

Using Sequences to Model Crises*

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Summary

The logic of historical explanation obliges one to understand temporality as a moderator of various effects on political outcomes. Temporal problems remain in the empirical analysis of political phenomena, however, especially as it pertains to categorical data and long-term time-dependence. Many theories in political science assert that sequencing matters or that political outcomes are path-dependent, but they remain untested (or improperly tested) assertions for which sequence analysis may be valuable. We briefly review the disciplinary origins of sequence analysis. We then apply the method to understand bargaining between actors during national crises. Finally, we explore the robustness of a commonly used sequence analysis metric. The ability to demonstrate and to separate sequential effects from accumulative effects—made possible through sequence analysis—constitutes a major step in political science towards analyses that are truly time-sensitive.

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1 Introduction

The logic of historical explanation obliges one to understand temporality as a moderator of various effects on political outcomes. Temporal problems remain in the empirical analysis of political phenomena, however, especially as it pertains to categorical data and long-term time-dependence. Many theories in political science assert that sequencing matters or that political outcomes are path-dependent, but they remain untested (or improperly tested) assertions for which sequence analysis may be valuable. We briefly review the disciplinary origins of sequence analysis. We then apply the method to understand bargaining between actors during national crises. Finally, we explore the robustness of a commonly used sequence analysis metric. The ability to demonstrate and to separate sequential effects from accumulative effects—made possible through sequence analysis—constitutes a major step in political science towards analyses that are truly time-sensitive.

2 Analyzing Sequences: concepts and conceptualization

There is a long and rich tradition of using historical processes to explain political outcomes (Thelen 1999; 2000). Pierson (2004) reminds us that politics occur in time, and it is an undercurrent of classic literature in political science (Dahl 1971, Moore 1966, North 1981). Beyond simply acknowledging the importance of time, scholars have argued for the differentiation of duration, tempo, acceleration, and timing (Abbott 1992; 2001, Grzymala-Busse 2011, Mahoney 2000, Pierson 2000; 2004, Page 2006, Slater and Simmons 2010). The unresolved debate over what affects the timing of democratization (Mansfield and Snyder 2007) represents a broader concern among scholars regarding how political processes are moderated by time. The challenges that this presents are two-fold: the first is to identify different temporal processes qualitatively; the second is to involve them in empirical treatments. As Grzymala-Busse (2011) notes, it is important to distinguish

temporal processes from causal mechanisms, as some causes may operate under specific temporal conditions. A process is outcome-dependent if the outcome in a period depends on past outcomes or upon the time period. If the long-run distribution of past outcomes matter, the process is said to exhibit path dependence (Page 2006). To this end, the notion of path dependence has been revived to address empirical problems related to ‘informative regress’ and increasing returns in political processes (Freeman 2010, Jackson and Kollman 2012, Lin and Cohen 2010, Page 2006, Slater and Simmons 2010, Walker 2010, Kreuzer 2013).

Existing approaches to handling time-dependence include the use of multivariate statistical methods involving successive time points, factor analysis, and cluster analysis. Yet, each of these methods has the weakness that each time-point is treated independently from others. Longitudinal methods are more capable of handling different forms of time-dependence. In event history analysis, ‘time’ refers to the length of time before a transition from one state to another. This treatment accounts for duration with precision, but it neglects transitions between multiple categories. Time-series methods takes time seriously insofar as what happens in one instant can be conditioned by prior moments. Autoregressive, integrated, and moving average models also account for prior states and average effects. Such models are more appropriate for accounting the evolution and correlation of strictly continuous variables on frequent time points, but many social science data are categorical and contingent. Some of the most advanced models for time-dependent categorical data include Hidden Markov Models and higher-order Markov models. However, Hidden Markov methods do not allow one to ascertain similarities between sequences and to handle easily a large number of varied sequences. As such, temporal problems remain in the empirical analysis of political phenomena, especially at the nexus of categorical data and time-dependence.¹

Sequence analysis—which is more commonly found in sociology—is a method to process sequence data, with sequences being defined as a series of states or events. It includes tools to code and format sequences, to compare them by pairs, to cluster and represent groups of similar order, to calculate specific statistics for sequences and groups of sequences, and to

extract prototypical sequences. Sequences can be composed of a number of different units of time (e.g., hours, days, weeks, months, years), whether they refer to states or events. States denote properties or status of the unit of observation (e.g. Republican, military dictatorship), while events denote a change between states (e.g. holds elections, coup d'etat) (Blanchard 2011; 2013). Sequences made of events ignore duration and focus on the order of punctual experiences, while sequences made of states deal with both duration and order. For logical reasons, statistical sequences cannot mix states and events (Blanchard 2011; 2013). These receive slightly different treatments, though they are essentially equivalent from a statistical perspective. The full set of elements from which the steps in a sequence can be chosen is referred to as the alphabet (Blanchard 2011, Gabadinho et al. 2011). A sequence, then, is a succession of elements chosen from an alphabet, where succession denotes order.

Sequence analysis—herein denoted as SqA—refers to the systematic study of a population of sequences. The approach was used originally in computer science to detect dissimilarities between long strings of codes. Sociologists and demographers have used this approach to consider such topics as job careers and life trajectories (Brzinsky-Fay and Kohler 2010), critical transitions from education to work to retirement (Abbott 1995), policy diffusion (Abbott and DeViney 1992), patterns of violence (Stovel 2001), elite careers (Lemercier 2005), legislative processes (Borghetto forthcoming), and activism (Fillieule and Blanchard 2011).² Though sequence analysis is very much alive in other social sciences, it is only beginning to be used in political science.³ Most notably, SqA has been evoked in a recent symposium in political science on how historical time is conceived (Blanchard 2013, Kreuzer 2013).

The application of SqA seems conceptually promising for explaining political phenomena at various levels of analysis. At the individual level, one might consider trajectories that involve electoral decision making, party positions, social status, political involvement, and public opinion. It can also be a useful tool for analyzing the particular words, sentences, and paragraphs invoked in political discourse. At the organizational level, one may focus on the development of parties, trade unions, activist groups, and rebels. At the

macrolevel, SqA can help explain the development of political regimes and how timing affects the transition to or from democracy. SqA can even supersede nations to explain patterns of international activity, such as the diffusion of norms, conflict behavior, and large-scale geopolitical sequences.⁴ As noted by Blanchard (2011), some of the primary objectives of sequence analysis are to describe and represent, compare and classify, identify dominant patterns, and explain and model sequences.⁵ We briefly address each of these broad objectives below.

Treating as a sequence a string of related elements that are associated with a common unit allows one to visualize and consider how the elements are related. A standard way to visualize sequences is with a sequence index plot, in which sequences are stacked and temporally aligned (usually horizontally). A sequence density plot is similar to a sequence index plot. Rather than showing the sample of sequences, however, it sorts the elements that make up the alphabet by frequency at each successive position. An example of a sequence index plot and sequence density plot are shown in our application, below. In addition, sequence frequency plots can be used to display the most frequent sequences, each one with a bar of its successive states, in order of their frequencies. An example of a sequence frequency plot is available in the online appendix (B).

The core of Sequence Analysis lies in the algorithm used for distance comparison—that is, the metric by which sequences are quantifiably compared. A critical question at the heart of dissimilarity calculation is which element of time should be preserved and how weights should be applied. There are several common metrics by which to compute sequence similarity. Some examples include Longest Common Prefix (LCP), Longest Common Subsequence (LCS), and Optimal Matching (OM) (Gabadinho et al. 2011).⁶ Optimal Matching is the most commonly used metric for sequence comparison (Elzinga 2008).⁷ By matching, it generates edit distances that are the minimal cost, in terms of insertions, deletions and substitutions, for transforming one sequence into another. The optimal matching algorithm compares two sequences state-by-state and determines the set of

operations that would align them at the lowest cost, producing an $n \times n$ matrix of dissimilarity, or distance between them. Once the dissimilarity algorithm and cost scheme are decided, there are a variety of ways in which one can analyze sequences through the use of the resulting dissimilarity matrix. One method is to use cluster analysis to sort sequences into like groups, thereby enabling visual comparison.⁸

Sequence analysis also has the capacity to search for sequences that share common subsequences. Subsequences refer to non-unit sections of sequences (i.e., successions of two or more states or events inside longer successions). The more common subsequences two sequences share, and the longer these common subsequences are, the more similar the two sequences are. To search for patterns within a sample of sequences—read as subsequences—the LCS and LCP algorithms are useful tools. In addition, one can cluster sequences on the basis of optimal matching and generate and rank the frequency of subsequences in a sample.

Finally, as a modeling technique, sequence groups created through hierarchical clustering can be included in cross-tabulations and logistic regression models.⁹ Given a theory about order, one can also use a distance calculation to compute similarity to a theoretically important sequence, whether it is an example (case-study) or an ideal-sequence (hypothetical). By taking the distance values computed for each sequence in a sample, one has a continuous predictor of outcome that rests on the principles of order (Grzymala-Busse 2011). Such an approach provides a direct test of whether, and to what extent, sequential theories about politics hold true.

By incorporating aspects of Sequence Analysis into quantitative models, one can more easily quantify and test arguments about sequencing. Proponents of ‘democratic sequencing,’ for example, assert that if reforms occur in the wrong order, then democratization can result in sub-optimal outcomes such as empowering illiberal leaders, engendering violent nationalism, and instigating civil conflict and interstate wars. To the extent that the order of democratization matters, the probability of successful governance differs (Carothers 2007a, Carothers 2007b, Mansfield and Snyder 2007, Fukuyama 2011, Hobson 2012). The ability

to quantitatively test such arguments—which are in part derived from extant arguments in qualitative comparative politics—would substantially advance the understanding of how politics as a process affects development.

3 Application: crisis bargaining patterns

As a demonstration we consider the effect of actors’ behavior in national crises. Our aim is to see whether different patterns of cooperation or conflict are associated with specific factors that pertain to a crisis. Do patterns of bargaining reinforce or undermine democracy, in that actors in different types of countries bargain in different ways? We focus on actors’ behavior during national crises because crises entail a “sequence of interaction” between actors (Snyder and Diesing 1977) in “a noisy, dangerous, and unavoidable learning process” (Fearon 1992).

Our investigation entails assessing actors’ behavior across forty-seven crises in twelve countries. We selected twelve cases to represent different levels of democracy, transitions, and predictability (Casper and Tufis 2003). First, we used the Polity IV scale to divide countries into democracies, autocracies, and anocracies (countries that fell between these two regime types), with six as the threshold value (Marshall and Jaggers 2003).¹⁰ We then coded each country as stable, transitioned, or unstable over time, based on whether it remained in its respective category, moved uni-directionally to another category, or experienced more than one transition over the period 1951-1992.¹¹ The above decision rules led to five categories: stable democracies, cases that switched to democracy, countries that were unstable, cases that switched to autocracy, and stable autocracies. Finally, we selected predictable and unpredictable cases based on the residuals from a naïve model of democracy (i.e. the difference between a case’s actual and predicted levels of democracy) (Casper and Tufis 2003). A country-year was considered “predictable” by the democracy model if its value fell within one standard deviation of the mean of the residuals.¹² As a result, the cases that were selected

represent different countries with different levels of democracy and transition histories, and cases that would be considered unpredictable and predictable according to a naive model of democracy (Casper and Tufis 2003).

Once we selected the twelve cases, we identified crises that occurred or were occurring within the case during the years 1950-1999. Our definition of a crisis follows Banks (1999) and can be of four types: riots, anti-government demonstrations, revolutions, and guerilla warfare (see Appendix A online). By definition, crises occur between the effective government and an opposition, which can have formerly been part of the government. Our decision to code moves as occurring between two actors draws on the unitary actor assumption, which treats one or more people or groups as a unified actor. Our use of the term ‘actor’ refers to one or more people or groups who are united by explicitly stated shared goals. According to our framework, each crisis contains an actor representing the government, and a relevant opposition. Where this criterion is not met, we code it as a different crisis. Our investigation of the twelve countries resulted in 47 crises over the period 1950-1999.

Using Keesing’s World News Archives, we detailed the reported events in Keesing’s from the time the crisis began until the date that it ended, or from the start to the end of our window of observation. For each of the 47 crises in our twelve countries, we coded the actions—to which we refer as the ‘moves’—of each actor using the Intranational Political Interactions Conflict Scale (Davis, Leeds and Moore 1998) (Appendix A online). The scale ranges roughly from 1000 to -1000 and differentiates the types of actions that can be taken by an actor, ranking them according to cooperativeness (0 to 1000) and “conflictualness” (0 to -1000).¹³ Out of a series of political events we denoted the most significant action—or verb—taken by each actor and assigned to it the corresponding number on the conflict scale. We began each series with the move of the actor acting on the part of the government, denoted by M_t . M stands for the actor’s move and t represents the point in time of the move. We then coded the response of the opposing actor, denoted by M_{t+1} . We continued to code the most significant response by each actor in the protracted series, thereby constructing a

series of alternating moves between the two primary actors. The time reference by which we constructed the crisis sequences is internal as opposed to external (pertaining to how a sequence unfolds rather than calendar time). We are less interested in the duration of crises or the duration of spells in a crisis, but rather the order in which the spells in a crises occurred. Nevertheless, duration (sequences based on calendar time) can be accommodated by SqA.

Figure 1 shows a sequence index plot of the crisis sequences, whereas figure 2 shows the sequence density plot of the same information. Each line represents a crisis in one of our twelve cases and is labeled with the name of the case and the crisis (e.g., *country_crisis name*). There are 47 crises in our dataset which vary in length between 4 and 38 moves. The average length of a crisis in our sample is eight states long. The most frequent state in our data is that of less to moderately negative events (IPI -100 through -500). This is true of both the mean and the modal state across sequences. The mean number of moderately negative moves in a sequence is six; the next highest occurrence is highly negative events, with a mean of four moves per series. Based on sequence averages, a randomly drawn series should be predominantly composed of moderately and highly conflictual moves. Neutrality is highest at the beginning and end of sequences, and the likelihood of cooperative moves generally increases with sequence length. As indicated by the frequency plot, virtually no two sequences are perfectly alike—the ten most common sequences represent, in effect, ten of our series. Appendix B (online) provides additional descriptive figures on the crisis sequences.

[Figure 1 about here]

[Figure 2 about here]

We used the Optimal Matching algorithm to calculate sequence similarity. The substitution costs that we chose reflect the distance between states (e.g., comparing 200 to -200 yields a cost of 400). We also set the insertion-deletion cost arbitrarily high to ensure that all comparisons incurred substitution costs. To better understand how to distinguish crisis bargaining patterns, we clustered our sample into six groups using the Ward (1963) hierarchical clustering algorithm. Our choice of six clusters was determined by rounding to

the largest integer less than or equal to the square root of our sample size ($\sqrt{47} \approx 6.85$).¹⁴

Given the considerable variation in the lengths of the crises, we calculated sequence similarity based on the first four moves of each crisis. Restricting our comparison to the first four moves of each crisis accommodates the shortest crisis in our sample, such that crisis length has no effect on how the sequences are clustered.¹⁵ The results shown here therefore focus on potential relationships between how crises begin (initial reciprocation) and features of the crisis. The clusters created based on the comparing the first four moves of each crisis can be seen in figure 3.

[Figure 3 about here]

After clustering the crises based on how they began, we sought to determine whether any factors are significantly associated with the clusters into which they had been sorted. In accordance with our theory, we test the following covariates: prior cooperation, shared interests, crisis origin, and cohesiveness (Casper and Wilson 2012). If there was no prior crisis in our sample or the last crisis did not end on a cooperative note, we denoted the absence of *prior cooperation* with 0, and 1 if there was prior cooperation. Similarly, we coded *shared interests* as a dummy variable indicating whether or not the government and opposition had shared interests (i.e., wanted a similar outcome or had a similar goal). For example, during the Clean Hands investigation in Italy, both the government and opposition had a vested interest in maintaining normal government functions, unlike those involved in the Northern League crisis. *Endogenous crises* were coded as 1 if the problem over which the actors were bargaining originated within the country. Myanmar_Oil Crisis, for example, was created by fluctuations in the worldwide price of oil. Similarly, the crisis Italy_Labor Unrest originated with the end of the Bretton Woods system and increasing oil prices. Lastly, we coded the variable *cohesiveness* by denoting, at each move, whether any of the two ‘actors’ encountered significant in-group opposition. An example of a lack of cohesiveness can be found in Italy_Northern League, when Umberto Bossi radicalized his discourse and withdrew from the coalition government, thus polarizing the League and losing support.

We were also interested in identifying whether the beginning of a crisis was affected by the issue over which the crisis began. Based on our *a priori* knowledge about each crisis, given by its unique name, we identified the general “theme” of each. We denoted each crisis by one of the following subject labels: coups; civil war; economic crisis; elections; government-specific; leader-specific; labor; protests; purges; rebels; separatists; and transition. Lastly, we also examined whether clusters were significantly related to crisis length. By virtue of our specification (comparing the first four moves of each crisis), crisis length should not have impacted clustering. To the extent that they are related it therefore suggests that how the crises began affected how long they lasted.

Crámer’s V is used when the number of possible values for two categorical variables is unequal, yielding a different number of rows and columns in the data matrix. Thus, this correlation measure is appropriate for measuring the association between cluster number and each of our dummy variables (Cramér 1946). Like other measures of correlational association, Crámer’s V ranges from 0 (no relationship) to 1 (perfect relationship). The p-value associated with the Crámer’s V statistic indicates the probability that the cell counts are due to chance. For each of the seven covariates, the p-value associated with the Crámer V statistic is below 0.01, indicating that none of the associations are random.

Figure 4 shows a plot of the Crámer’s V statistic associated with each variable and the clusters. According to Crewson (2012), a Crámer’s V statistic greater than 0.5 characterizes a high level of association between two variables. The results suggest that previous cooperation is not strongly related to the manner in which crises were clustered, nor are endogenous crises differently grouped. Shared interest is strongly associated with how crises were clustered however, which suggests that the order in which a crisis is initiated is affected by the correspondence of actors’ goals. Actor cohesiveness, both government and opposition, also seems to affect how a crisis begins.

[Figure 4 about here]

Interestingly, the general theme of a crisis is also strongly associated with cluster

number. This may suggest that how a crisis begins is also affected by the nature of the crisis (*what is the crisis about?*). Nevertheless, the level of association between cluster and subject is similar to that of shared interests. It may reflect the fact that some issues are inherently zero-sum, such as bargaining over secession. Most notably, the clusters are strongly associated with crisis length. Though we intentionally prevented crisis length from affecting how crises were clustered, there is still a strong association. This suggests, therefore, that how crises begin affect their duration.

Our investigation of actors' behavior across forty-seven crises in twelve countries focused on the "sequence of interaction" between actors (Snyder and Diesing 1977). Using sequence analysis, we demonstrated that our sample of crises divide into unique subgroups with common bargaining patterns and features. The clusters, which we discerned based on pattern commonalities, are significantly associated with shared interests, crisis origin, and actor cohesiveness. Bargaining patterns are thus affected by known factors in a crisis which reinforce or undermine democracy. While just a beginning into a larger empirical agenda, our results bode well for explaining a nuanced dimension of bargaining—namely, order of action—and for developing a new approach to studying political sequencing.

To add to this agenda, scholars must carefully consider the assumptions and decisions that are necessary to compare qualitative sequences quantitatively. Doing so will serve to better explain how patterns of bargaining reinforce or undermined democracy and will more broadly yield exciting new insights into complex political processes. Further extensions of this work explores bargaining sequences through Comparative Historical Analysis. As an example, however, it illustrates the promise of SqA applications in political science to questions of order and sequence.

4 Robustness

Though optimal matching is just one of several types of sequence analysis algorithms (methods for comparing pairs of sequences), almost all applications of sequence analysis in the social sciences have used the OM algorithm (Abbott and Tsay 2000, Hollister 2009). Little is known about the robustness of OM classification, however, which limits its usability beyond description (Hollister 2009). A number of studies have added confidence to the validity and reliability of the OM algorithm. Abbott’s and Tsay’s (2000) review of social science research utilizing OM alignment in sequence analysis evaluates nearly all articles, conference papers, and dissertations using the method at the time. They discuss issues related to OM alignment and how various authors have dealt with them. They conclude that OM is a legitimate classification method that is not based on a probability model of sequence generation, and that it produces reliable and valid results. Previously, Forrest and Abbott (1990) had tested the impact of intercoder reliability on OM results. The authors had five coders independently code sequence data that they had analyzed in previous work (Forrest and Abbott 1986). The authors found that coding decisions and the level of detail varied by coder. Analyzing the variation by applying OM and using data-reduction techniques, however, they found that the aggregated results based on each dataset resembled each other. Their robustness test also suggested the reliability and validity of OM for divergent datasets. In addition, Halpin (2010) addresses the critique that the OM algorithm is inadequate for analyzing “episodic” data (data for which the length of time spent in each state also matters). Modifying the algorithm to make it sensitive to spell length, the author demonstrates that standard usage of OM is reasonably robust to continuous-time sequences.

Existing studies that take the robustness of OM into account have demonstrated the ability of OM to accommodate both continuous and discrete-time data, and that it is relatively unaffected by intercoder reliability. Our introduction and application of sequence analysis also aims to contribute to robustness tests of the algorithm. Beyond encouraging its use and adaptation to suit the needs of political science research, we also want to establish

some of the current limits of the application. In an attempt to shed light on the limitations of SqA through the use of OM for political science research, we present the results of a simulation exercise in which we subjected the OM algorithm to a series of robustness tests. Primarily, we examine the extent to which OM is affected by error, which is a common concern for social scientists (Adcock and Collier 2001). We demonstrate that the statistical logic undergirding simple matching algorithms is sufficient to handle a number of problems that affect social science data. The value added of such tests is that it establishes confidence in the ability of OM to identify dominant patterns in incomplete or erroneous data, which surpasses that of human coders. Though we recommend a healthy skepticism towards its adoption into political science research, our tests confirm the validity and reliability of OM as a tool for analyzing sequences. We also comment on the sensitivity of OM to sample size, subsequences, and disproportionate sequences.

To set up the simulation exercise, we constructed known parameters of a latent concept by performing 1000 random draws from a normal distribution and then associated them with three discrete categories (see Appendix C online). We associated each category with a particular sequence that was 20 moves long, constructed based on five possible states (an alphabet of five). In each robustness test we affected the sample with some form of error and then applied OM and clustered the sequences into three groups. For the purpose of this exercise we chose to use an insertion-deletion cost of 1 and a substitution cost of 2. This is the most common decision rule among studies that use sequence analysis, and the choice to apply a cost of 2 to substitution reflects that substitution is similar to inserting (1) and deleting (1) a state.

If we had perfect information about the sequences, the OM algorithm would sort them into perfect predictors of y . That is to say, when we apply the OM algorithm and cluster the sequences into three clusters, cluster assignment perfectly sorts out the sequences into three homogenous groups. As social scientists, however, we know that there is likely error in our data. Sources of error in social science data include measurement error, systematic

biases, inter-coder unreliability, and random error (noise). As such, in our robustness check of the OM algorithm we consider some of the major sources of error that can arise in analyzing political science data.

In the first test, we introduced systematic error. This was accomplished by randomly selecting a cross-section (column) of data and randomizing everything in that column. This would be akin to having a time-period of data in which a global shock affected all reported values (e.g., war, natural disasters). We incrementally increased the amount of systematic error in the data from 1 to 20 columns, the total number of moves. We found that the OM algorithm is capable of nearly perfectly classifying sequences where up to half of the data have been affected by systematic error, as shown in figure 5 (see also Appendix C online). Beyond this amount of systematic error, the OM algorithm begins to falter. The OM algorithm is thus capable of handling a large amount of error where there are missing or incomplete moves affecting the entire sample of sequences.

[Figure 5 about here]

Secondly, we allowed the lengths of the sequences to differ. For each observation (row of time-series data), we selected a number of states between 1 and 18 to randomly delete from sequences in our simulated dataset, thereby creating samples with sequences of different lengths. A related example of this issue would be having data on subjects with different rates of survival/mortality (i.e., presidents, regimes). The OM algorithm can handle differences in lengths up to about 65 percent of the original length before it begins to classify them differently. Put another way, for a sample of data which is a maximum of 20 moves long and composed of five different states, the OM can fairly easily compare them with sequences that are 7 moves long (a difference of 13). Thirdly, we changed the dimensions of the data to create four datasets that differ by the number and length of the sequences. The different dimensions of the datasets (expressed as rows by columns) that we created were 10 x 100, 100 x 100, 1000 x 10, and 1000 x 100, respectively. Out of necessity, we affected half of each dataset with systematic error. When we applied the OM algorithm, we discovered that this

method was particularly sensitive to the overall length of sequences as opposed to the number of sequences. Thus, the OM algorithm works best for longer sequences and is not affected by the number of sequences. As expected, the method is best suited for time-series over cross-sectional applications.

Fourthly, we introduced random error. This problem is commonly expected where there is “noise” in the data, most likely due to missingness. As this issue is perhaps the biggest concern to social scientists, we randomly selected from 1 to 20,000 observations (the number of simulated observations) and replaced them with a random selection. In figure 6, half of the dataset has been randomized. The OM algorithm perfectly handles up to 12 percent random error before it begins to misclassify the sequences with some probability. One can think of this variability as forming confidence intervals over the range of random error, although the algorithm seems fairly robust to a large proportion of random errors. Figure 7 shows how well the OM algorithm classifies sequences that are twenty states long, with increasing random error. In the above example—where half of the data were randomized—the OM algorithm correctly classified about 70 percent of the sequences.

[Figure 6 about here]

[Figure 7 about here]

Finally, we repeatedly substituted within our sample a subsequence that was five states long to discern whether the OM algorithm would be misled by alternative patterns in the data. Surprisingly, the introduction of this new subsequence to a dataset which had longer common subsequences had no effect on classification. This suggests that pattern-matching algorithms prioritize dominant patterns at the expense of sub-sequences that might be attractive to human coders. Thus, researchers interested in identifying “tempo” should be aware of how they look for sub-sequences in the data (Blanchard 2013).

Based on our robustness tests of the OM algorithm, we determined that it can handle a great deal of systematic error, differences in length, random error, and even “misleading” sub-patterns in the data. Nevertheless, the algorithm is clearly not without flaws—what is

more, its ability to compare sequences is diminished in the presence of more than one of these problems. These are issues that must be considered when using the metric to represent sequence similarities. Scholars who are interested in pursuing the use of sequence analysis in political science—primarily through the use of the OM algorithm—can be fairly confident about the systematic and random error in their data and secondary subsequences, and more wary of sequence length and the differences in length between sequences.

As it regards the use of clustering algorithms as a complement to sequence analysis, we assert that sequence clusters can be thought of as latent classes. The latent classes created by clustering are derived from the sequence from which ‘like’ groups emerge. To this end, clusters created on the basis of a distance metric such as OM can be used as the dependent variable—e.g., *what determines whether an observation develops into Y?*—or as the independent variable—*how do like sequences affect Y?* There is, of course, no standard method for discerning groups from the distances calculated by OM. There are a variety of ways in which clusters can be calculated. One approach would be to try various clustering methods and to select the method which has the biggest impact on model fit. It is also possible to calculate the similarity of each sequence with its assigned cluster and to treat the ‘worst-fitting’ sequences as outliers as another form of robustness check when using sequences or clusters in statistical models. The impact of clustering methods on predictive accuracy is nevertheless a separate topic—clustering is but one way to utilize the information produced by matching algorithms such as OM.

A superficial test of the robustness of the Optimal Matching algorithm for sequence analysis of flawed data shows surprisingly positive results. Fortunately, its use can be dramatically improved upon by considering (and attempting to mitigate) each of these issues in turn. Furthermore, selecting costs that are more theoretically motivated or which aim to mitigate data problems can make the analysis even more accurate. Abbott and Tsay (2000) highlight the need to test the effects of different cost schemes on OM classification.¹⁶ An option that is just beginning to be explored, and which can further the aims of enhancing

Optimal Matching, is how to apply weights to states about which one is more confident.¹⁷ Another issue that we did not explore here was the effect on OM of increasing the number of states that comprise the ‘alphabet’. That is, in considering the ability of OM to correctly identify dominant patterns, scholars should consider the relative impacts of the size of the alphabet. As a general rule, however, the more parsimonious the better. As is the case with all statistical models, one leverages nuance for generalizability.

In summary, our exercise undergirds our introduction of SqA by demonstrating that a common procedure for comparing sequences is fairly robust to a number of problems and that it is thus a promising statistical technique for political science research. Further development of the OM algorithm offers to take the study of sequences and dominant patterns in political science a greater distance. We encourage political scientists to approach the method with a healthy degree of skepticism, but also to note the logical simplicity and transparency of OM as a means of comparing and quantifying the sequential nature of political phenomena.

5 Conclusion

Our brief description of sequence analysis highlights the way in which it can be used in political science to bridge the gap between qualitative arguments about order and sequence and quantitative methods. Sequence analytic methods are compatible with both qualitative and quantitative approaches. As an approach, it is simple, flexible, and easy to interpret. It provides a simple yet sophisticated way to test sequencing, and also allows for a great deal of flexibility without a substantial loss in degrees of freedom. It also provides easy to interpret clusters. As we demonstrated in the robustness tests of Optimal Matching, however, the matching algorithms that are at the core of SqA can misclassify with some probability. This is a feature that can perhaps be better exploited in the future. All the same, using clusters derived from a distance metric is equivalent to adding dummy variables to account for the uniqueness of sequences. It is not necessarily more theoretically appealing, but sequence

analysis does provide some empirical credibility to such claims. With sequence analysis there is also some probability of obscuring “true” patterns in favor of dominant themes in discrete data. The OM algorithm is obviously sensitive to different forms of error, the extent to which we have begun to uncover. Nevertheless, sequence analysis and the distance metrics by which to do it are still in development and show surprisingly robust results.¹⁸

For the benefit of expanding political science research on sequences, future work ought to aim to compare the OM algorithm to different metrics such as the LCP and LCS, compare the impacts of different types of error together, and perhaps use this information to construct a measure of uncertainty (other than entropy) regarding the distance values that such metrics produce. As an empirical approach, however, sequence analysis constitutes a promising agenda for quantitatively evaluating time- and order-dependent information. More broadly, however, this approach encourages a renewed focus on the types of time-dependence and ways to model them in political science (Abbott 2001, Jackson and Kollman 2012, Pierson 2004, Page 2006, Grzymala-Busse 2011).

Notes

¹Ratkovic and Eng (2009) also offer a method based on sequential segmentation splines for identifying the location and the number of discontinuities in a series of observations. Their method nevertheless derives discrete ‘jumps’ from continuous data.

²See also Blanchard, Bühlmann and Gauthier (2014).

³A subset of the literature on crisis forecasting has used sequence analysis to explore patterns of international conflict (Schrodt and Gerner 2000, D’Orazio and Yonamine 2012).

⁴A promising area of research for which identifying dominant patterns is useful is in providing tests of the assertion that particular events or sequences constitute critical junctures that determine whether particular outcomes become ‘locked-in’ (Collier and Collier 1991)

⁵Refer also to Blanchard (2013)

⁶The LCP metric looks for the longest substring of states that two sequences have in common, starting from the beginning (hence, *prefix*). The LCS is similar to LCP; it searches for common subsequences, which are not necessarily constituted of adjacent symbols and need not begin the same way. For more information on these metrics, refer to Gabadinho et al. (2011).

⁷Though not without its criticisms, chief among them being the difficulty of interpreting the method, the OM algorithm is a forerunner among algorithms for calculating sequence similarity. It is also quite efficient, in that it uses the minimal number of operations to match two sequences (Elzinga 2008).

⁸It is important to note that clustering is analytically distinct from classification. Clustering—which is also a kind of ‘unsupervised learning’ in machine learning—is simply trying to figure out what clusters emerge from the data, while classification—which is supervised learning—uses sequences for predictive purposes.

⁹Given a set of N items to be clustered, and an $n \times n$ distance matrix, the basic process of hierarchical clustering is as follows: start by assigning each item to its own cluster, such that if you have N items, you have N clusters. Let the distances between clusters be a function of the distances between the items they contain. Find the closest pair of clusters and merge them into a single cluster, reducing the number of clusters by one. Recompute the distances between the remaining clusters and repeat.

¹⁰Governments for each country-year were coded as democratic if they scored 6 or higher on Polity’s democracy scale. Similarly, governments for each country-year were coded as autocracies if they scored 6 or higher on Polity’s autocracy scale. Finally, governments in country-years that scored lower than 6 on both the democracy and the autocracy scales were coded as middle-ranged cases.

¹¹For example, cases of redemocratization would fall in this category: both the Philippines and Brazil had been democratic, and then experienced authoritarian regimes, before returning to democracy.

¹²Since the democracy model predicted 66.5% of the country-years, we used this as the cut-off point between predicted and unpredicted cases. Thus, countries were coded as predicted cases if for more than 66.5% of their years the residuals were within one standard deviation of the mean. Similarly, countries were coded as unpredicted cases if for more than 66.5% of the years the residuals were more than one standard deviation of the mean (Casper 2002, Casper and Tufis 2003).

¹³Our use of the term “conflictualness” is borrowed from Stoll (2013).

¹⁴Taking the square root of a sample is a well-known rule-of-thumb for calculating the optimal number of bins in a histogram. Hypothetically, each bin would therefore contain a number of observations equal to the square root of the sample. The observation that the marginal impact of an additional cluster affects fewer than this number suggests that—just as an additional bin would be unnecessary—an additional cluster is unnecessary. Clustering the sequences into 7 clusters (as opposed to 6) affects only one sequence. See figure in Appendix B (online).

¹⁵It is important to note that we obtain similar results when we do not restrict our sequences to four moves. There are other ways of treating sequences of uneven lengths, which we did not address. For example, one way of dealing with discrepant sequence lengths include proportionalizing the states in each sequence to make them of equal lengths, as exemplified by Blanchard (2005). Moreover, one could adjust costs to discount operations for later states. Each approach has unique drawbacks as well as advantages.

¹⁶For issues related to cost selection, see Elzinga 2008.

¹⁷For an example of applying weights to enhance sequence comparison, see Halpin 2010.

¹⁸See Abbott and Tsay (2000) and Hollister (2009) for a review of SqA-appropriate matching algorithms.

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Tables and Figures

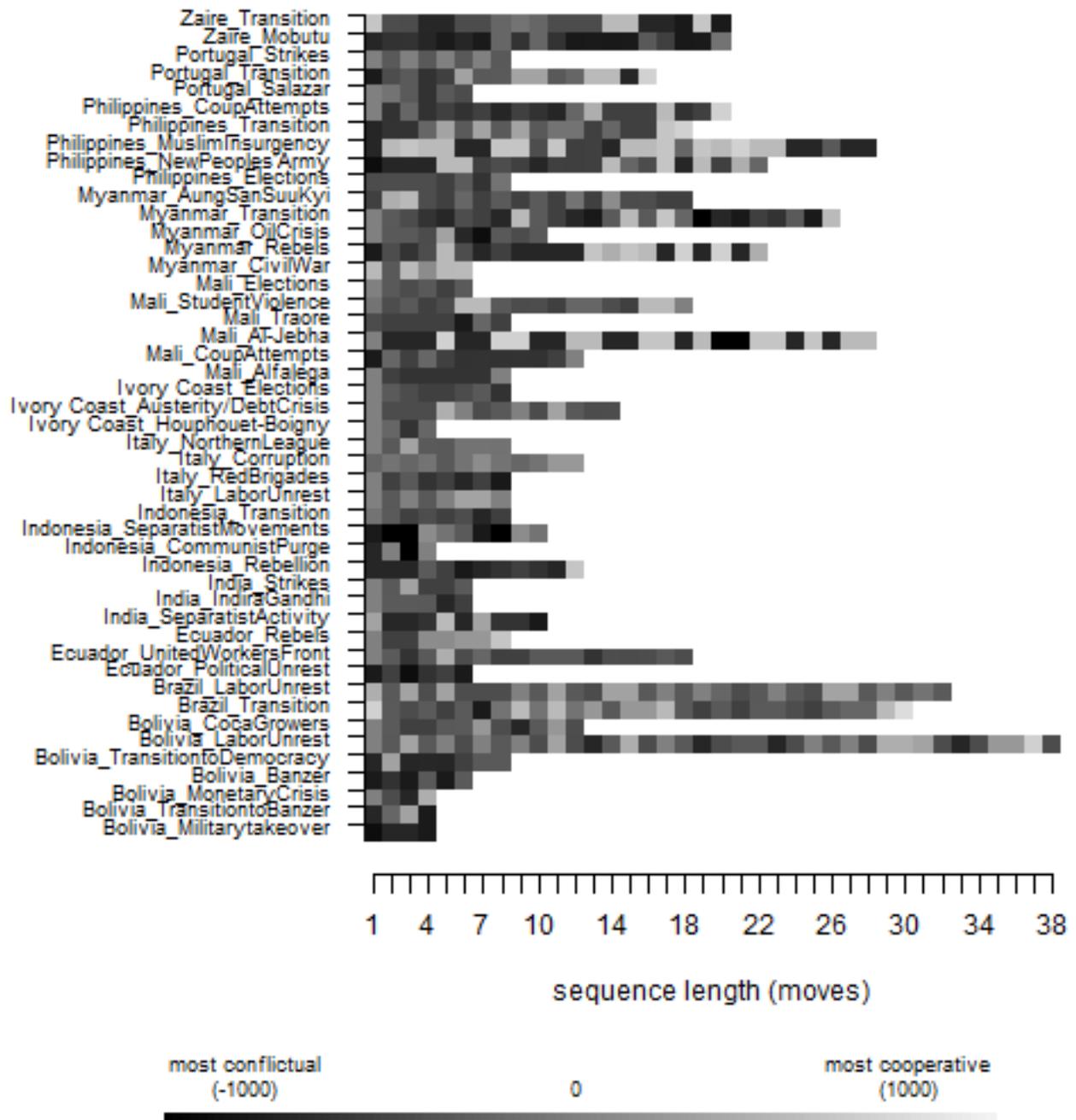


Figure 1: Sequence index plot

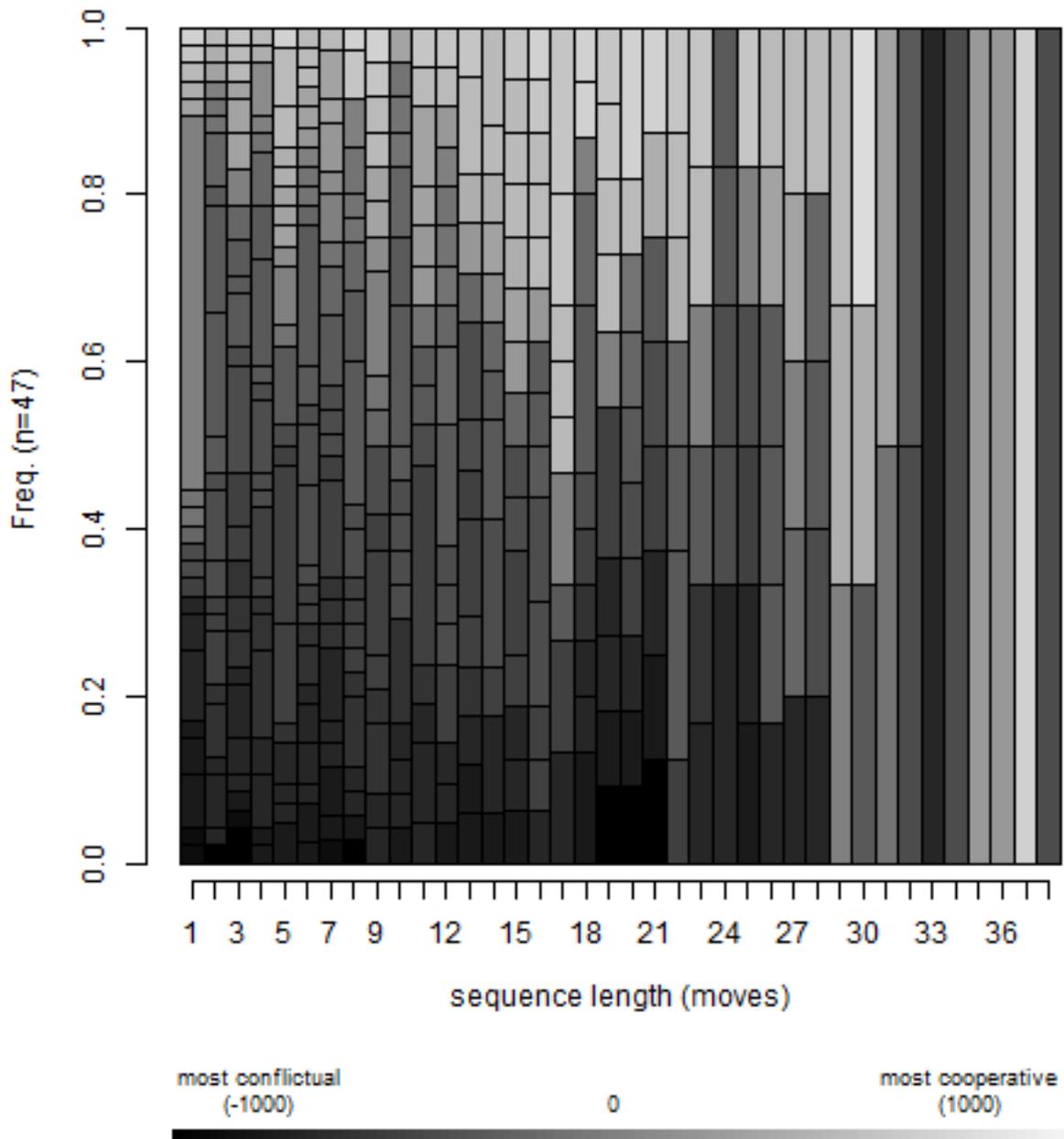


Figure 2: Sequence density plot

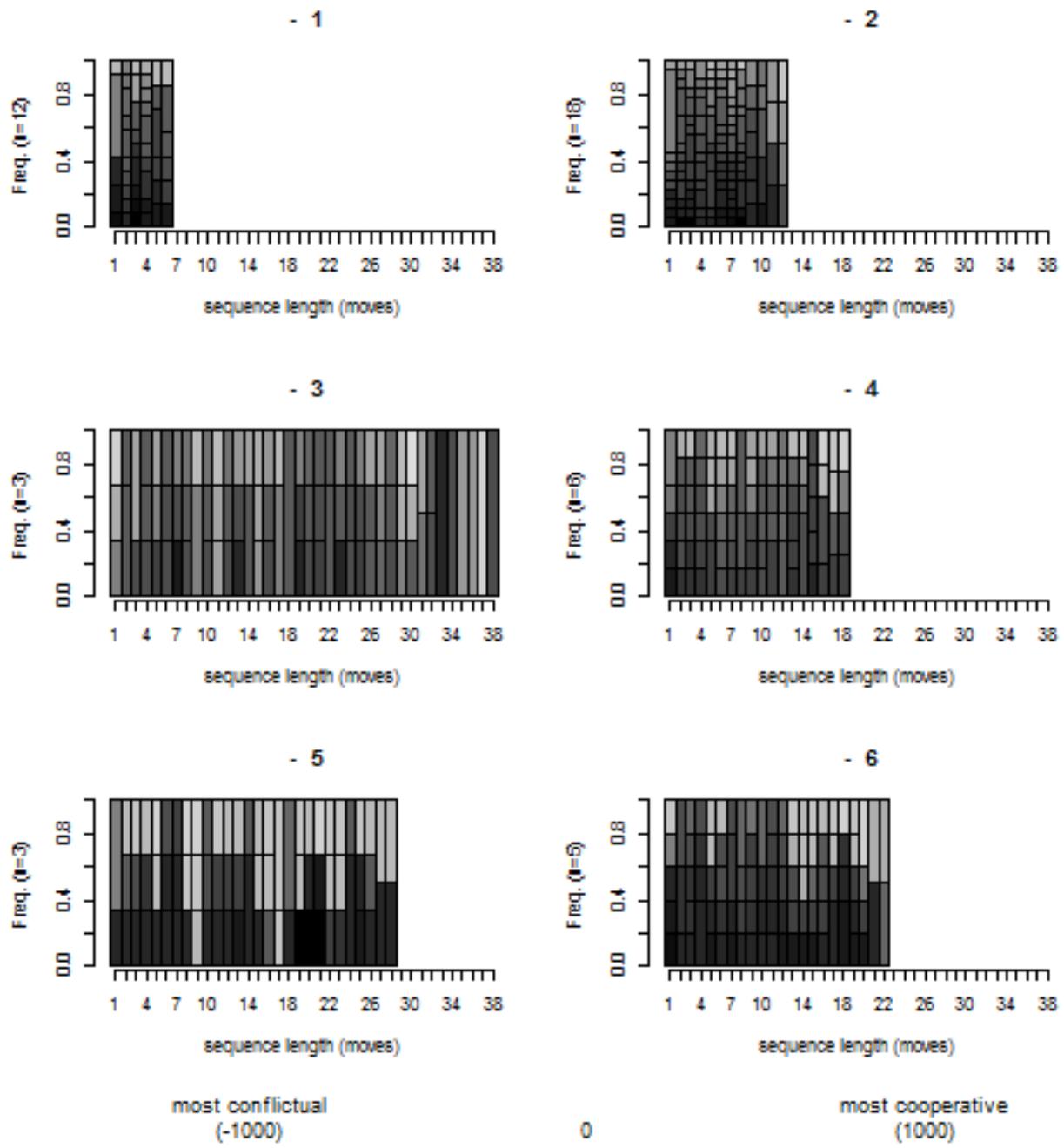


Figure 3: Sequence density plot by cluster, using Ward (1963)

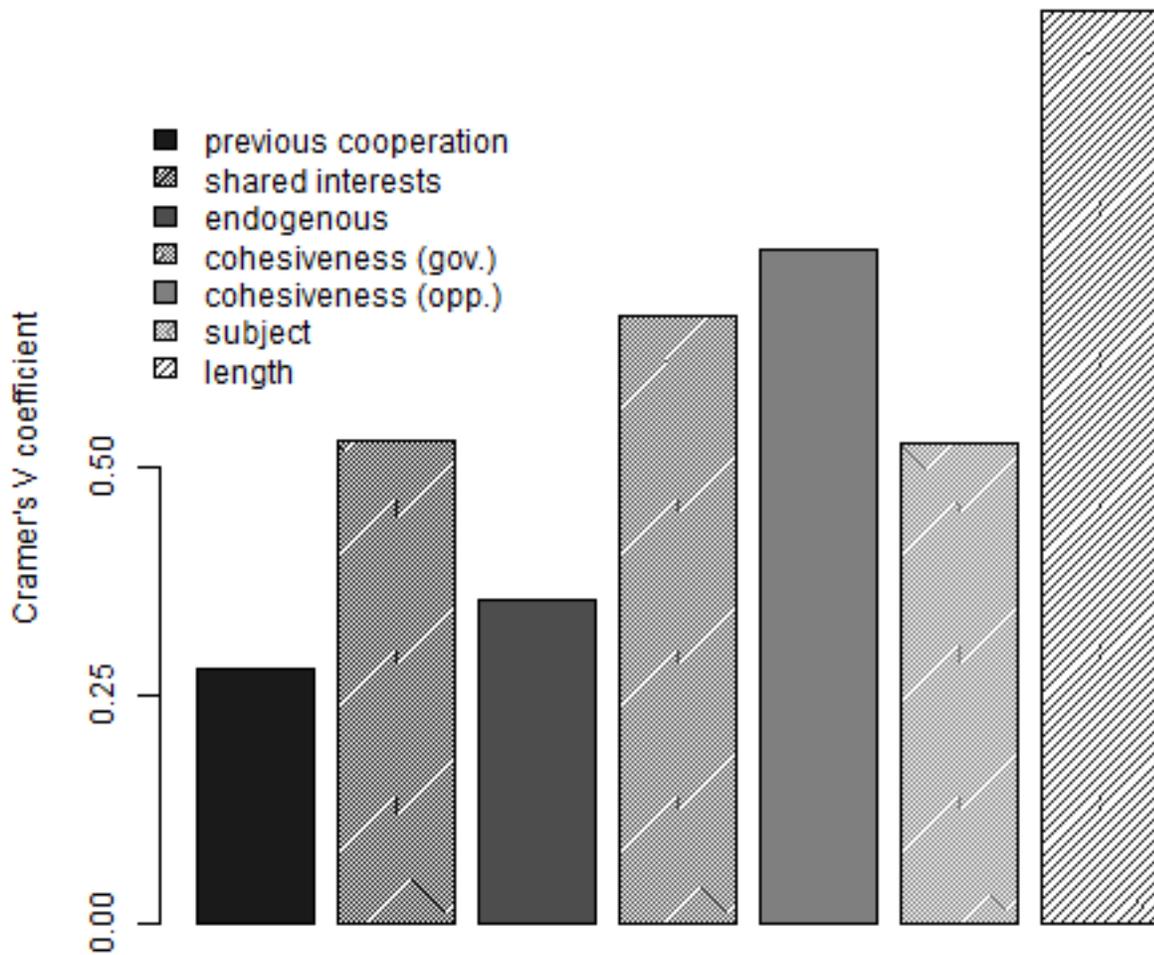


Figure 4: Bar plot:
 Crámer V coefficients, by covariate
above 0.50 denotes threshold for strong association

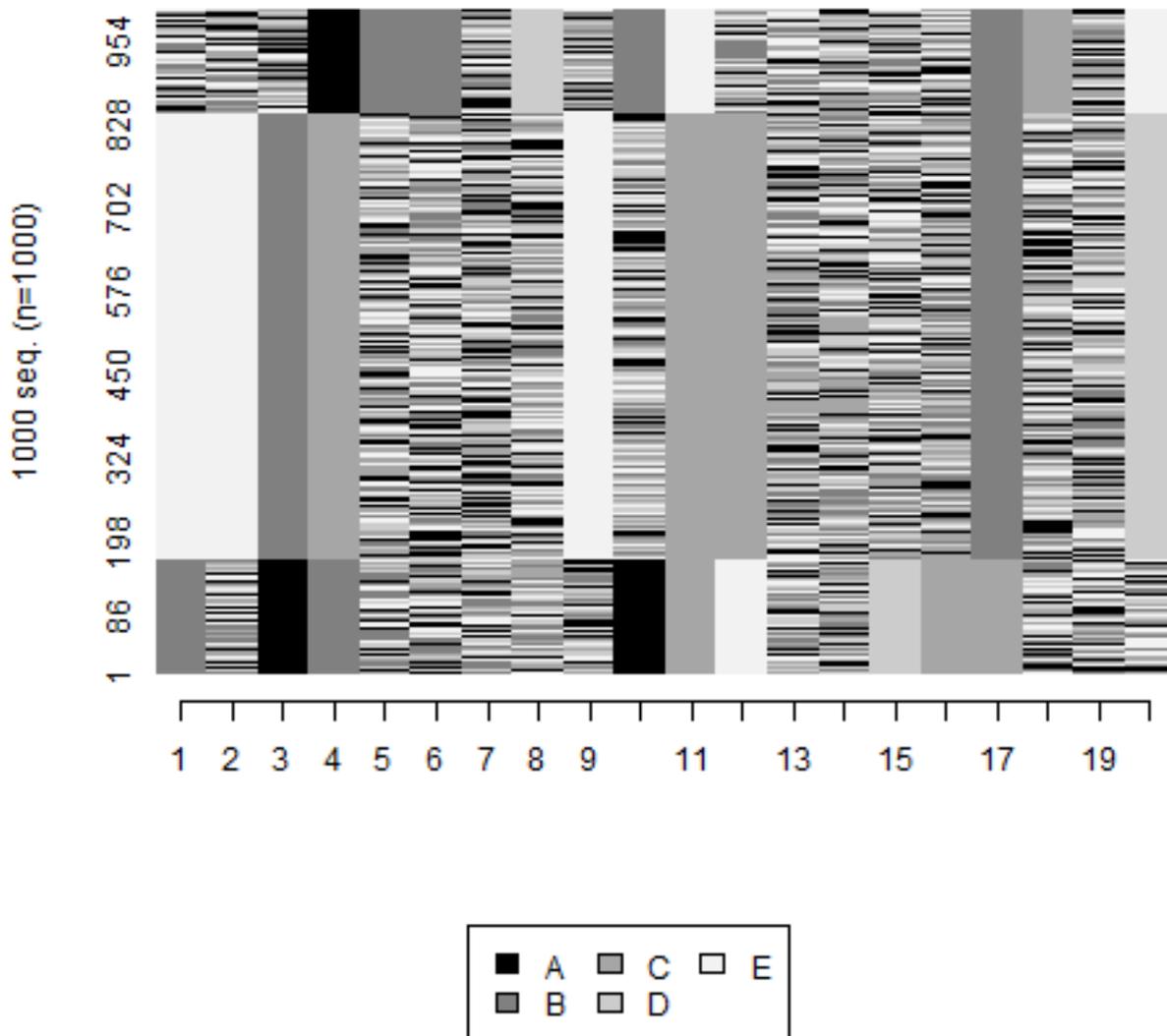


Figure 5: Sequence index plot:
 simulated sequences
 (0.5 affected by systematic error)

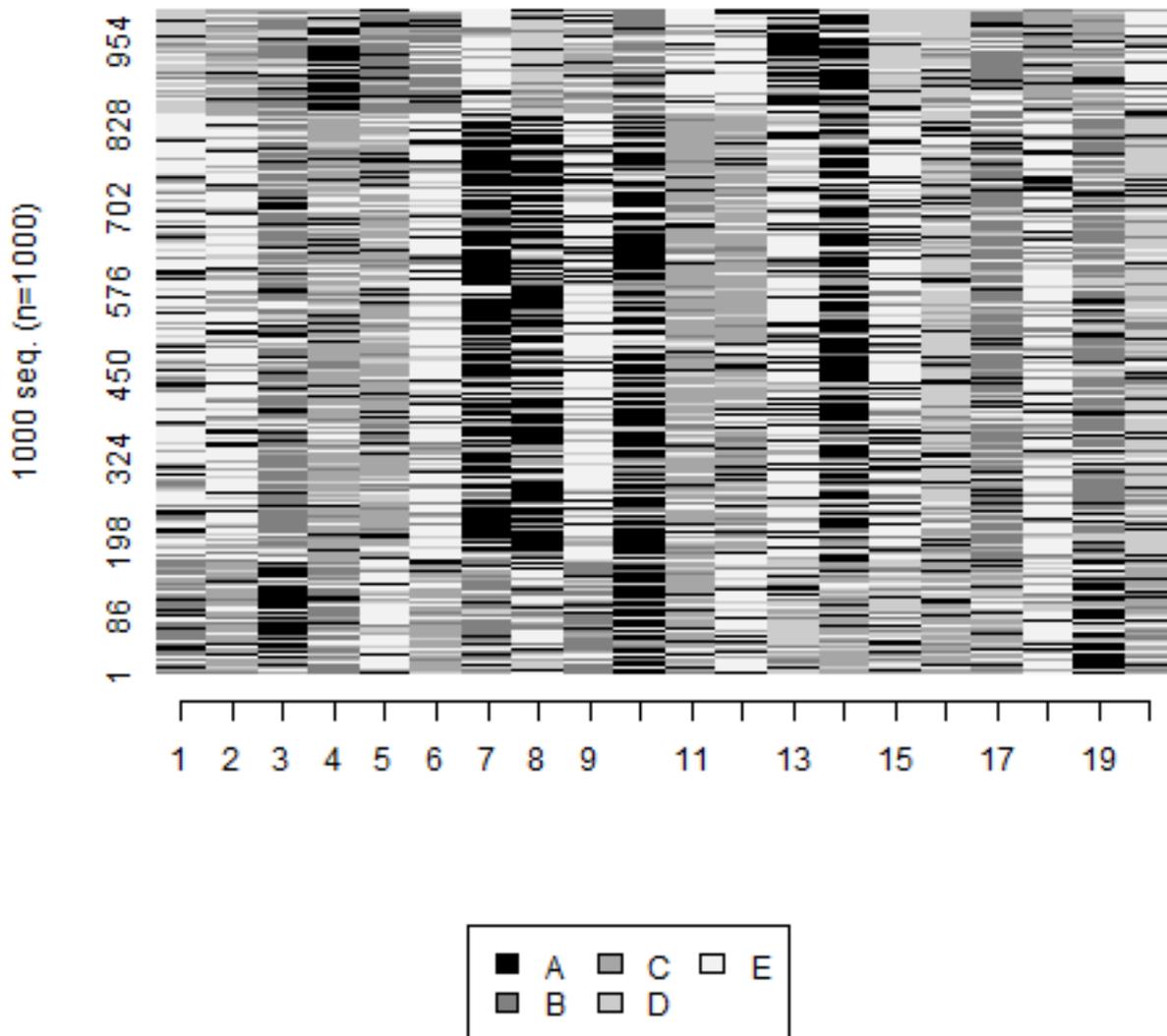


Figure 6: Sequence index plot:
 simulated sequences
 (0.5 affected by random error)

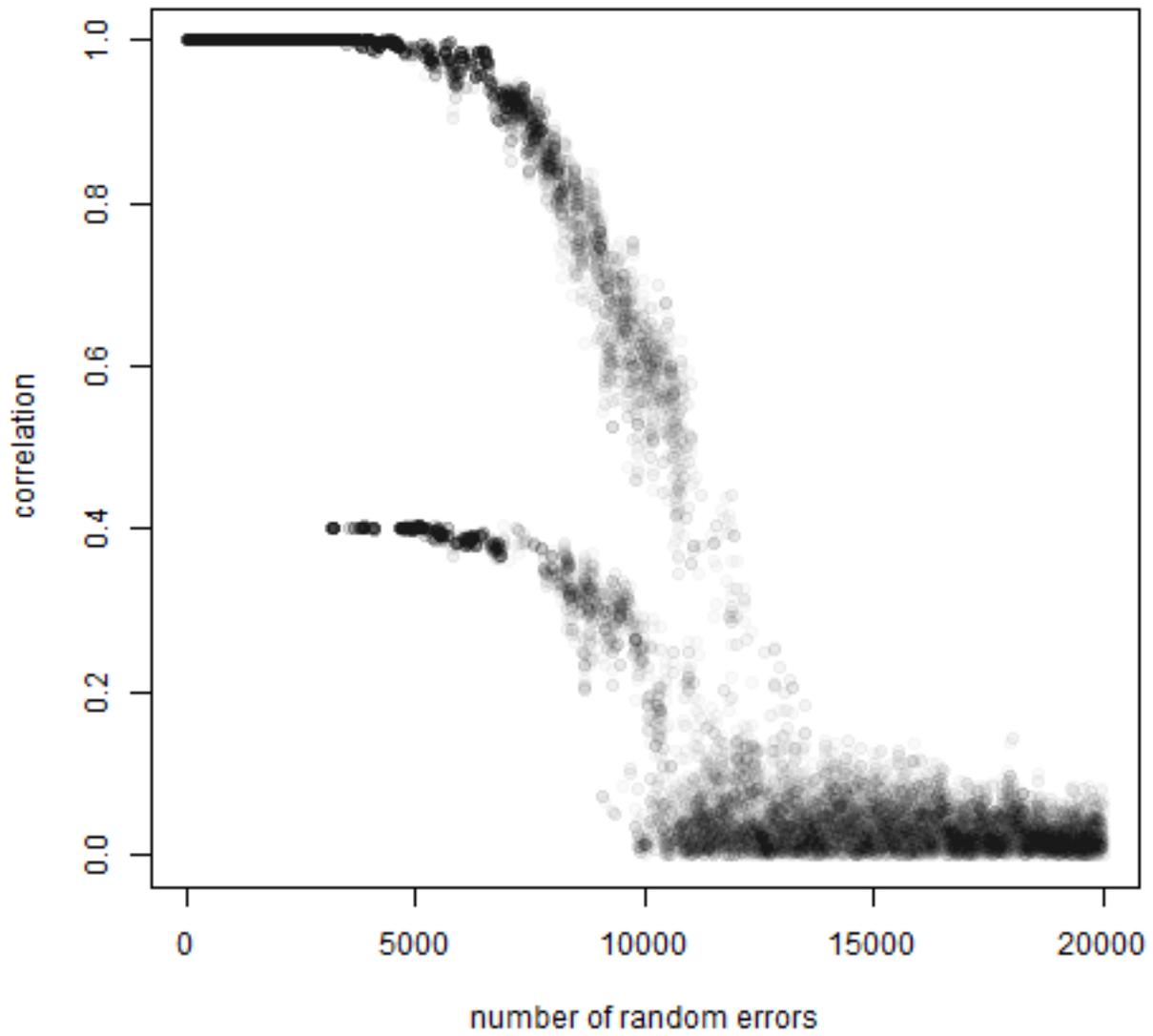


Figure 7: Correlation plot:
Simulated sequences with increasing random error, using OM