assignment to treatment conditional on pre-treatment covariates (Dehejia and Wahba, 2002, p. 151). Blackford (2009) gives several other arguments for propensity score matching. For instance, more subjects can be preserved than when matching on multiple covariates, so the resulting groups are more similar to the overall population and less bias is introduced. Furthermore, it is much easier to match on one variable than on multiple dimensions (Dehejia and Wahba, 2002; Smith and Todd, 2003). However, when matching on multiple covariates two subjects may have very similar propensity scores even when their individual characteristics differ widely. In other words, propensity score matching does not guarantee that the paired subjects will be impressionistically similar. For this reason, some researchers use propensity scores but also require paired subjects to have quite similar covariate values according to certain predefined conditions. Propensity scores must be derived from pre-treatment variables (e.g., Rubin, 1991), particularly those likely to be both related to group assignment and relevant for the dependent variables; however, they may not be variables caused by group assignment or later outcomes (Blackford, 2006, p. 98). Propensity scores can be estimated in a number of ways, including a logistic regression model fit to pre-treatment covariates.

Unfortunately, we do not always have enough information for estimating propensity scores before treatment, and using variables that are themselves affected by the treatment or variables that are not related to the outcome results in overmatching, matching that is superfluous or erroneous and which
harmsthe statistical efficiency or the validity of the study; e.g., [Rothman et al., 2008]). For example, if we view the presence of Autism Spectrum Disorder (ASD) in a subject as a “treatment effect”, it is not clear what one could use as a “pre-treatment” variable. There are many factors known to be related to autism risk, including gender, the number of affected siblings, birth order, genetic issues such as de novo mutations, and the presence of certain environmental toxins and air pollution during gestation (e.g., [Chaste and Leboyer, 2012]), but many of these risk factors are difficult or impossible to measure long after birth. When we do not have that information, it may be tempting to use whatever is available to estimate propensity scores. Note however that autism is often comorbid with intellectual disability (in about 50–70% of all cases; see [Matson and Shoemaker, 2009]), so we cannot exclude the possibility that intellectual (dis)ability is affected by having autism (although it could be the other way around, or both could be the result of a common underlying neurological condition). The situation is similar for Specific Language Impairment (SLI), another developmental disorder: IQ is generally lower in children with SLI, but it is not clear whether or not the condition causes the lower average IQ. In either case, using IQ to estimate propensity scores may produce overmatching.

Post-hoc matching may still be appropriate in those cases where propensity scores cannot be estimated due to a lack of suitable pre-treatment covariates. While it does not guarantee an unbiased estimate of the treatment effect, post-hoc matching does eliminate the possibility that an observed difference is due simply to group differences in the matched covariates. For example, for children with a neurodevelopmental disorder, the “post-treatment” covariates might be cognitive and/or language abilities measured using standard instruments. Performing analyses on data matched with respect to these covariates does not ensure that the actual effect of treatment (here, presence or absence of a development disorder) is properly measured, but it does ensure that any group differences in the outcome variables are unmediated by group differences in these covariates.

In other cases, including those for which propensity scores cannot be estimated, one may alternatively use another type of matching we refer to as group-matching. Group-matching ensures that the statistical distribution of covariates is similar between groups of subjects—instead of at the individual level, as in pair-matching—by ensuring that the groups are not significantly different with respect to the covariates at some given \( \alpha \)-level; [Mervis and Klein-Tasman, 2004], for example, propose using \( \alpha > 0.5 \) or \( \alpha > 0.2 \). The statistics used for matching are often based on comparison of group means—[Rubin, 1973] refers to this as mean-matching—but one may also wish to take other statistical properties, like variance, into account. [Rubin, 1973] examines both matching approaches and reports group-matching works well when the dependent variable is linearly related to the matching variables. Moreover, matched groups can easily be analyzed using standard statistical techniques such as mixed-effect linear models ([Pinheiro and Bates, 2000; Bates, 2005, 2010]). [Shaked and Yirmiya, 2004, p. 37] reports that “larger effect sizes were yielded when participants... were matched on a group basis, rather than on a one-to-one basis, with the comparison participants.”

The computational implementation of group-matching has received very little attention. For instance, in a 2004 special issue of the Journal of Autism and Developmental Disorders, focused on the question of subject matching, implementation was discussed only by one paper: [Mervis and Klein-Tasman, 2004] describe a procedure for matching on one variable, and it is not clear whether the procedure was implemented computationally. We are unaware of prior work on group-matching with multiple variables, a situation in which propensity scores may also be difficult to estimate or to use.

In this paper, we introduce and evaluate multiple algorithms for group-matching that uses complex matching criteria involving one or more covariates. We have made available our implementation of those algorithms to the research community via the ldamatch R package. Rather than illustrating the use of this thoroughly-documented package via code snippets, we describe these algorithms and evaluate their effectiveness and performance by applying them to artificial and real-world data sets.
2 Problem statement

Let us suppose that we have $G$ groups comprising a total of $N$ subjects, with group membership for the subjects indicated by the vector $g_1, \ldots, g_N$. Each subject also has an associated covariate vector $c_i$, $i = 1 \ldots N$. We wish to find an optimal subset of subjects denoted by the boolean indicator variables $s_1, \ldots, s_N$ subject to some criteria. Without loss of generality, let us assume that the criteria are a set of one or more statistical tests that typify the similarity of the covariate distribution between the groups, and possibly also constrain the expected group size proportions or bound the maximum number of subjects that can be removed, overall or from particular groups. The statistical tests $t_j, j = 1 \ldots T$ defining these criteria are assumed to be functions from $g_i, c_i, s_i$, $i = 1 \ldots N$ to $p$-values $\in [0, 1]$. We say that the difference between groups is non-significant if the $p$-values from each statistical test is above a pre-specified threshold $\alpha_j$; for example, $\alpha_j$ might be 0.2 or 0.5. Note that matching does not consider the dependent variables targeted by the larger study.

Our goal is to find solutions that meet the following expectations, in decreasing order of importance. First, we want to preserve as many subjects as possible. Second, we may have certain preferences related to group membership: either want to maintain the ratio of the group sizes close to a given ratio (such as the original group size ratio), or we may prefer to keep subjects in certain groups more than in others; this can be implemented by specifying a precedence among the groups. Third, we want to minimize differences between the groups. For each criterion we track the ratio of the actual $p$-value to the desired threshold $p$-value. To combine this ratio across all criteria, we take the minimum:

$$r = \min_{j=1 \ldots T} \frac{p_j}{\alpha_j}$$

We maximize $r$, halting when $r \geq 1$. When comparing possible matched subject configurations, these metrics can be used, in the above priority ordering, to select a unique solution. Solutions for which the above metrics are identical are assumed to be equivalent.

The above problem formulation is an optimization problem in which one seeks optimal values for boolean variables $s_1, \ldots, s_N$ such that $s_i$ is true if and only if subject $s_i$ is preserved by the matching. Were we to evaluate all possible combinations, there would thus be $2^N$ such solutions, making the evaluation exponential in the number of subjects $N$. We are interested in the solutions with the highest total number of subjects, so we can introduce a lower bound $n$ defined such that we do not consider solutions which entail the removal of more than $n$ subjects. There are

$$\sum_{i=0}^{n} \binom{N}{i} = 1 + N + \binom{N}{2} + \ldots + \binom{N}{n}$$

solutions that satisfy this constraint. Clearly, exhaustive search quickly becomes intractable if many subjects must be removed to find a solution. Furthermore, exclusion of any remaining part of the search space may result in a suboptimal solution.

The matching problem is a discrete optimization problem, more specifically an integer program—though not necessarily an integer linear program—which are known to be NP-hard (Nemhauser and Wolsey, 1999, p. 8f.). Integer linear programs can be solved in polynomial time using a relaxation to linear program and then mapping the real values found onto integers. However, a solution found via this relaxation may not be optimal, or even feasible. Furthermore, this relaxation limits the types of statistical criteria that may be used. Here we take a different approach. First, we propose heuristics which search a well-defined subset of the hypothesis space. The following two sections describe and evaluate these heuristics.
3 Matching algorithms

Below we describe several search strategies that evaluate a subset of all possible subject configurations denoted by $s_i, i = 1 \ldots N$, with the goal of finding one which satisfies all statistical criteria at the required $\alpha$-levels. We walk the search space with the aim of optimizing the measures described above. Here we briefly describe these algorithms, referring to them by the names used in Idamatch R package.

3.1 Random search (random)

This algorithm randomly samples the search space for a given number of iterations choosing the subjects to keep randomly according to the binomial distribution, gradually decreasing the expected value of their count from $N$ (the number of subjects) to $G$ (the number of groups). The search stops after the specified number of iterations $I$ and yields the best solutions found. This is a non-deterministic algorithm with $O(I \cdot T)$ running time, that is, it depends only on the required number of iterations and on how long it takes to evaluate the statistical tests for any particular subject configuration.

3.2 Test-statistic search (heuristic2)

This is a constructive algorithm: it constructs a solution in a series of steps, always choosing the next step such that it brings us nearer to a solution (see for example Genova and Guliashki, 2011). The basic idea is that we use the value of $r$ (which indicates how well the groups are matched) to decide which way to proceed when walking the search space, that is, which subject to remove next to attain the largest improvement in the target criteria. In every step, it calculates $r$ after removing each remaining subject in turn, and then removes the subject that results in the highest $r$. If multiple configurations with the same number of subjects meet our criteria, we take advantage of the other metrics to rank them and choose the first one. This is a deterministic algorithm, with a computational complexity of $O(N^2 \cdot T)$; that is, it is quadratic in the number of subjects. This approach was used in van Santen et al. (2010) for selecting a matched subset of subjects for analysis.

3.3 Test-statistic search with lookahead (heuristic3 and heuristic4)

Intuitively an issue with the heuristic2 algorithm is that it is not able to proceed toward the global optimum when the step in that direction results in a local drop in $r$. For example, when two subjects need to be removed with extreme covariate values on the opposite ends of the scale, the removal of either subject makes the group balance worse.

We addressed the above issue in the heuristic3 and heuristic4 algorithms by looking ahead several steps during the search. Lookahead has been utilized for various problems, including vehicle routing problems (Atkinson, 1994), decision tree induction (Dong and Kothari, 2001), and composition of finite-state automata (Allauzen et al. 2010), but we are unaware of it being applied to the matching problem. These two heuristics differ in how they decide on their next step.

Both algorithms first identify one or more sets of $L$ subjects, denoted here by $S$, whose removal results in the biggest improvement (more than one set if they are equivalent on our metrics), then remove one subject from those sets. Note that this way it is possible to reach one of the best sets found $L$ steps later, but it does not commit to removing $L$ particular subjects at this point, as it may find a still better combination in later steps. In heuristic3, removal decisions are made solely on the basis of $r$, whereas heuristic4 prefers to eliminate a subject which is a candidate for removal in the highest number of subject sets. Thus heuristic4 makes as minimal a future commitment as possible.
More formally, the algorithm for choosing the next subject for removal in heuristic3 is as follows:

1. Initialize \( l \) as \( L \) (the lookahead) and \( C \) as \( S \) (the candidates sets for removal, having the highest \( r \) values, consisting of \( L \) subjects each).
2. If \( l = 1 \), choose the subject to be removed randomly from \( C \) and exit.
3. Decrement \( l \) (i.e., \( l \leftarrow l - 1 \)).
4. Let \( S_l \) be all subject subsets of size \( l \) from \( C \).
5. For each subject subset in \( S_l \), calculate \( r \) with its subjects removed.
6. Let \( C \) be the subject sets from \( S_l \) with the highest \( r \) value.
7. Go to step 2.

The algorithm for choosing the next subject for removal in heuristic4 is as follows:

1. Count the number of times each subject occurs in \( S \) and keep the ones with the largest count as candidates.
2. If more than one candidate remains, calculate \( r \) for each one and keep the ones with the highest \( r \).
3. If still more than one candidate remains, choose one of them randomly.

Both algorithms are non-deterministic (as they choose randomly among seemingly equivalent options), and follow a depth-first search strategy. Their complexity is \( O(N^{L+1} \cdot T) \) where \( N \) is the number of subjects and \( L \) is the degree of lookahead. Both algorithms are equivalent to heuristic2 when \( L = 1 \).

The ldamatch implementation makes it possible to remove several subjects without recalculating the \( r \) values. It can be time-consuming to calculate the \( r \) value for such data sets, and these values may not change much after removing one subject, particularly when working with very large groups. The user can limit the maximum number of subjects removed in each step (specifying it as a number or as a percentage of the remaining subjects) and when the algorithm should revert to calculating \( r \) after each step (e.g., when \( r \) reaches some specified value). This lazy recomputation technique does not change assymptotic complexity, but in practice, it speeds up search substantially without major degradation in quality. As seen below, allowing the removal of 100 subjects before recomputing \( r \) may reduce the running time by more than an order of magnitude.

3.4 Exhaustive search (exhaustive)

While exhaustive search is simple, it is often infeasible for large problems. We implemented an exhaustive search algorithm that is feasible when only a few subjects need to be removed to reach well-matched subject groups. We can estimate an upper bound on the number of subjects that need to be removed using the heuristics, and based on that number, we can estimate the maximum running time of exhaustive search. Having this algorithm at our disposal can give us the optimal solution in certain cases and can enable us to assess how well other approaches fare. Consider a fictious example when the exhaustive search is feasible for a seemingly complex matching problem. Given two groups, each containing 20 subjects, and assuming that the computer can process 1,000 out of the \( 2^{20+20} \) subject configurations per second (which is over 1.099 \( \cdot 10^{12} \) configurations), evaluating all cases would take over 34 years. However, if a heuristic finds a solution that meets the matching criteria by removing five subjects, then we estimate that exhaustive search will complete in 13 minutes or less, which makes running an exhaustive search feasible. If it turns out during the process that the optimal solution requires the removal of only three subjects, then it will finish in less than 11 seconds.
The ldamatch package implements exhaustive search using a breadth-first strategy. Our criteria rank candidate solutions first based on the total number of subjects retained, and second by favoring smaller divergence from the desired group proportions. Deviation from the desired group proportions are measured using the Kullback-Leibler (K–L) divergence (see e.g. Cover and Thomas, 2006). When multiple solutions are available with the same size and K–L divergence, we favor those with higher values of $r$.

4 Evaluation

An optimal matching can be found using exhaustive search, but this is not feasible for large or complex problems. Moreover, even when exhaustive search is feasible, it may be preferable to find an approximate solution if one can do so in a fraction of the time. The heuristics generally find a solution, but we do not know if they do indeed work in all cases and when they do, how much worse these solutions are compared to the optimal one (i.e., their approximation bounds).

4.1 Procedures

Our goal is to characterize these heuristics: their execution time, and the quality of the solutions, comparing to an optimal solution found via exhaustive search when possible. With this knowledge, we should be able to choose a suitable algorithm for the task at hand and to estimate the quality of approximation with respect to the optimal solution. For this purpose, we evaluate the algorithms on several data sets: artificial “subjects” from multivariate normal distributions with diverse parameters, and real data sets, containing either a small group of subjects or a large number of items. We analyze the results to gain an understanding of the pros and cons of the proposed algorithms.

4.1.1 The matching process

Since every matching algorithm has its own respective drawbacks and benefits, we do not commit to using any one of them, but rather make use of several and select the best output. We use exhaustive search when heuristics indicate that it will be feasible.

We hypothesized that heuristics would find better solutions when stricter criteria are used. For example, they sometime preserves more subjects when matching not just means, but overall distributional shape (Facon et al., 2011), or when required to keep all subjects from one of the groups. This may be because stricter criteria can help to guide them into a direction that will prove to be globally optimal. In other words, additional criteria may help the system to make better local decisions and thus to attain better global decisions. We can take advantage of this by matching the groups using both more and less strict criteria and comparing the outputs.

4.1.2 Computational resources

We ran all evaluations in parallel using the Slurm Workload Manager to launch jobs across a large, heterogeneous computing cluster. The exhaustive, heuristic3, and heuristic4 algorithms were run in multithreaded mode. The nodes of the cluster were commodity x86–64 machines running Ubuntu Linux, with 24 CPUs and 24 logical cores per node. CPU frequency varied from 1600 to 3000 MHz.

4.2 Evaluation on synthetic data

We first synthesize sets of items to be matched by randomly sampling multivariate distributions. We sample from multivariate normal distributions used to approximate an enormous number of naturally-
occurring phenomena. This allows us to evaluate the algorithms for various parametric distributions without the difficulties of collecting real data sets with desired properties.

### 4.2.1 Data generation

Each synthetic data set is generated as follows. A random covariance matrix is generated using the `genPositiveDefMat` function of the `clusterGeneration` R package, then two random samples were drawn from that distribution: a larger sample and a smaller sample with a shifted mean. We refer to the former sample as “basic items” and the latter as “intruders”. We combine the two samples into one data set with the expectation that the matching procedure will identify and exclude many intruders.

We created 36 parameter sets based on the following meta-parameters:

- number of all items: 100, 150, or 200 (to have a variety of configurations to evaluate).
- total number of covariates: 2 to 4.
- number of covariates that differ between the basic items and the intruders: 2 to 4 (e.g., 2 of 3)
- number of intruders: 10
- group sizes: 50% of items in either group
- means of each covariate: a random number drawn from a uniform distribution over (1.0, 2.0).
- difference between the means of the basic items and the intruders: between 0.5 and 1.0 times the diagonal of the covariance matrix
- variances of each covariate: the mean multiplied by a random number from a uniform distribution over (1.0, 10.0)
- \( p \)-value for the basic subjects: between 0.2 and 0.5
- \( p \)-value for all subjects: < 0.1

We set the \( p \)-value threshold for the matching algorithms to 0.2. This choice of \( p \)-values is intended to bias the algorithms toward excluding intruders. However, when there is distributional overlap between the basic items and the intruders, it is possible to achieve a match without excluding all intruders; it is also possible that basic items will be excluded.

We created 5 random data sets for each of the 36 collections of parameters, and ran each method for each data set: the proposed heuristics, and four results from 1, 10, 100, or 1,000 runs of random search. The criteria used are the \( p \)-values from Welch’s \( t \)-test and the Anderson–Darling test, enforcing a match both on means and distributional shapes.

### 4.2.2 Metrics

Our evaluation metrics are the following:

- the percentage of excluded items and of excluded intruders
- the balanced divergence, the Kullback–Leibler divergence of the group ratios from the expected ratios (i.e., those for the original group ratios)
- criteria \( p \)-values after matching
- (“wall clock”) execution time
Table 1: Results from running the matching algorithms on synthetic data sets; the median result across all data sets is reported. # solutions: number of unique solutions; % E. items: the percentage of excluded items; % E. intruders: the percentage of excluded items which were intruders; BD: balanced divergence; \( p \): the \( p \)-value from Welch’s \( t \)-test or the Anderson-Darling test (whichever is smaller) for the matched groups; \( r_n \): the best of \( n \) random algorithm runs; \( h_2 \): heuristic2; \( h_3 \): heuristic3; \( h_4 \): heuristic4; \( \lambda \): lookahead.

| algorithm | # solutions | % E. items | % E. intruders | BD  | \( p \) | time       |
|-----------|-------------|------------|----------------|-----|-------|------------|
| \( r_1 \) | 0           | 97         | 100            | .00 | .52   | < 1 minute |
| \( r_{10} \) | 1           | 37         | 40             | .84 | .28   | < 1 minute |
| \( r_{100} \) | 1           | 9          | 10             | .24 | .24   | < 1 minute |
| \( r_{1000} \) | 1           | 4          | 10             | .06 | .22   | < 1 minute |
| \( h_2 \) | 1           | 2          | 10             | .12 | .22   | 1 minute   |
| \( h_3 \) (\( \lambda = 1 \)) | 17         | 2          | 10             | .05 | .21   | 2 minutes  |
| \( h_4 \) (\( \lambda = 1 \)) | 18         | 2          | 11             | .05 | .21   | 2 minutes  |
| \( h_3 \) (\( \lambda = 2 \)) | 78         | 2          | 10             | .02 | .21   | 2 hours    |
| \( h_4 \) (\( \lambda = 2 \)) | 74         | 2          | 10             | .02 | .21   | 2 hours    |
| \( h_3 \) (\( \lambda = 3 \)) | 216        | 2          | 7              | .02 | .21   | 45 hours   |
| \( h_4 \) (\( \lambda = 3 \)) | 221        | 2          | 7              | .02 | .21   | 45 hours   |
| exhaustive | 2           | 2          | 10             | .02 | .22   | 3 hours    |

4.2.3 Results

We find (see Table 1) that the random algorithm identified matched groups about 30% of the time when it was run a single time, excluding over 97% of the items on average. When preserving the best of 10 runs, the success rate increases to 99%, and 100% for 100 or 1000 runs. At the same time, the percentage of excluded items decreases dramatically. This is significantly worse than the results from the heuristics, though running times are comparable.

The heuristics succeed in finding a solution in every case. The percentage of excluded subjects did not differ between them for the task at hand: they generally find similar solutions, but running times increases exponentially as lookahead is increased. A lookahead of 3 does not improve match quality, but does find significantly more solutions that satisfied our criteria. The heuristics do not quite meet performance of exhaustive search. Exhaustive search is not only feasible for most of these data sets (over 80% of the time when we allowed it to run for up to five days), but even takes lesss time to run than heuristics with a lookahead of 3.

In summary, the heuristics are preferable to the random algorithms, at least for this simulated data. However, they still do not always reach the performance of the exhaustive algorithm, and can take very long to run when a large lookahead is used.

4.3 Matching subjects on neurocognitive measures

In this section, we describe the application of the matching algorithms to the subject pool of the CSLU ERPA Corpus (Gorman et al., 2015, 2016; MacFarlane et al., 2017). This enables us to evaluate the algorithms on real-world data. First we summarize our goals for the matching task, then we describe a process for finding a solution. Finally we present some properties of the results and compare the algorithms. For more information on this data set and the matching problem it poses, see Kiss 2017.
4.3.1  Matching criteria

Our goal is to find four sets of subjects from four groups such that various group pairs are matched on a separate set of covariates. The four groups are:

- ALN: Autism with normal language
- ALI: Autism with language impairment
- SLI: Specific Language Impairment
- TD: typical development

All groups are to be matched on age. Furthermore, particular pairs of groups are to be matched on the following covariates:

- SLI and ALI: performance IQ (PIQ) and verbal IQ (VIQ)
- ALI and ALN: ADOS score (Lord et al., 2000)
- ALN and TD: PIQ and VIQ

There are 113 subjects in all, comprised of 43 TD, 25 ALN, 26 ALI, and 19 SLI diagnostic cases. We wish to keep all subjects with SLI (the smallest group in our corpus), and as many as possible from the ALI, ALN, and TD groups, in decreasing order of preference. The criteria require a two-tailed \( \alpha > .2 \) on Welch’s \( t \)-test and, optionally, the Anderson–Darling test.

A pilot experiment revealed that matching each pair of groups independently gave different subsets of subjects for each pair. This was considered undesirable as we want to find just one set of subjects that meets all of the criteria above while also optimizing the group size and other metrics. We address this problem by matching the groups simultaneously, globally optimizing the solution. The basic idea of this approach is to create one complex set of matching criteria that contains everything we require in the final solution, and then use that to work with all subjects from all groups at the same time. We therefore implemented infrastructure components that allow us to:

1. specify complex sets of matching criteria, including various criterion functions and thresholds for various sets of groups
2. calculate \( r \) (the minimum \( p \)-value–threshold ratio) based on a combination of test statistics
3. calculate evaluation metrics for how well a set of subjects suits the matching criteria
4. enforce an ordering among the possible subject configurations; that is, being able to decide which one of two subject sets has better evaluation metrics

4.3.2  Results

Using ldamatch, we apply the simultaneous optimization approach as outlined above to the CSLU ERPA ADOS Corpus. Results are given in Table 2, which uses the Welch’s \( t \)-test criterion, and Table 3, which combines the \( t \)-test and the Anderson–Darling test. Exhaustive search is infeasible for this problem. In contrast, the random algorithm practically always finds a solution, but the quality of the solution is much worse than that obtained with heuristics. Regarding these heuristics, we can see that there is not a large difference between the algorithms in the number of subjects retained. Of the 113 candidate subjects, the best solutions preserved at most one more than the others. However, the heuristic solutions are differentiated by the degree to which they are able to preserve the desired group size proportions and how many equivalent solutions they produce.
Table 2: Results from ten replications of matching subjects from the ERPA data set on verbal IQ and chronological age using Welch’s $t$-test at $\alpha = .2$. # excluded: the number of subjects excluded (best of ten); # solutions: number of unique solutions (greatest of ten); time: wall clock execution time; $r_{1000}$: the best of 1,000 runs of the random algorithm; $h_2$: heuristic2; $h_3$: heuristic3; $h_4$: heuristic4; $\lambda$: lookahead; # solutions: number of unique solutions.

| algorithm | # excluded | # solutions | time       |
|-----------|------------|-------------|------------|
| $r_{1000}$ | 54         | 1           | < 1 minute |
| $h_2$     | 18         | 1           | < 1 minute |
| $h_3 (\lambda = 1)$ | 17       | 16          | < 1 minute |
| $h_4 (\lambda = 1)$ | 17       | 12          | < 1 minute |
| $h_3 (\lambda = 2)$ | 17       | 96          | 22 minutes |
| $h_4 (\lambda = 2)$ | 17       | 165         | 22 minutes |
| $h_3 (\lambda = 3)$ | 17       | 39          | 9 hours    |
| $h_4 (\lambda = 3)$ | 17       | 468         | 10 hours   |

Table 3: Results from ten replications of matching subjects from the ERPA data set on verbal IQ, performance IQ, ADOS severity score, and chronological age using Welch’s $t$-test and the Anderson–Darling test at $\alpha = .2$. # excluded: the number of subjects excluded (best of ten); # solutions: number of unique solutions (greatest of ten); time: wall clock execution time; $r_{1000}$: the best of 1,000 runs of the random algorithm; $h_2$: heuristic2; $h_3$: heuristic3; $h_4$: heuristic4; $\lambda$: lookahead; # solutions: number of unique solutions.

| algorithm | # excluded | # solutions | time        |
|-----------|------------|-------------|-------------|
| $r_{1000}$ | 59         | 1           | < 1 minute  |
| $h_2$     | 27         | 1           | 10 minutes  |
| $h_3 (\lambda = 1)$ | 21       | 11          | 14 minutes  |
| $h_4 (\lambda = 1)$ | 21       | 11          | 14 minutes  |
| $h_3 (\lambda = 2)$ | 19       | 35          | 8 hours     |
| $h_4 (\lambda = 2)$ | 19       | 30          | 8 hours     |
| $h_3 (\lambda = 3)$ | 19       | 55          | 212 hours   |
| $h_4 (\lambda = 3)$ | 19       | 40          | 211 hours   |
4.4 Matching verbs on frequency

Much of the prior work on matching is focused on quasi-experimental, between-subjects studies in which differences between two or more groups of human subjects is one of the primary sources of variance. However, the matching procedures described above can just as easily be applied to linguistic “items”—such as words—used as stimuli in experimental or observational designs. As an example, we illustrate the matching of regular and irregular English verbs on frequency and related attributes. The regular verbs include all those verbs which form their past tense by the addition of the suffix spelled \(-ed\) and pronounced as \([t\), \([d\) or \([\theta]\), depending on the final segment of the verb stem. In contrast, the irregular verbs either undergo stem changes in the past tense (e.g., become-\textit{became}, leave-left, think-thought) or have a past tense forms that are identical to their present tense forms (e.g., cut, hit, shut). The regular verbs greatly outnumber the irregular verbs, and it is well-known that the irregular verbs have higher average token frequencies than regular verbs (Marcus et al., 1992). These two imbalances conspire to make this a particularly challenging matching problem, though word frequency is an extremely important covariate for many behavioral tasks.

The inventory of English verbs used here was created by combining of a list of verbs from the English Lexicon Project (Balota et al., 2007), a list of irregular verbs extracted from the CELEX-2 lexical database (Baayen et al., 1996), and word frequencies norms from SUBTLEX-US database (Brysbaert and New, 2009). This data set contains 3,727 verbs, of which 134 are irregular.

4.4.1 Matching criteria

Table 4 shows experiments matching regular and irregular verbs on word frequency using the criterion \(p(t) \geq .2\). A second set of experiments, shown in Table 5, matches these groups on both word frequency as well as the conditional probability of the verb given its “base” (i.e., citation form or lemma), a measure proposed by Lignos and Gorman (2012).

4.4.2 Results

Each algorithm is applied ten times; the tables display the number of times the algorithms produce outcomes, and the range of the resulting values. For both sets of experiments, the only feasible approaches are heuristic3 and heuristic4 with limited lookahead. We also experiment with another method to speed up computation. Let \(\rho\) denote the frequency with which \(r\), the \(p\)-value/threshold ratio, is updated. Whereas we use \(\rho = 1\) above—that is, \(r\) is recomputed every iteration—we also perform matching with \(\rho = 10\) and \(\rho = 100\). When \(\rho = 10\), for instance, this produces a considerable speed-up and the resulting matches are only slightly degraded from the solutions obtained with \(\rho = 1\). However, high values of \(\rho\) do not result in usable matches.

5 Discussion

The most important difference between the algorithms is running time. The relatively-simple heuristic2 returns a solution in seconds or minutes for the problems considered here, whereas algorithms with relatively large look-aheads may require hours or even days of parallel computation. Nevertheless, in certain cases it may be worth running such methods for many days. For instance, one may wish to commit a large amount of compute time simply to preserve one or two more subjects when there is a substantial marginal cost associated with each subject’s data, and the resulting solution may be used in multiple projects and/or publications. For instance, both Kiss (2017) and MacFarlane et al. (2017) use the CSLU ERPA Corpus look-ahead subject-matches, which required several days of computation.
| Algorithm | # Outcomes | # EI | # ER | Time       |
|-----------|------------|------|------|------------|
| $h_3$ ($\lambda = 1$) | 10 | 49 | 1,060 | 18 hours |
| $h_4$ ($\lambda = 1$) | 10 | 49 | 1,060 | 18 hours |
| $h_3$ ($\lambda = 1, \rho = 10$) | 10 | 49 | 1,060 | 7 hours |
| $h_4$ ($\lambda = 1, \rho = 10$) | 10 | 49 | 1,060 | 7 hours |
| $h_3$ ($\lambda = 1, \rho = 100$) | 10 | 50 | 1,082 | 17 minutes |
| $h_4$ ($\lambda = 1, \rho = 100$) | 10 | 51 | 1,104 | 19 minutes |

Table 4: Results from ten replications of matching regular and irregular verbs on word frequency at $\alpha = .2$. # outcomes: number of successful runs; # EI: number of excluded irregular verbs (best of successful runs); # ER: number of excluded regular verbs (best of successful runs); time: minimum wall clock execution time across successful replications. $h_3$: heuristic3; $h_4$: heuristic4; $\lambda$: lookahead; $\rho$: number of items removed before recomputing item scores.

| Algorithm | # Outcomes | # EI | # ER | Time       |
|-----------|------------|------|------|------------|
| $h_3$ ($\lambda = 1$) | 9 | 63 | 2,811 | 81 hours |
| $h_4$ ($\lambda = 1$) | 10 | 63 | 2,970 | 82 hours |
| $h_3$ ($\lambda = 1, \rho = 10$) | 6 | 63 | 2,598 | 9 hours |
| $h_4$ ($\lambda = 1, \rho = 10$) | 3 | 63 | 3,195 | 9 hours |
| $h_3$ ($\lambda = 1, \rho = 100$) | 8 | 63 | 2,953 | 1 hour |
| $h_4$ ($\lambda = 1, \rho = 100$) | 7 | 63 | 3,005 | 1 hour |

Table 5: Results from ten replications of matching regular and irregular verbs on word frequency and the conditional probability of word given morphological base ($pformbase$) at $\alpha = .2$. In all successful experiments, a large number of entries must be removed to satisfy the criterion; failed experiments are omitted. # outcomes: number of successful runs; # EI: number of excluded irregular verbs (best of successful runs); # ER: number of excluded regular verbs (best of successful runs); time: minimum wall clock execution time across successful replications. $h_3$: heuristic3; $h_4$: heuristic4; $\lambda$: lookahead; $\rho$: maximum number of items removed before recomputing item scores.
The heuristic3 and heuristic4 methods often identify multiple solutions which are roughly equivalent with respect to the provided criteria. This can be useful to confirm that findings generalize across various subsamples matched to the same criteria. Alternatively, since there is a stochastic element to the proposed heuristics, replications may result in slightly different outcomes, and so one may wish to run these heuristics repeatedly times and analyze the best solution.

While the heuristics we pose here have proved effective for our purposes, future work could frame the matching problem using integer linear programs or their the linear relaxations. Alternatively, one could use local-improvement algorithms (Aarts and Lenstra, 2003) to refine solutions found via heuristic.

The above experiments used p-values from null hypothesis tests as criteria for matching. However, since our stated goal is to create groups which were equivalent—not to accept or reject the null hypothesis—future work could use Bayesian statistical methods which allow one directly estimate the probability that experimental groups are “practically equivalent” with respect to their covariates (e.g., Benavoli et al., 2017).

6 Conclusions

We have proposed an approach for matching groups of subjects or items so as to minimize covariate differences between the groups. Evaluation of the proposed methods for matching found that even the simplest algorithms often find acceptable solutions, and these solutions are improved using methods which are computationally more intensive. The implementations above are available to the research community in the form of the R package ldamatch, which can be obtained from the CRAN repository.

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