

Case Selection via Matching

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Abstract

This article shows how statistical matching methods can be used to select “most similar” cases for qualitative analysis. I first offer a methodological justification for research designs based on selecting most similar cases. I then discuss the applicability of existing matching methods to the task of selecting most similar cases and propose adaptations to meet the unique requirements of qualitative analysis. Through several applications, I show that matching methods have advantages over traditional selection in “most similar” case designs: They ensure that most similar cases are in fact most similar; they make scope conditions, assumptions, and measurement explicit; and they make case selection transparent and replicable.

Keywords

case selection, matching, most similar systems, qualitative methods, research design

Can statistical matching methods be used for selecting cases in qualitative case study research? Qualitative methodologists have used matching as an analogy for the logic of “most similar” case study research and some suggest that it is a viable way of selecting cases for paired analysis (Gerring 2007; Levy 2008; Lieberman 2015; Seawright and Gerring 2008; Tarrow 2010).

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Yet to my knowledge, only one qualitative study—Madrigal, Alpízar, and Schlüter (2011)—has explicitly used matching to select cases, indicating that either the analytic benefits are not clear or the methods are not sufficiently developed to meet researcher needs. This article offers a methodological justification for most similar case designs, explains the benefits of using matching for qualitative case selection, shows how existing matching algorithms can be adapted to meet the needs of qualitative analysts, and walks through examples in which these methods are applied to real case selection problems using new, freely available software.

Selecting cases with statistical matching methods has several advantages. First, researchers can be confident that selected cases that are in fact similar, especially when there are many relevant variables. When identical cases are not available, researchers must trade off similarity on some variables for similarity on others. Statistical matching offers a principled way to make these trade-offs and provides tools for assessing the quality of the resulting case pairings. Selecting cases with matching is transparent, replicable, and protects researchers against the criticism that the cases were intentionally chosen in ways that might bias the findings. Importantly, it does not require that researchers adopt a “statistical worldview” when analyzing cases (Mahoney and Goertz 2006). In fact, although statistical matching is closely associated with causal inference and the counterfactual model of causation (Neyman 1923; Rubin 1973), researchers do not have to adopt this counterfactual model, or even the broad goal of causal inference. Instead, the machinery of matching can be co-opted for a different purpose: to select most similar cases that are, in fact, most similar.

I begin by arguing for a new understanding of the inferential logic that motivates most similar case selection strategies and the process tracing analysis that typically follows. I then give an overview of statistical matching methods. Because most existing matching algorithms are not ideally suited for qualitative case selection, I explain which methods can be most usefully adapted to the needs of case study analysts. I illustrate the benefits of matching with applications to the work of Madrighal et al. (2011), Haverland (2006), and Lieberman (2003), followed by a summary of the benefits and costs to researchers.

Design and Inference With Most Similar Cases

Case selection is the process of choosing cases for case study research. Following Gerring (2004), I define a *case* as “a spatially bounded phenomenon . . . observed at a single point in time or over some delimited period of time”

(p. 342). A *case study* is “an intensive study of a single unit for the purpose of understanding a larger class of (similar) units” (p. 342). Virtually, all qualitative methodologists agree that systematic, nonrandom case selection is crucial to case study research, although there is disagreement about which selection strategies have the most merit.¹ Seawright and Gerring (2008) describe seven general strategies of case selection for causal inference: *typical*, *diverse*, *extreme*, *deviant*, *influential*, *most similar*, and *most different*.² Statistical matching methods will primarily be useful for designs that pair (or group) cases based on similarity—namely, most similar and “most different” case selection. In this article, I focus on applications of matching to most similar case selection, leaving most different case selection and other strategies for future research.³

Most similar case selection entails choosing two or more cases that have similar characteristics. This strategy is genealogically related to Mill’s (1858) method of difference and was developed and clarified by Przeworski and Teune (1970) as the method of “most similar systems,” and Lijphart (1971) as the Comparative Method.⁴ It features prominently in recent texts on case selection (Gerring 2007) and is a relatively common strategy for designing research in several disciplines.⁵ Most similar case selection proceeds by (1) defining the relevant universe of cases, (2) identifying key variables of interest that should be similar across the target cases, (3) identifying a variable or variables that should vary meaningfully across the target cases, and (4) selecting the desired number of cases—often a pair but sometimes more—that have the specified similarities and differences. Often, analysts begin this process with one case already in mind and follow the steps mentioned previously to identify a second case that is similar.

Are Credible Inferences Possible With Most Similar Case Designs?

Despite the popularity of most similar case designs, defenses of this approach in the methodological literature are surprisingly weak, and some argue that the approach is less helpful than other approaches (Seawright n.d.). Given that the purpose of this study is to improve the execution of these designs, I begin by presenting a stronger justification.

Texts on qualitative methodology often treat most similar case selection as a precursor to a correlational analysis—essentially an “intuitive regression” with very few cases. From this perspective, the paired cases serve as mutual counterfactuals, answering the question “what might have happened under different circumstances?” By comparing very similar cases, qualitative methodologists have argued that they can approximate the logic of a

randomized experiment (Lieberman 2003:8; Tarrow 2010:244). Assuming that plausible “natural experiments” can be identified, the resulting similarity between cases “controls” for potential confounding of the relationship of theoretical interest. Any remaining correlation between a variable of interest and the outcome is causal.⁶

This characterization of most similar case selection as a precursor to small-n intuitive regression is misleading because it is not methodologically sound and it is not what most researchers actually do. If researchers *did* primarily use intuitive regression to analyze small numbers of similar cases, the results would be unpersuasive for the same reasons that a randomized experiment with a handful of cases would be uninformative—the design is statistically underpowered. Additionally, researchers would have to argue that any random error in the process of generating outcomes is negligible relative to the magnitude of the causal effect and that there are no unobserved confounders.⁷ Finally, this characterization does not recognize that many most similar case designs also condition on the outcome variable in some way during the case selection process (e.g., ensuring that the outcome of interest occurs in at least one case).

Luckily, most similar case analysis is not small-n regression. Instead of merely reporting correlations, case study analysts almost universally describe the process by which each outcome came about in each case (Caporaso 2009; Tarrow 2010; Tilly 2002). Tarrow (2010:238) argues that parallel process tracing is an integral part of most similar case analysis and that it gives greater inferential leverage than the “logic of correlation” because process tracing can unpack the causal mechanisms that underlie a correlation. George and Bennett (2005) further explain the role of process tracing in most similar case analysis, which they refer to as “controlled comparison:”

[P]rocess-tracing can serve to make up for the limitations of a particular controlled comparison. When it is not possible to find cases similar in every respect but one—the basic requirement of controlled comparisons—one or more of the *several* independent variables identified may have causal impact. Process-tracing can help to assess whether each of the potential causal variables in the imperfectly matched cases can, or cannot, be ruled out as having causal significance. If all but one of the independent variables that differ between the two cases can be ruled out via a process-tracing procedure . . . a stronger (though still not definitive) basis exists for attributing causal significance to the remaining variable. (p. 215)

But what specifically is process tracing, and how does it strengthen a most similar case design? George and Bennett (2005) define process tracing as

“attempts to identify the intervening causal process—the causal chain and causal mechanism—between an independent variable (or variables) and the outcome of the dependent variable” (p. 207). Because it is causal inference, process tracing must rely on inferences about counterfactual states of the world (Neyman 1923; Pearl 2000; Rubin 1973).⁸ At each step of a causal chain, the scholar must infer what would have happened if the preceding links had been different. And at each step, confounders might lead the researcher to conclude that a false pathway is in fact real. In short, each step in a process tracing chain requires a causal estimate with nonexperimental data.

Seen from this light, it is surprising that process tracing is possible at all, given the difficulty of obtaining even a single unbiased causal estimate in many nonexperimental settings. Process tracing requires many such estimates; how does it achieve causal inference without the quantitative machinery that allows other cases to serve as counterfactuals? Some methodologists have argued that process tracing overcomes this challenge by replacing *data set observations* with one or more *causal process observations*—defined as an “insight or piece of data that provides information about context, process or mechanism, and that contributes distinctive leverage in causal inference” (Brady and Collier 2004:227). These often resemble a “smoking gun” that points to the operation of some causal mechanism. Subsequent work has tried to unpack whether and how causal process observations facilitate causal inference (Beck 2006, 2010; Collier, Brady, and Seawright 2010; Mahoney 2012), but this is an active area of research and methodologists do not yet agree.

I argue that process tracing primarily uses thought experiments, rather than data, to inform counterfactual statements.⁹ Observing a smoking gun is powerful because a researcher can imagine a world without the smoking gun, *not* because the researcher is comparing the this instance of a smoking gun with other noninstances in a specific data set. Instead, the researcher makes counterfactual assumptions, based on experience, of how things “typically” behave and thus how alternative worlds might have played out. Because these counterfactual assumptions are based on experience, causal links in the process tracing chain are most believable if they are “short” and can be reduced to common experiences. In defense of this position, George and Bennett (2005) quote historian Clayton Roberts arguing that a proper causal explanation involves “minute tracing of the explanatory narrative to the point where the events to be explained are microscopic and the covering laws correspondingly more certain” (Roberts 1996:66).

Effective process tracing requires two types of evidence. First, it requires “measurement evidence” that the events in the purported causal chain happened. Case studies are ideal for measurement because researchers can focus

their efforts on discerning what events actually occurred in a particular case. This descriptive inference does not rely on counterfactual claims. Second, it requires “identifying evidence” that identifies the causal relationship (in the statistical sense) by ruling out confounding variables and processes. Unfortunately, “proving the negative and demonstrating that a particular process did not occur can be notoriously difficult” (George and Bennett 2005:218). This is where a research design featuring carefully matched cases helps to rule out alternative causes. The case selection and process tracing components of the typical most similar case analysis can thus complement each other to produce more reliable inferences than either could achieve in isolation.

Properly understood, most similar case analysis is analogous to the two stage empirical strategy proposed by Ho et al. (2007a) for making causal inference in quantitative observational studies: (1) use statistical matching to create a sample in which units have similar background characteristics and (2) use a parametric model (such as regression) to account for the confounding due to remaining differences between units. Intuitively, step 1 attempts to find a subset of observations in an observational data set that looks as if they could have come from a randomized experiment. Practically, this means constructing a subsample in which the units vary meaningfully on the key variable of interest—the *treatment*—but are similar in all other ways. In most cases, this matching procedure creates a subsample that looks more similar than the original data. However, differences may persist between the treatment and control groups that cannot be fixed without the matched subset becoming too small for the subsequent analysis to be informative. To account for remaining differences in a matched data set, Ho et al. (2007a) propose using a parametric model such as ordinary least square to estimate causal quantities of interest in the matched sample. This research procedure is “doubly robust”—causal inference is possible if *either* the matching works *or* the parametric model works.

I argue that qualitative scholars are doing something similar when combining most similar case selection with process tracing. First, they condition on some confounders when selecting cases to ensure that those confounders are not the cause of any effect they see. Then, they deal with the rest of the empirical variation among the cases by using process tracing in the same way that quantitative analysts use regression to interpolate between nonidentical cases. Although this design is no longer a “natural experiment” because some covariates could be correlated with treatment assignment, it reduces the inferential burden at the process tracing stage. Rather than contending with all potential alternative causes through process tracing, the analyst must only

contend with those not addressed at the matching stage. In some sense, the procedure follows the logic of double robustness because the case selection and process tracing guard against each other's failures. Although this analogy is informal, it suggests a strong justification for most similar case analysis.

Statistical Matching for Case Selection

How can statistical matching help advance the analytical goals of case study researchers using most similar case designs? As shown previously, the inferential leverage in a most similar case design relies partially (though not solely) on the similarity of the cases. Finding sufficiently similar cases can be challenging, and the analyst must persuade the reader that the paired cases are indeed the most similar. Matching helps with these challenges.

A Review of Statistical Matching Methods

Statistical matching is an approach to purposeful case selection in large-n studies with the goal of finding comparable units within a data set. Matching is useful for making causal inferences in large-n data sets (Rosenbaum 2002; Rubin 1973) and is closely associated with the Neyman-Rubin causal model (Neyman 1923; Rubin 1973). The logic is simple: If units *A* and *B* are identical and *A* receives a treatment while *B* receives control, then subsequent differences between the units can be attributed to the treatment. Matching, like regression, is a way of conditioning on covariates. Rather than “controlling for” a variable by including it in a regression model, matching “controls for” a variable by only allowing comparisons between units that have sufficiently similar levels of the variable.

Although matching was developed to facilitate causal inference via statistical analysis, the primary role of matching is to create matched samples with similar units, a goal shared by qualitative researchers using most similar case designs. Qualitative researchers can use matching to find similar cases without adopting the assumptions or quantitative machinery that follows matching in quantitative studies.

Before describing specific matching methods, I describe the general features of the problem that matching is trying to solve. Matching identifies treated and control units that are “close” to each other in a *k*-dimensional space defined by the *k* covariates that need to be conditioned on to estimate unbiased causal effects. In general, as the number of covariates grows, the distance between units in the covariate space also grows, so matching with

more covariates means that matched pairs are further apart.¹⁰ For this reason, it can be detrimental to condition on variables that are not confounders because matching on these variables makes reduces similarity on actual confounders. On the other hand, analysts rarely have enough information to definitively declare that a variable is not a confounder.

There are many matching methods, primarily distinguishable by the distance metrics they use to determine similarity. Here, I describe the most common and most important methods.

Exact matching. Exact matching identifies units that are identical on observed covariates. It is ideal for both quantitative studies and qualitative controlled comparison, but it is often difficult to find exact matches, especially when the covariates used for matching take on many values.

Coarsened exact matching. Coarsened exact matching (CEM; Iacus, King, and Porro 2011, 2012) follows a similar logic to exact matching but works for data sets where exact matches are not possible. Matching proceeds by first coarsening each continuous variable into categories preferably based on substantive knowledge. For example, one might reasonably coarsen *years of education* into categories corresponding to primary school, secondary school, and college. This would allow a freshman in high school to match with a senior in high school, but not with someone who had started college. Each covariate is coarsened based on these user-defined categories and exact matching is done on the coarsened variables. Units are matched together if they fall within the same stratum of the coarsenings. Observations that fall a stratum with no units in the opposite treatment are discarded.

Mahalanobis matching. This family of algorithms identifies similar units by minimizing pairwise Mahalanobis distance,¹¹ a generalization of Euclidean distance that accounts for correlations between variables (Rubin 1973).

Propensity score matching. Propensity score matching (Rosenbaum and Rubin 1983) relies on the insight that the propensity of each observation to receive treatment is a balancing score, meaning that conditioning on the true propensity score will, in expectation, balance the covariate distributions of treatment and control groups. In practice, analysts typically estimate propensity scores using logistic regression and match observations that have similar propensity scores.

Genetic matching. Genetic matching (Diamond and Sekhon 2013) uses a genetic algorithm to optimally choose weights for each matching variable. These variable weights imply a distance metric that is then used to produce a matched sample that minimizes a loss function based on global differences between treated and control distributions.¹² At each iteration, the algorithm starts with a proposal for the variable weights, introduces many random versions of this vector, and tests to see which version improves covariate similarity the most. The starting proposal for each iteration is the best set of weights from the previous iteration; this repeats until balance is optimized. Genetic matching takes as its inputs the matrix of matching variables augmented with a column that is the estimated propensity score. Because of this, genetic matching is a generalization of Mahalanobis and propensity score matching and will reproduce the results of these algorithms if they are optimal.

Adapting Matching Methods for Case Selection Goals

Which matching methods are most useful for qualitative case selection? Matching methods are not inherently good or bad on their own merits—their utility is based entirely on whether they can help the analyst find a subsample of similar units. A matching method that works well for one application may perform poorly for others. In general, I find that versions of exact matching and Mahalanobis matching are most likely to be helpful for case selection. Propensity score matching is unlikely to be helpful (contrary to Seawright and Gerring 2008).

Exact matching is ideal for selecting most similar cases because it mirrors what qualitative scholars are already doing when possible. Exact matching creates pairs of cases that are identical on the matching variables—the exact procedure described in qualitative methods texts as the proper way of selecting most similar cases. Using exact matching for case selection is thus simply taking what qualitative scholars already are doing, but carrying out the matching on a computer (which has benefits, described subsequently). Exact matching should be the first tool that any analyst should turn to. Quantitative analysts rarely use exact matching because they need substantial sample sizes for subsequent analysis and often only a few exact matches can be found in a data set. In contrast, case study researchers only need a small number of exact matches for analysis, so exact matching may be more feasible for case study research.

Which methods are most useful for selecting similar cases when exact matches are not available? When confronting this situation, case study

practitioners often take the step of coarsening or dichotomizing variables on which they cannot find exact matches (Gerring 2007:133). This is exactly the same procedure as CEM, so CEM offers a principled way of thinking about these choices and selecting matches. CEM implements the method that most qualitative scholars already choose when there are no exact matches available. Thus, analysts can garner the benefits of using statistical software to perform the case selection while retaining exactly the same procedure that they would have used if selecting cases by hand.

Mahalanobis matching offers a different way of matching cases when exact matches do not exist. Mahalanobis matching identifies units located close together in the k -dimensional space defined by the covariates. Although this does not exactly mirror what qualitative scholars typically do when there are no exact matches, it does provide the outcome that analysts typically want: the paired cases will be as close together as the existing data allow. This method can be combined with other methods. If it is particularly important to condition on some covariate X_1 , then exact matching can be used for this covariate, followed by Mahalanobis matching on the other covariates within the strata defined by exact matches on X_1 .

Propensity score matching is probably not ideal for selecting similar cases for qualitative analysis because it first summarizes the k covariate values for a single case using a scalar (the propensity score) and then matches units on this scalar. Although matching on propensity scores may balance aggregate covariate distributions, individual matches are often far apart in the covariate space. As such, selecting two cases with similar propensity scores may not produce matches that have similar values of the control variables. Similarly, Genetic matching (as currently implemented) minimizes a loss function defined in terms of global balance, so paired units are not necessarily close in the covariate space. However, genetic matching provides technology for weighting covariates by their importance that is useful to case study analysts.

Matching methods rarely work “off the shelf” for qualitative case selection because they are intended to precede statistical analysis rather than process tracing. The most obvious problem is that existing computer software for matching is not tailored to the specific needs of case study scholars. Software for matching is readily available (Ho et al. 2007a, 2007b) but is tailored to producing an entire data set of matched treatment and control units rather than answering questions such as “which three cases are most like case x ?” I provide software that implements matching routines specifically for case selection.¹³ With this software, users can find one or more cases that best match a particular case of interest using matching methods described in this article. If the researcher does not have a particular case in mind, the software

can find the closest possible matched pairs in terms of specified covariates. Unlike statistical matching software, I do not require users to specify a “treatment” variable because some qualitative analysts do not have one at the case selection stage. Other analysts do have a treatment variable in mind; my software has options to maximize the variance or “spread” of a continuous variable of particular interest while matching as closely as possible on several other variables (King, Keohane, and Verba 1994:140).

One difference between case selection for quantitative and qualitative research is that case study analysts often condition on the outcome variable during case selection, most frequently by choosing cases where a rare outcome of interest is present. This differs from the statistical matching framework and requires modification to existing matching routines. Conditioning on the outcome no longer allows unbiased estimation of the correlation between treatment and outcome (Geddes 1990), but may still meet the analytical goals of case study researchers. If so, the methods mentioned previously can be adapted to maximize case similarity subject to some constraint on the values of the outcome variable, although researchers should be aware that constraints will often reduce the number or quality of available matches.

Analysts often know that some covariates are more likely than others to be important alternative causes of the phenomenon of interest. This type of information is easily incorporated into the matching framework, and matching can help researchers express to readers the extent to which one variable matters more than another. This can be done by weighting the variable highly in the matching analysis, or even requiring that it be matched exactly. Because readers might question the relative importance of these variables, researchers could check the robustness of their case selection to alternative weights. There is no “correct” weighting—generally, variables that are strong confounds and difficult to account for in the subsequent process tracing should receive the most weight when matching.

In some settings, researchers can use existing data sets to match cases. In others, the researcher needs data that are partially or completely unavailable. If the missing information can be coded in general terms, then analysts can code the variables themselves and pass this data set to the matching routine. This does not mean that every variable must be quantified—categorical coding is adequate for matching.

If missing information is difficult to collect for more than a few cases, one viable strategy is to first match on easily measured variables and then measure difficult variables for the cases that are most promising. However, it is crucial to note that if information is missing for many cases, then the analyst

does not have enough information to pursue a most similar case design with respect to the missing information. Any matching of cases, whether carried out mentally by the researcher or using statistical software requires data to make the comparison. If the criteria for matching cases are too vague to be written down, they are probably too vague to be used at all.

Another strategy for dealing with missing information is match on proxy variables or comparing cases that are widely considered to be “natural pairs.” For example, matching countries by geographic region can hold many confounders constant, even though geography itself may not be a confounder. This is also a solution for situations when data are “missing” because analysts do not know which variables are confounders. If the confounder set is partially unknown, controlling for categories that of broad similarity between cases can increase similarity on a large number of known and unknown dimensions. However, if the major confounders *can* be specified and data are available, analysts should demonstrate that matching on these types of broad proxy variables does not compromise the goal of finding the best matches on the specific matching variables.

Taking the idea of “natural pairs” to its logical conclusion, the best match for unit i_t (where t indexes time) may be i_{t-1} .¹⁴ In quantitative settings, analysts sometimes avoid matching the same unit in different time periods because it might violate a crucial assumption of the Neyman-Rubin causal model that the potential outcomes of compared units are independent.¹⁵ However, qualitative researchers might wish to focus on such pairings, either because they can account for the independence or because their analytic goals do not require independent cases. A design that compares units i_t and i_{t-1} will control for any time-invariant factors whether information is missing or not.

Illustrations

In this section, I illustrate the process of case selection via matching on two applied examples.

Madrigal, Alpizar, and Schlüter (2011)

Madrigal et al. (2011) seek to explain the performance of community-based drinking water provision organizations (CBDWOs) in rural Costa Rica. To my knowledge, their study is the only published research that uses statistical matching for case selection, so it is instructive to see how matching was implemented and whether it improves the study.

Madrigal et al. (2011) are explicit that their primary goal is to “study causal pathways instead of measuring the causal effect of selected variables on outcomes” (p. 1665). Because of their theoretical approach, they are most interested in the influence of CBDWO governance structures on water infrastructure condition, consumer satisfaction, and financial health. Citing Seawright and Gerring (2008), they use matching as a case selection method to “reduce the number of potential explicative variables [and] focus on the role of governance structures” (p. 1665).

Madrigal et al. (2011) use modified propensity score matching to select four cases that meet several constraints. They restrict the sample to cases in the Metropolitan Region of Costa Rica (one of seven administrative regions) on substantive grounds: that it allows “better control of geographical and climatic characteristics” and eliminates the possibility that “peculiarities of the relationship between ICAA regional administrative units and local CBDWO might affect their performance” (p. 1665).¹⁶ Within this subset, they estimate a propensity score model with organizational type as the outcome and cases characteristics as predictors. They then “[reduce] the population of cases to those located within a 95 percent confidence interval around the median propensity score” and select “the four cases closest to the median assuring that they differ in terms of water quality” (see Note 6). Thus, they condition on the outcome—specifically selecting a high- and low-performing CBDWO from each of the two types of CBDWO governance.¹⁷ Their goal with this procedure is to analyze cases that are similar to each other *and* representative of the other cases in some sense.

Unfortunately for replication purposes, the identities of the selected cases are obscured to protect the communities, so we cannot evaluate the performance of this case selection method relative to other possibilities. However, this serves to illustrate that matching helps readers evaluate the quality of case selection, even when standards of ethical research require that the identities of cases remain secret. This may be one of matching’s greatest benefits for qualitative work.

The authors provide replication data for most of the matching procedure, although the final selection stage is omitted and key indicators that would identify the selected cases are either missing or modified. I use this data set to illustrate why the propensity score matching used by Madrigal et al. (2011) may be less than ideal. For comparison, I identify the best match in terms of the propensity scores estimated by the authors and the best match in terms of Mahalanobis distance. Table 1 shows case information about the best pairing generated by each distance metric. I find that Mahalanobis matching produces a matched pair that is more similar in the scale of the covariates, with

Table 1. A Comparison of the Similarity of the Best Case Pairings From Propensity Score Matching and Mahalanobis Distance Matching.

	Best Propensity Score Pairing			Best Mahalanobis Distance Pairing		
	Case 5	Case 134	Difference	Case 78	Case 79	Difference
ln(Population)	4.83	4.87	-0.039	5.10	5.21	-0.12
Precipitation	3,500	3,000	500	2,000	2,000	0
Distance to hotel	21,599	39,831	-18,231	43,868	47,386	-3,518
Distance to national park	9,465	12,906	-3,441	20,868	19,427	1,441
Distance to municipality	332	384	-52	382	348	33
ln(Distance to San Jose)	10.26	10.17	0.082	9.18	9.17	0.006

Note: Data supplied by the authors. The units of the variables are unknown.

smaller absolute differences for five of the six covariates. This pattern persists when I examine more matches recommended by each method.

This illustrates my contention that propensity score methods are not well suited for case selection because similarity on the propensity score does not imply similarity on any single control variable. As a result, propensity scores will not necessarily produce matches that are similar in the ways qualitative researchers want. It is likely that Madrigal et al. (2011) could have identified even more compelling matches if they had used Mahalanobis matching instead of propensity score matching, but it is impossible to be sure without knowing the specific cases they selected.

Haverland (2006)

Haverland (2006) argues that studies of Europeanization—the effect of the European Union (EU) on member-state political structures—have a “no-variance” problem because case study analysts have primarily used designs featuring only EU members. Haverland argues that with no variance in EU membership, it is difficult to assess the effects of the EU because hypotheticals and process tracing alone do not provide reliable counterfactuals of what might have happened to states in Europe without EU membership.

Table 2. The Best Matched Pairs of European Union (EU) Members to Non-EU Members, Based on Mahalanobis Distance Calculated on the Variables in the Table.

Pair	Country	European Union	<i>d</i>	Political Freedom	Civil Liberties	GDP per capita	Trade	Socialist
1	Austria	Yes	0.02	1	1	19,242	58b	0
	Australia	No		1	1	20,019	56b	0
2	The Netherlands	Yes	0.04	1	1	19,109	179b	0
	Canada	No		1	1	20,230	181b	0
3	Denmark	Yes	0.08	1	1	20,897	46b	0
	Norway	No		1	1	22,365	42b	0
4	Sweden	Yes	0.09	1	1	19,867	77b	0
	Australia	No		1	1	20,019	56b	0
5	Denmark	Yes	0.14	1	1	20,897	46b	0
	Australia	No		1	1	20,019	56b	0

Note: GDP = gross domestic product. Mahalanobis distance is denoted “*d*.” Trade figures are in billions. Political freedoms and Civil Liberties are scaled from 1 to 7, with 1 indicating “most free.”

Haverland is skeptical that a most similar design will produce good inferences. The non-EU states he considers most similar to EU members—Norway and Switzerland—are enmeshed in the European milieu and may be influenced by Europeanization without formal membership. Instead, he argues that future research might profitably analyze “moderately similar” cases such as Australia, Canada, New Zealand, and the United States (p. 141). His criterion for these cases is that they are “stable and liberal democracies with a capitalist economy” that are “so ‘remote’ from the EU that often it can be plausibly argued that indirect EU effects also do not reach them” (p. 141).

I use matching to implement the case selection strategy advocated by Haverland. I operationalize Haverland’s matching criteria by collecting data on political freedom, civil liberties (Freedom House 2006), gross domestic product (GDP) per capita, trade (Gleditsch 2004), and socialism averaged between 1980 and 1992 (prior to the signing of the Treaty of Maastricht) for 26 of the 28 current EU members,¹⁸ and 151 non-EU states. It would be exceptionally taxing to manually consider each of the 3,926 possible pairings between EU and non-EU states. I use the software described previously to identify pairs of similar EU and non-EU cases based on Mahalanobis distance calculated for these five variables.

Table 2 shows the first five matched pairs in order of match quality. This list (and the longer list that I do not reproduce here) provides new ideas about

which countries might serve as cases to evaluate the effects of Europeanization. I find that some expert intuitions may be incorrect. Haverland identifies Norway and Switzerland as the two cases that are obviously most similar to EU members, but although Norway appears high on the list (as a match for Denmark), Switzerland is only the 45th best match for *any* EU country.¹⁹ Although Haverland considers Australia to be a moderately similar case to the EU countries, I find that it is the best possible non-EU pairing for three of the five EU cases—Austria, Sweden, and Denmark. It is in fact a legitimately most similar case based on a reasonable operationalization of Haverland's own criteria. There is no need to settle for moderately similar cases.

Table 2 does not feature any of the largest economies in the EU because these countries do not have non-EU counterparts that are as similar as the pairs listed. There may be other reasons to analyze these large economies (including intrinsic importance). I illustrate how to find matches for a specific case by using the same variables to identify matches for Germany using Mahalanobis distance matching. The resulting top matches—Japan, the United States, Canada, Union of Soviet Socialist Republics (USSR)/Russia, and South Korea—corroborate Haverland's intuition that Canada is similar to Germany (p. 141) and offer some additional options for consideration. However, the Mahalanobis distances between these matches range from 5.4 to 30.9, indicating that these matches are substantially less similar than those in Table 2.²⁰

If any of the above-mentioned matches are surprising, it indicates that either the analyst's heuristic sense of similarity is wrong or that additional matching criteria should be considered. Matching methods can help analysts elicit their own beliefs about which variables ought to be matched to make a pair of case studies persuasive. Perhaps new variables should be included, the current variables should be transformed to account for nonlinearities, or some variables should be weighted more heavily than others to construct matches that better fit a heuristic sense of similarity.

To show how such variable weighting works, I analyze the robustness of the Germany case pairings to alternative weightings of the covariates. The covariates can be divided into political variables (political freedom, civil liberties, and socialist history) and economic variables (GDP per capita and trade) and I explore how trading off the relative importance of these results in different case pairings. I start by giving the economic variables weights of 1 and gradually decreasing these weights to 0 while simultaneously starting the weights of the political variables at 0 and increasing them to 1.²¹ For each weight combination, I recalculate the list of matches for Germany and then record the average rank (meaning position on the list) of the five cases chosen

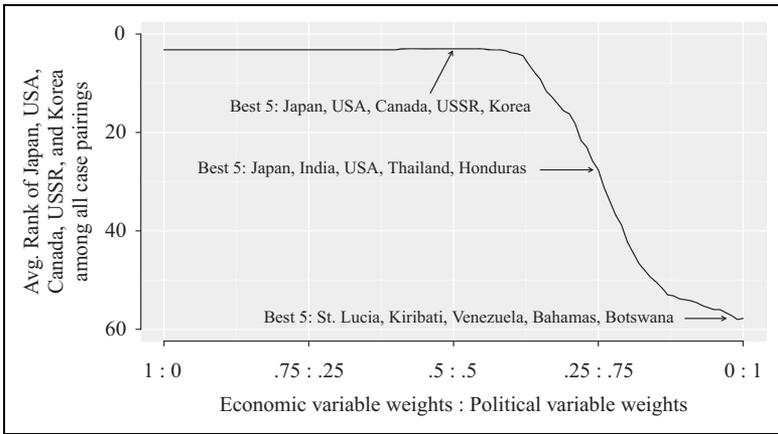


Figure 1. Changes in the average positions of Japan, United States, Canada, Union of Soviet Socialist Republics (USSR), and Korea on the list of best matches for Germany depending on different weights for economic and political variables. The five best matches for Germany are listed for the weighting combinations 0.5:0.5, 0.25:0.75, and 0:1.

originally: Japan, the United States, Canada, USSR/Russia, and South Korea. For any weighting that ranks these cases at the top, the average rank will be 3.5. If these cases are poor matches, they will appear further down the list and the average rank will increase.

The results in Figure 1 show that the case selection depends on the relative weight assigned to economic and political variables. The economic variables appear to dominate, so the top matches are stable as long as at least 40 percent of the weight is on economic variables. However, if the political variables are weighted highly, then the matches change substantially. The original matches move far down the list, while other cases take their place at the top. With all of the weight placed on the political variables, the best matches for Germany are Saint Lucia, Kiribati, Venezuela, the Bahamas, and Botswana. These matches surprise me, indicating that (1) I do not have an accurate sense of which cases have Freedom House scores similar to Germany between 1980 and 1993 and (2) the economic variables are important to my own heuristic sense of what it means for a country to be “like Germany.” This style of robustness analysis could accompany any presentation of most similar case selection to show whether the cases chosen are sensitive to the importance placed on each matching variable.

How Can Matching Improve Case Selection?

The previous sections show that several statistical matching methods can be adapted to serve the goals of case study researchers; this section discusses how matching improves upon current case selection practices.

Matching Aids Transparency and Replicability

One of the well-known adages of small-*n* research is that “the cases you choose affect the answer you get” (Geddes 1990:131). Analysts can strengthen confidence in their findings by providing precise information on how cases were selected, preferably in the form of a publicly available replication archive (Dafoe 2014).

It is almost universal in most similar case studies to spend at least some portion of the research describing the case selection. However, scholars rarely provide any discussion or data on alternative cases they considered but did not choose. Matching improves the credibility of case selection by providing comparisons to the cases *not* selected.

To illustrate, I reexamine Evan Lieberman’s (2003) study comparing how definitions of “national political community” influenced the politics and outcomes of tax collection in South Africa and Brazil. Lieberman is concerned that economic development and tax revenues from international trade might have influenced tax policy, so he sets out to show that these factors are virtually identical for the South African and Brazilian cases and cannot be the causes of the differences he observes.²² Lieberman’s extensive discussion (pp. 106-121) describes compelling similarities between the cases and his figures show that GDP per capita and *tax revenue from trade* in Brazil and South Africa have trended similarly over time. However, there is no discussion of alternative case pairings and without comparisons to other countries, it is difficult to tell just how similar these trends are.

To illustrate how comparison to other countries could make Lieberman’s case selection more even more persuasive, Figure 2 shows cross-national GDP per capita data from 1950 to 1990 for 175 countries, with South Africa and Brazil highlighted for comparison. This figure is directly analogous to Lieberman’s figure 4.1 (2003:114), except that other countries are included as well.²³ Although it is difficult to pick out the individual trend lines for the other 173 countries, it appears that Brazil and South Africa are indeed relatively similar.

To formalize this comparison, I use statistical matching methods to show how close Brazil and South Africa’s GDP per capita trend lines are relative to

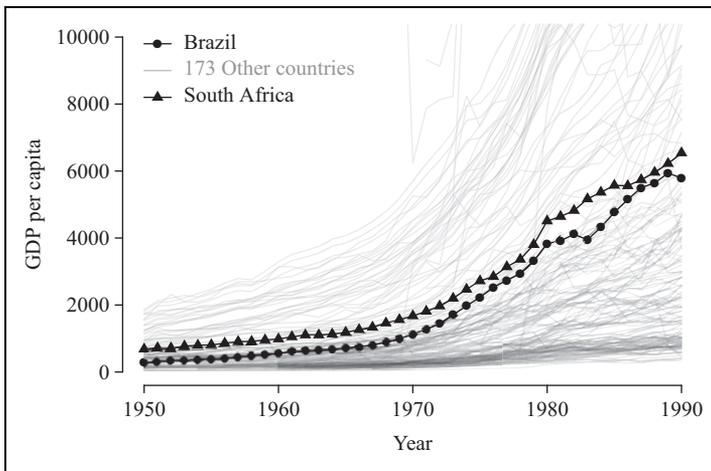


Figure 2. Trends in gross domestic product (GDP) per capita between 1950 and 1990 for 175 countries including South Africa and Brazil.

Source: Gleditsch (2004).

other possible cases that could have been chosen. I first discard any countries that do not have a complete GDP per capita time series between 1950 and 1990, which leaves 85 countries for matching. I reformat the time-series cross-sectional data into a cross section, with countries in the rows of the data matrix and yearly values of GDP per capita in the columns. I then calculate Euclidean distance²⁴ between each observation, producing a measure of similarity between trends in the same scale as Figure 2.

The left panel of Figure 3 shows the resulting matches if I begin with Brazil and identify the most similar countries based on GDP per capita trends. For a most similar case design, South Africa should be the best match for Brazil among the possible matched pairs we could have chosen (or nearly so). South Africa ranks highly, but there are nine other countries²⁵ that are better matches. However, rather than weighing all years equally, it may be preferable to give greater weight to the more recent past. The right panel of Figure 3 shows the results of a revised matching procedure with very little weight given to the distant past and logarithmically increasing weight over time. This produces a different ordering of matches; South Africa is now the fifth best match for Brazil out of 85 possible matches.

Given that similar GDP per capita trends are only one of several criteria that Lieberman uses for case selection, this result is quite encouraging. The

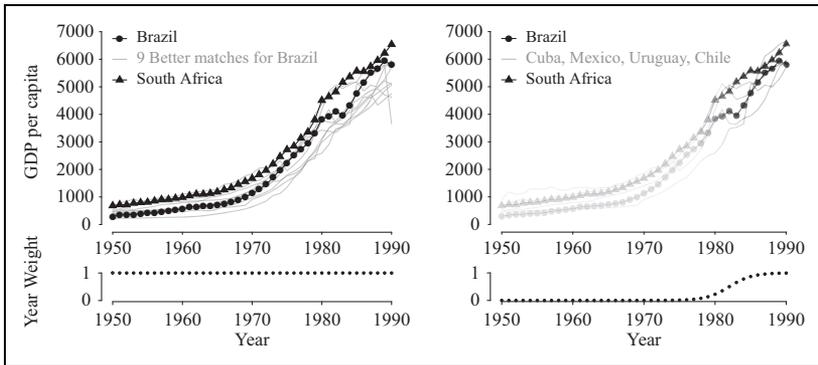


Figure 3. Trends in gross domestic product (GDP) per capita for South Africa, Brazil, and countries that match Brazil better than South Africa. Left: matching with equal weight across years (shown subsequently). Right: matching with no weight on early years and increasing weight on recent years (shown subsequently and by transparency).

matching analysis shows that relative to other countries, the trends and levels of GDP per capita in South Africa and Brazil are very similar. Differential rates of economic development are unlikely to be the cause of the differential tax policies he observes.

This illustration demonstrates the benefits of transparency about which cases were considered. Often, scholars doing this style of research select countries that are within the same region, but leave it ambiguous whether they considered countries outside of the region as potential cases. If extra-regional cases were considered but rejected, then this suggests that the cases really are similar on the covariates matched by the analyst. By only considering matches within the same region, the researcher is implicitly assuming that *region* must be matched exactly, regardless of the other covariates under consideration. Often, this is defensible because cases within regions tend to have had more similar histories and characteristics, but this decision should be explicit in the research design.

Similarly, field research is most practically carried out in countries where one speaks the language or has experience, but these might not always be the most similar cases. Matching helps by allowing analysts to compare the quality of matched pairs with and without a geographic or linguistic constraint. To illustrate, I replicate the matching from the Europeanization application in the Illustrations section with the constraint that at least 50 percent of the population must speak English to some degree.²⁶ In fact, this is no constraint

at all—the list of best matches is essentially identical to Table 2. In contrast, when I consider a similar constraint that all cases must have an adequate Francophone population, I get a drastically different set of best matches—namely, Luxembourg–Switzerland, Belgium–Switzerland, France–Switzerland, and the improbable combinations of Luxembourg–Djibouti and Luxembourg–Congo.²⁷ Analysts and readers might rightly worry that this language-constrained case selection strategy will not result in sufficiently similar cases.

The use of matching for case selection can also help researchers by tying their hands during the case selection process. Analysts often know something about the cases they are considering and could be accused of selecting cases that seem likely to lend additional support to a preferred hypothesis. Matching offers an additional way to reassure readers against such claims. A researcher looking for a second fieldwork site to confirm findings from a first case can avoid concerns about cherry-picking by specifying a list of covariates for matching, a list of cases to consider, and a list of constraints (such as language requirements or countries that are prohibitive for field work), and then selecting the case most similar to their first case given the constraints.

Costs and Limitations

Selecting cases with statistical matching also entails costs and has limitations, but I argue that most of these are actually benefits in disguise. The first obvious cost is the need to acquire matching software and learn how to use it. This is easily mitigated: I provide software for each of the routines discussed in this article, along with annotated code to recreate all of the illustrations mentioned previously.

A second cost is that the data for matching must be entered into a machine-readable format. This is easy for researchers using preexisting data sets, but it can be taxing for scholars who are relying on their own personal knowledge of cases to enter all of that knowledge into a spreadsheet. The benefit of this effort is that by transferring the data from one's head to a spreadsheet, the criteria for case selection are explicit rather than implicit, aiding both the researcher and subsequent readers evaluating the research design.

Perhaps the most severe limitation is missing data. In many instances, case study researchers are undertaking small-*n* analysis precisely because they lack the large, cross-case data sets that seem ideal for case selection via matching. Often, key pieces of information are missing for some of the cases that otherwise would be eligible for selection. Statistical matching methods cannot calculate the similarity of cases with missing data, meaning that only cases with no missing data on the matching variables can be considered.

I have suggested solutions to this problem in Statistical Matching for Case Selection section. Here, I will argue that this “problem” is a feature rather than a bug. One benefit of using matching is that it reveals the limits of what the researcher knows about the world and avoids the false pretense of a most similar case design when such a design is impossible. By definition, paired cases cannot be most similar unless other cases were also considered that were less similar. Only cases without missing data can be fully compared, meaning that only units with no missing data are eligible for selection regardless of how the researcher actually chooses the cases. Matching makes this eligibility criterion transparent but the problem lurks even if matching is not used.

Some researchers who have incomplete data nevertheless argue that their cases are “similar enough” to rule out confounding from one or more factors. By stating that cases are “similar enough,” researchers are appealing to auxiliary information about the strength of the confounding that might be induced by the control variables. If two cases are not identical, but still seem “close enough,” this indicates that the researcher’s priors tell them that minor differences in a potential confounder are not worrisome. Although common in practice, this approach differs substantially from the formal logic of most similar case design. Using matching for case selection makes it clear when this shift in the logic of inquiry occurs.

Case selection via matching can also be criticized from the opposite direction: When enough data are available to select cases from a relatively large pool, perhaps regression analysis should be preferred over qualitative case studies. This critique ignores the goals of case study researchers, most of whom are trying to trace causal mechanisms. This focus on mechanisms is almost entirely lost in a regression analysis of the pool of eligible cases. In fact, the advice to “just run a regression” lays bare some of the trade-offs for researchers choosing between process tracing and regression. Process tracing of mechanisms offers substantial information about individual cases but is too costly to carry out for more than a few cases. In contrast, a large-*n* regression is easy to implement but provides dubious causal inferences in most observational settings and gives little insight into mechanisms. The choice to select cases and process trace reveals the researcher’s belief that tracing mechanisms will ultimately lend more support for a theory than correlating inputs with outcomes.

Conclusion

Statistical matching methods have much to offer qualitative researchers facing the task of most similar case selection. Several existing matching methods are formalized versions of the case selection rules already used by many

qualitative researchers, but case selection via matching does not require adoption of a “statistical worldview.” Statistical matching methods offer substantial improvements over traditional practices of case selection: They ensure that most similar cases are in fact most similar, they make scope conditions, assumptions, and measurement explicit, and they make case selection transparent and replicable. The costs of using matching to select cases are modest and surmountable. I provide freely available software that makes the matching methods in this article accessible to researchers, along with code to walk readers through each of the examples mentioned previously. Matching requires researchers to enter data about their cases into a computer-readable form, but this promotes transparency and makes the resulting scholarship more credible. Case study analysts would do well to consider matching when selecting most similar cases.

Author’s Note

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Notes

1. The primary advocates for random sampling are Fearon and Laitin (2008) who randomly sample 25 cases for qualitative analysis of the causes of civil wars. Random sampling is more problematic with fewer cases.
2. Others suggest additional the criteria of data availability, “large within-case variance in values on the independent, dependent, or condition variables,” and “intrinsic importance” (Van Evera 1997:77).

3. An interesting twist on most similar and most different research designs are case selection strategies that use most different cases with the same outcome (MDSO) and most similar cases with a different outcome (MSDO; Berg-Schlusser and De Meur 2009; De Meur and Berg-Schlusser 1996). These authors have a rather different matching method for pairing cases, using a Boolean distance metric after discretizing the variables of interest. Matching could also be modified to fit this situation and would allow the user to use continuous covariates without discretizing them.
4. See also Collier (1993) and Meckstroth (1975).
5. A search in Google Scholar for “most similar systems” returned 2,260 search results. The same search on JSTOR returns 149 results, mostly in Political Science, Sociology, and International Relations (as of January 24, 2014).
6. In practice, credible natural experiments can be hard to find (Dunning 2012; Sekhon and Titiunik 2012).
7. We can be much more confident about the conclusions of most similar case analysis when testing deterministic theories (Dion 1998).
8. For discussion and contrasting views, see Woodward (2007), Bogen (2004), and Salmon (1994).
9. See Fearon (1991) for a methodological statement on the links between counterfactuals with and without case comparisons.
10. I refer to “matched pairs,” but statistical matching can also incorporate varying treatment-control ratios.
11. Squared Mahalanobis distance is defined for two $p \times 1$ vectors x and y as $D^2 = (x - y)' \Sigma^{-1} (x - y)$ where Σ is the covariance matrix of the $p \times p$ distribution.
12. The matched sample is produced by using the $k \times k$ diagonal weight matrix W in a generalization of the mahalanobis distance formula $D^{2*} = (x - y)' (\Sigma^{-1/2})' W \Sigma^{-1/2} (x - y)$ to match observations where $\Sigma^{-1/2}$ is a Cholesky decomposition such that $\Sigma^{-1/2} (\Sigma^{-1/2})' = \Sigma$. The default loss function is to minimize the largest p value from paired t -tests and Kolmogorov–Smirnov tests for all matching variables.
13. Matching software is available at <http://cran.r-project.org/web/packages/case-Match/index.html>.
14. This is the small- n equivalent of fixed effects regression.
15. The Neyman–Rubin causal model requires the stable unit treatment value assumption which is that the potential outcomes of each unit are independent of the treatment assignment of the other units. Both qualitative and quantitative researchers must account for learning and interactions between units to make credible inference.
16. ICAA stands for the “Costa Rican Institute of Water and Sewerage,” a government institution that oversees provision of drinking water.

17. The two governance structures are CAAR—Comités de Acueductos y Alcantarillados Rurales, and ASADAS—Asociaciones Administradoras de Sistemas de Acueductos y Alcantarillados Sanitarios
18. The Czech Republic and Slovakia are excluded because they were unified during this time period.
19. Switzerland is the seventh best match for Denmark, after Norway, Australia, Iceland, San Marino, New Zealand, and Liechtenstein. Switzerland matches poorly because it has a combination of trade and gross domestic product (GDP) per capita that is relatively far from others in the data.
20. Mahalanobis distance does not have interpretable units, so it cannot be used as an absolute measure of match quality, but when calculated over the same variables in a single data set, higher distances indicate worse matches.
21. I implement weights following the approach of Greevy et al. (2012).
22. Lieberman's study is an example of both most similar case selection (Lieberman 2003:8) and "nested analysis" (Lieberman 2005, 2003:32-34), suggesting that these designs are not mutually exclusive.
23. I change the analysis slightly by extending the data to 1990 and not correcting for purchasing power parity. Starting with 1950 is comparable to Lieberman's analysis because he extrapolated all of the data prior to 1950. Data are from Gleditsch (2004).
24. Euclidean distance is a special case of Mahalanobis distance where the covariance matrix is substituted with an identity matrix of the same dimensions. My software implements both Euclidean and Mahalanobis distance matching.
25. The nine better matches are Mexico, Costa Rica, Cuba, Yugoslavia/Serbia, Panama, Czechoslovakia, Romania, and Chile.
26. Data on the approximate number of English speakers by country are from http://en.wikipedia.org/wiki/List_of_countries_by_English-speaking_population (available on request).
27. Data on the approximate number of French speakers by country are from http://en.wikipedia.org/wiki/List_of_countries_where_French_is_an_official_language (available on request).

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