

# Text as Policy:

## Measuring Policy Similarity through Bill Text Reuse

Fridolin Linder, Bruce Desmarais, Matt Burgess, Eugenia Giraudi

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### **Abstract**

The identification of substantively similar policy proposals in both proposed and adopted legislation is important to scholars of public policy diffusion and legislative politics. Conventional, manual, approaches are prohibitively costly in constructing datasets that accurately represent policymaking across policy domains, geographic units, and/or time. We propose the use of text-sequencing algorithms, applied to legislative text, to identify bills that introduce similar policy proposals. We present three ground truth tests, applied to a corpus of 500,000 bills from US-state legislatures. First, we show that bills introduced by ideologically similar sponsors are more likely to exhibit a high degree of text reuse. Second, we show that bills classified by the National Council of State Legislatures as covering the same policies exhibit a high degree of text re-use. Third, we show that rates of text reuse across state borders correlate strongly with the diffusion networks recently introduced by Desmarais, Harden and Boehmke (2015).

# 1 Introduction

The diffusion of public policy has been a central focus in political science research since at least [Walker \(1969\)](#). Research on public policy adoption and diffusion has conventionally relied on modestly-sized, hand-coded datasets that record when a set of jurisdictions adopt one or a handful of similar policies ([Boehmke and Skinner, 2012](#)). In this paper we draw upon a voluminous and comprehensive source of data with which to measure the consideration and adoption of similar policies – the text of legislation considered in US state legislatures. We take an automated, text-as-data, approach to the analysis of bill text. This vastly increases the volume of data that can be included in policy adoption research.

Through the development of automated text-analytic methods of measuring policy diffusion we consider several methodological challenges and broader conceptual hurdles. The central methodological puzzles are two-fold. First, we need to extract segments of text in pieces of legislation that communicate similar policy enactments. Second, we need to develop a method for quantitatively scoring the reused text between bills. The main conceptual puzzle with which we engage is the potential ambiguity regarding whether two policies should be considered the same for the purposes of policy diffusion research. Considering precedents in the literature, we argue for conceptualizing policy adoption in terms of a continuum of similarity rather than a dichotomy of equivalence.

We take a multi-pronged approach to evaluating the performance of text reuse in measuring the consideration and adoption of similar laws. First, we investigate the relationship between the ideological distance of the legislators that proposed two bills and the text reuse scores between these bills. Second, we assess the how well policy diffusion networks that have been established by previous research can be predicted using the amount of text reuse between states. And third, we use data on equivalent bills collected by the

National Council of State Legislatures to build an evaluation data set containing true policy overlap to assess the accuracy of text reuse in predicting policy overlap. We find that a high degree of text reuse between bills provides a precise signal of the presence of similar policies within the bills.

## 2 Background

The measurement task on which we are focused is the identification of comparable policy actions (e.g., adoption, consideration) across jurisdictions—US states in particular. Scholars of public policy, legislative politics, and related areas have used measurements of comparable policy actions in a variety of research tasks. These include the study of policy diffusion (Karch, 2007), the comparison of policies on a select legislative issue (e.g., Huber et al., 2001; Mycoff et al., 2009), and influence/adoption of model legislation introduced by advocacy organizations (e.g., Garrett and Jansa, 2015; Burgess et al., 2016). In each of these areas of research, scholars make use of measurements of consistent policy actions across jurisdictions. Below we review a variety of methods, and conceptual definitions that researchers have used in measuring consistent policy actions.

Public policy research on cross-jurisdiction comparable policy actions has conventionally involved the manual identification of related policies across states, countries or local governments in one or a handful of policy areas (e.g., Walker, 1969; Berry and Berry, 1990; Simmons and Elkins, 2004; Gilardi et al., 2009; Krause, 2011). This is a manual approach to measurement at the monadic level. In the area of policy diffusion research, recognizing the limitations of monadic levels of measurement, researchers have developed dyadic approaches to studying the diffusion relationships between states (Volden, 2006; Boehmke, 2009). In the most recent iteration of dyadic approaches, Desmarais et al. (2015) apply network inference algorithms to US state adoption sequences in over 100 policy domains

to empirically infer the underlying network through which policies diffuse. In another recent innovation in measurement for policy analysis, [Garrett and Jansa \(2015\)](#) analyze the text of US state legislation to identify the influence of model legislation, as introduced by interest groups.

We now consider the coding rules used in past research to define sets of equivalent, or at least similar, policies. Perhaps the broadest approach—studying policies adopted within a domain, but moving the status quo in opposite directions—is represented by [Glick \(1992\)](#). Glick studies judicial enactments related to the “right to die”—the right of patients or their representatives to end the use of life-preserving medical technology. He considers an adoption to include any judicial enactment on this topic, whether they restrict medical providers’ deference to the patients or enact broad patients’ rights. [Berry and Berry \(1990\)](#) look at policy change in a uniform direction—states’ adoption of lotteries. Lotteries, of course, vary in terms of their rules and financial models, but all of the policies studied by [Berry and Berry \(1990\)](#) moved the status quo from no state lottery to the existence of a state lottery. [Volden \(2006\)](#) considers a broad array of state laws—those implemented for the Federal Health and Human Services Children’s Health Insurance Program (CHIP). CHIP laws were coded for six policy characteristics and then analyzed for diffusion dynamics. Lastly, [Mooney and Lee \(1995\)](#) provides an example of quantitative coding of policies adopted in a given domain. They code the permissiveness of state abortion laws (pre *Roe v. Wade*) on a five-point scale. These examples convey the variability with which scholars have defined the set of policies that are considered to be comparable across state borders.

### 3 Detecting Policy Similarity through Text Reuse

The above review of the ways in which researchers have defined comparable policies offers clarity regarding the implicit concepts underlying policy comparability. We see that policies that are considered comparable exhibit two qualities. First, they often, but do not always, move the status quo in a similar direction. This could be thought of as ideological similarity. Second, they enact policy in similar domains—either narrowly or broadly conceived. Before we describe the algorithm we use for detecting text re-use, and validate that algorithm, we draw upon these two concepts to define the latent variable we seek to measure through the assessment of text overlap. Specifically, we are motivated by the fact that researchers do not typically focus on strictly equivalent policies. Rather, they deem policies comparable if they are highly similar along one or two dimensions—policy domain and (optionally) ideological direction.

We see past work that has identified sets of comparable policies as focusing on sets of policies that meet some threshold of similarity. As such, the latent variable that we argue below is measured effectively through text re-use is *policy similarity*. The text in legislation is an aggregate representation of the dimensions underlying the policies proposed therein. These dimensions include the domain of the policy, the ideological position enacted by the policy, the level of specificity in the policy enactment, and several other salient features of policy that are communicated through the text in legislation. We do not claim that the re-use of text can be used to measure these dimensions in a specific, dis-aggregated way. Rather, text re-use serves as a summary measure of the greatest overlap observed across all relevant policy dimensions represented in legislative text.

### 3.1 Detecting Text Reuse

To assess the maximal similarity of policies proposed in two pieces of legislation, we seek to identify large segments of equivalent or highly similar text (i.e., text reuse between bills). Alignment algorithms for discovering similar long sequences of text stand in contrast to bag-of-words methods, which are based on the comparison of word occurrence frequencies in documents. Bag-of-words methods may be effective for capturing broad topical areas in legislation, but will provide results that are too coarse for precisely assessing policy overlap. For example, in modeling bills in the US Congress using statistical topic models, arguably the canonical bag-of-words method for text analysis, [Gerrish and Blei \(2011\)](#) find that topic models for legislative text perform most effectively when parameterized with 64 topics to model a corpus of 4,447 bills. While 64 topics provides a fairly detailed categorization of the domains covered in legislation, it is unrealistic to think that this method can isolate individual policy proposals. Considering [Gerrish and Blei’s \(2011\)](#) results again, that would mean that the US Congress considers nearly seventy bills, on average, for each specific policy proposed.

There are a variety of algorithms designed to automatically detect text reuse between documents mostly originating in the plagiarism detection literature (see e.g. [Potthast et al., 2013](#), for an overview). In political science, [Wilkerson et al. \(2015\)](#) introduced the Smith-Waterman local alignment algorithm (SW algorithm) to detect overlapping language in congressional bills in order to trace policy ideas through the legislative process of the US Congress. We use the same algorithm to detect text reuse in US state bills, however, our implementation of the algorithm differs slightly. The SW algorithm was developed by [Smith and Waterman \(1981\)](#) in molecular biology, in order to match genetic sequences. Given two sequences (of genes or words) it calculates the optimal alignment (match) between these sequences.

Sequences in text that convey equivalent content matter often do not match perfectly. Formatting, white space, typographical errors, etc. would decrease the precision dramatically if only exact matches were used. The SW algorithm, therefore, returns the optimal alignment while allowing for mismatches and gaps. The extent to which such imperfections are tolerated is governed by parameters that are set by the researcher. There are three such parameters: the match score (reward for exactly matching words), the mismatch score (penalty for including words that do not match), and the gap score (penalty for including placeholder words in matching a shorter sequence to a longer sequence). The goal of the algorithm is to return the the alignment with the highest score given the input sequences and the parameters. Consider the following two excerpts from Alaska State Bill 203 (28th session) and North Carolina House Bill 366 (2015) respectively:

*”section 1.AS44.99 is amended by adding new sections to read: article 6. compact for a balanced budget (...)”*

*”chapter 143 is amended by adding a new article to read: article 80. compact for a balanced budget (...)”*

There is a large number of possibilities of how these sequences could be aligned. There is a trade-off between short sequences that match perfectly, and longer sequences with imperfections. For example, we could match just “is amended by adding new” or “compact for a balanced budget”. However, by adding a gap between “adding” and “new” in the first sequence and accepting the mismatches “article”-“section” and “6.”-“80.”, a longer alignment can be obtained: “is amended by adding (*a*) new (*article/section*) to read: article (*6./80.*)”.

Because there are so many different possibilities, it is computationally demanding to find the optimal alignment. [Smith and Waterman \(1981\)](#) therefore proposed a dynamic programming approach that is illustrated in Figure 1. Dynamic programming refers to algo-

rithms that divide a problem into sub-problems and store results of previous calculations for later ones. In the case of the SW algorithm, the property that makes it a dynamic problem is the fact that all the alignments of shorter sub-sequences of an optimal alignment of a sequence are themselves optimal. Intuitively, if the benefits of including a sub-sequence in an alignment outweigh the penalties from mismatches and gaps in that sub-sequence, that sub-sequence will contribute positively to longer alignments to which it is appended. To make this clearer consider the beginning of the sequences in the example above:

*“section 1.AS44.99 is amended”*

*“chapter 143 is amended”*

It is obvious that the best local alignment of the first three elements would be just “is” - “is” since the first two elements don’t match and therefore would just reduce the overall quality of the alignment. If we now consider the alignment of the first four words we know that we can discard all possible alignments that involve the first two elements because the quality of every alignment that involves these elements could be improved by dropping them. Re-using the result from the first three elements, the problem of aligning the first four elements is now reduced to the single decision about the elements “amended” and “amended”. This decision is easy to make because we only have to consider four possibilities: We match the elements and they are actually the same, we match the elements and they are not the same, we introduce a gap in one of the sequences or we decide to stop the alignment.

If the next two elements match, the decision is easy - we add them and increase the total alignment score. However, if they do not match the decision is more difficult. We only want to introduce a gap or mismatch if it pays off later (that is if we thereby can ‘reach’ another part of the sequence that matches again). But we only know that once we went through the whole sequence. The central idea is therefore to find all optimal alignments ending in all possible spots, keep these scores and after everything is calculated finding



the alignment that maximizes the overall quality. Therefore, after the decision is made the same procedure is applied to the next pair of sequence elements, and repeated until the end of both sequences is reached.

This intuition can be formalized in an algorithm that is based on a dynamic programming matrix that contains all optimal sub-alignments. A matrix is created where each combination of elements of the two sequences is assigned a cell. And an additional row and column of 0 is appended to the beginning of each sequence (to allow for a gap in the beginning of one sequence). The quality or alignment score of every possible alignment is then calculated cumulatively with the following algorithm. Denote the two sequences as  $\mathcal{A} = (a_1, a_2, \dots, a_n)$  and  $\mathcal{B} = (b_1, b_2, \dots, b_k)$ . Additionally let  $\delta$ ,  $\epsilon$  and  $\gamma$  be the match, mismatch and gap scores. Define the scoring function:

$$S(a_i, b_j) = \delta \mathbb{I}(a_i=b_j) + \epsilon \mathbb{I}(a_i \neq b_j) \quad (1)$$

Where  $\mathbb{I}(\cdot)$  is the indicator function. Then the entry for each cell  $M_{i,j}$ ,  $i = 1, 2, \dots, n$  and  $j = 1, 2, \dots, k$  of the matrix is filled by the following rule:

$$M_{i,j} = \max(M_{i-1,j-1} + S(a_i, b_j), M_{i-1,j} + \gamma, M_{i,j-1} + \gamma, 0) \quad (2)$$

The algorithm is visualized for the example above in Figure 1<sup>1</sup>. Each row corresponds to a word in the sentence from the Alaska bill and each column to the sentence from the North Carolina bill. On the right side of the matrix the optimal alignment is displayed.

The four values of which the maximum is chosen in Equation 2 describe four steps in this dynamic programming array. The first value corresponds to a diagonal step which means in the resulting alignment sequence elements  $a_i$  and  $b_j$  are matched and the score of the

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<sup>1</sup>An interactive version can be found at <http://fridolin-linder.com/2016/03/30/local-alignment.html>.

	-	chapter	143	is	amended	by	adding	a	new	article	to	read:	article	80.	compact	for	a	balanced	budget	Alignment Result	
-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	is	is
section	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	amended	amended
1.AS44.99	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	by	by
is	0	0	0	3	-2	-1	0	0	0	0	0	0	0	0	0	0	0	0	0	adding	adding
amended	0	0	0	2	6	-5	-4	-3	-2	-1	0	0	0	0	0	0	0	0	0	-	a
by	0	0	0	1	5	9	-8	-7	-6	-5	-4	-3	-2	-1	0	0	0	0	0	new	new
adding	0	0	0	0	4	8	12	-11	-10	-9	-8	-7	-6	-5	-4	-3	-2	-1	0	sections	article
new	0	0	0	0	3	7	11	10	14	-13	-12	-11	-10	-9	-8	-7	-6	-5	-4	to	to
sections	0	0	0	0	2	6	10	9	13	12	11	10	9	8	7	6	5	4	3	read:	read:
to	0	0	0	0	1	5	9	8	12	11	15	-14	-13	-12	-11	-10	-9	-8	-7	article	article
read:	0	0	0	0	0	4	8	7	11	10	14	18	-17	-16	-15	-14	-13	-12	-11	6.	80.
article	0	0	0	0	0	3	7	6	10	14	13	17	21	-20	-19	-18	-17	-16	-15	compact	compact
6.	0	0	0	0	0	2	6	5	9	13	12	16	20	19	18	17	16	15	14	for	for
compact	0	0	0	0	0	1	5	4	8	12	11	15	19	18	22	-21	-20	-19	-18	a	a
for	0	0	0	0	0	0	4	3	7	11	10	14	18	17	21	25	-24	-23	-22	balanced	balanced
a	0	0	0	0	0	0	3	7	6	10	9	13	17	16	20	24	28	-27	-26	budget	budget
balanced	0	0	0	0	0	0	2	6	5	9	8	12	16	15	19	23	27	31	-30		
budget	0	0	0	0	0	0	1	5	4	8	7	11	15	14	18	22	26	30	34		

Figure 1: Dynamic programming array of local alignment algorithm. The parameters in this instance are: Match Score: 5, Mismatch Score: -2, Gap Score: -1. The optimal alignment is displayed on the right side of the matrix. The left column corresponds to the text sequence in the rows of the matrix, the right column to the sequence in the columns. Mismatches are colored in red, gaps are indicated by "-" and orange color. The blue cells in the matrix display the path of the optimal alignment.

alignment is either increased by  $\delta$  if they match or decreased by  $\epsilon$  if they don't match. The second and third value describe a gap step either in horizontal or vertical direction. That is, if we move from cell  $(i, j)$  to cell  $(i + 1, j)$ , in the resulting alignment sequence element  $a_{i+1}$  is matched with a gap. On the other hand, if we move to cell  $(i, j + 1)$  sequence element  $b_{j+1}$  is matched with a gap in the resulting alignment. If the first three values are all  $\leq 0$ , the score in the cell is 0 meaning that no step is taken and every potential

alignment stops at this point. This can be observed in Figure 1. The blue path describes the optimal alignment. The first two elements in both sequences don't match, therefore the score remains zero. Therefore the resulting alignment starts at the fourth element of each sequence with four diagonal steps, each adding points ( $\delta = 5$ ) to the final score which reaches 20 at the alignment ending in "adding"- "adding". After that, a step to the right is taken, meaning that the additional "a" in the column sequence is matched with a gap in the row sequence (indicated by "-" and orange coloring in the result on the right hand side). The cumulative score of the alignment is reduced by  $\gamma = -1$  to 19. After that only diagonal steps are taken. Note that there are two mismatches each of which reduces the score by  $\epsilon = -2$ .

The optimal alignment is identified by finding the highest score in the matrix, at which the alignment ends, and back-tracing the path of the alignment. The steps in the path are chosen using Equation 2, and are indicated in Figure 1 by arrows pointing to the left, the upper left, up or no arrow. The back-tracing continues until a zero is encountered.

This algorithm is computationally intensive ( $\mathcal{O}(nk)$  in computation time and memory demand), but returns the globally optimal local alignment given the scoring parameters. We provide a proof of this in the appendix. The property follows from the recursive relation used to fill the dynamic programming matrix. An alignment that is constructed by adding one element to an already optimal alignment is optimal itself. Starting by aligning the first two elements of the sequence optimally (which is trivial), a globally optimal can be found by iteratively adding to this alignment.

In our analyses we use a slightly modified version of the local alignment algorithm, in which the first gap in a series of multiple gaps receives a higher penalty than the following ones (Wilkerson et al., 2015, use the same modification). This penalizes many small gaps and makes the algorithm produce longer gaps. The idea behind this modification is that someone who changes text in a bill might insert several words into an existing piece of

text. The fact that something was inserted should weigh heavier than the length of the insertion which is achieved by down-weighting gap extensions.

## 4 Policy Similarity in US State Legislation

Through the application of the SW algorithm to US state legislation, we will provide a quantitative measure of policy similarity between bill sections. We follow [Wilkerson et al. \(2015\)](#) in focusing on sections, as bills can contain many separate policy proposals. The similarity measures between sections that we identify can be aggregated up to the bill, legislator or state levels. The measures we provide can be used to test hypotheses regarding, among other topics, public policy diffusion, legislative politics, political parties, and interest groups.

### 4.1 Data

We apply the SW algorithm to a database of US state bills, collected by [Burgess et al. \(2016\)](#) and the Sunlight Foundation<sup>2</sup>. This data base contains approximately 500,000 bills from 2008 to 2015. Not all bills from all states are available for the whole time period. Figure 2 displays the year ranges and number of bills in the bill data base. This collection of bills is based on all bills that are available through the Sunlight Foundation’s [openstates.org](#) API. [openstates.org](#) is a website maintained by the Sunlight Foundation, in order to increase transparency in state politics. The Sunlight Foundation uses web scrapers to access all bills that are available on the websites of legislatures in all US states. This includes enacted legislation as well as bills that are still in the legislative process, or where not enacted.

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<sup>2</sup><http://sunlightfoundation.com/>

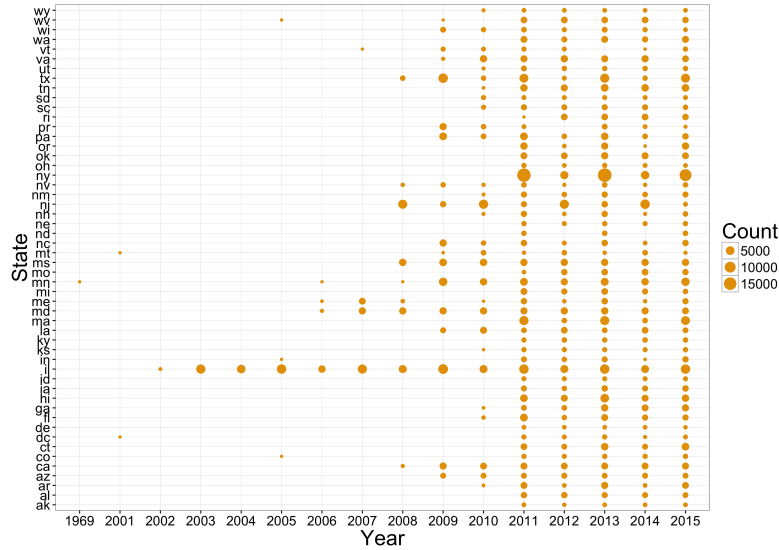


Figure 2: Description of the bill database. The horizontal bars display the time range for which bills are available for each state. The color of the bar indicates how many bills are available for this state.

Our approach of applying the SW algorithm is similar to [Wilkerson et al. \(2015\)](#) but differs in several key respects. The analysis consists of three major steps: 1) Pre-processing and selection of documents to compare, 2) alignment computation, 3) post hoc refinement (boiler plate removal).

## 4.2 Pre Processing and Selection

All bills are split up into sections in order to be able to detect all alignments between two bills. Because the SW algorithm only returns the one best alignment between two sequences, relevant information might be lost when considering every bill as one large sequence of words. The SW algorithm is computationally demanding and an exhaustive comparison of all possible bill-section-pairs is not feasible (with 500,000 bills, assuming each bill consists on average of four sections this would amount to about  $2 * 10^{12}$  comparisons). [Wilkerson et al. \(2015\)](#) encountered the same problem and excluded bills that don't have at least five matching 10-grams. Since this implies considerable exact character

matches, we see this as a too restrictive for our application. Because the text we are using originates in 50 different legislatures, exact character matches might obfuscate valuable text reuse just because of small formatting changes, changes of state names, etc. Instead we choose to rely on a procedure that is based on finding bills with similar language. We store all available bills in an Elastic Search database. Elastic search is an open source web search engine which is designed to find document that match a search query (Gormley and Tong, 2015). We utilize the ‘more like this’ query, which is designed to find documents that are similar to a given document. It works in the following way: From the focus document, the  $k$   $n$ -grams with the highest tf-idf scores are selected and transformed into a search vector that is representative of the query document. Then, for each document in the collection, a variation of the cosine similarity is calculated and the  $m$  bills with the highest scores are selected for further analysis. For this analysis we set  $k$  to 25,  $n$  to 5 and  $m$  to 1000<sup>3</sup>

### 4.3 Bill Alignment Computation

Once the candidate sections are selected, the alignments are calculated for all possible bill-section-dyads, section-pairs from the same bill and section pairs from the same state are excluded. We exclude same-state comparisons in the current analysis since our validation exercises are focused on cross-state comparisons. We refer to the two sections involved in each alignment process as ‘left’ and ‘right’ sections. The algorithm returns parts of the left and right section that are determined to be aligned as well as a score. We refer to these three pieces of information as an alignment.

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<sup>3</sup>For details on the exact algorithm we refer the reader to the elastic search documentation (<http://sunlightfoundation.com/> as well as the lucene engine documentation ([https://lucene.apache.org/core/4\\_9\\_0/core/org/apache/lucene/search/similarities/TFIDFSimilarity.html](https://lucene.apache.org/core/4_9_0/core/org/apache/lucene/search/similarities/TFIDFSimilarity.html)). In order to account for the possibility of selection bias being introduced to our analyses through the cap of 1000 similar bills, we analyzed the results with different numbers of pre-selected bills. We find that this parameter, when set to a sufficiently high value, does not lead to such bias because the set of potentially relevant bills is always much smaller than 1000.

Table 1: Alignment Examples. Yellow highlighting shows matching sections. Dashes stand for gaps introduced by the alignment algorithm. Non highlighted text are mismatches.

Left Text	Right Text	Score
<p><b>nj_214_A1167:</b> "the entire credit may not be taken for the taxable year in which the renewable energy property is placed in service but must be taken in five equal - installments beginning with the taxable year in which the renewable energy property is placed in service. if, in one of the years in which the installment of a credit accrues, the renewable energy property with respect to which the credit was claimed is disposed of, taken out of service, or moved out of state, the credit expires and the taxpayer may not take any remaining installment of the credit. the taxpayer may, however, take the portion of an installment that accrued in a previous year and was carried forward to the extent permitted under"</p>	<p><b>nc_2011_SB747:</b> "the entire credit may not be taken for the taxable year in which the facility - - is placed in service but must be taken in five equal annual installments beginning with the taxable year in which the facility - - is placed in service. if, in one of the years in which the installment of a credit accrues, the facility - - with respect to which the credit was claimed is disposed - - - of - or taken out of service, the credit expires and the taxpayer may not take any remaining installment of the credit. the taxpayer may, however, take the portion of an installment that accrued in a previous year and was carried forward to the extent permitted under"</p>	388
<p><b>nj_214_A1167:</b> "the entire credit may not be taken for the taxable year in which the renewable energy property is placed in service but must be taken in five equal installments - - - - beginning with the taxable year in which the"</p>	<p><b>ga_2011_12_HB146:</b> "the entire credit may not be taken for the - year in which the - - property is placed in service but must be taken in four equal installments over four successive taxable years beginning with the taxable year in which the"</p>	110
<p><b>nj_214_A1167:</b> "the entire credit may not be taken for the taxable year in which the" renewable energy property is placed in service but must be taken in five equal installments beginning with the taxable year in which the</p>	<p><b>nc_2009_SB305:</b> "the entire credit may not be taken for the taxable year in which the costs are paid - - - - but must be taken in five equal installments beginning with the taxable year in which the"</p>	108

From this procedure we obtain ca.  $10^9$  individual alignments (that is, shared text between two sections of two bills) which corresponds to about  $2 * 10^6$  bill dyads ( $1.3 * 10^6$  bill dyads excluding within-state alignments). Figure 3 displays the cumulative frequency distribution of the alignments. The vast majority of alignments are very small (less than 10). We use the alignment score as the quantitative measure of policy similarity. However, as we discuss below, due to the presence of extreme outliers, we work with this measure on the log scale. In order to aggregate the alignments to the bill level, we sum the alignment scores for each section pair of the corresponding bill dyad. Table 1 displays three examples of section alignments. The ‘Left Text’ and ‘Right Text’ columns display the optimal alignment for the two sections the alignment score is displayed in the ‘Score’ column. This example shows the reuse of legislative text in three states (New Jersey, North Carolina and Georgia).

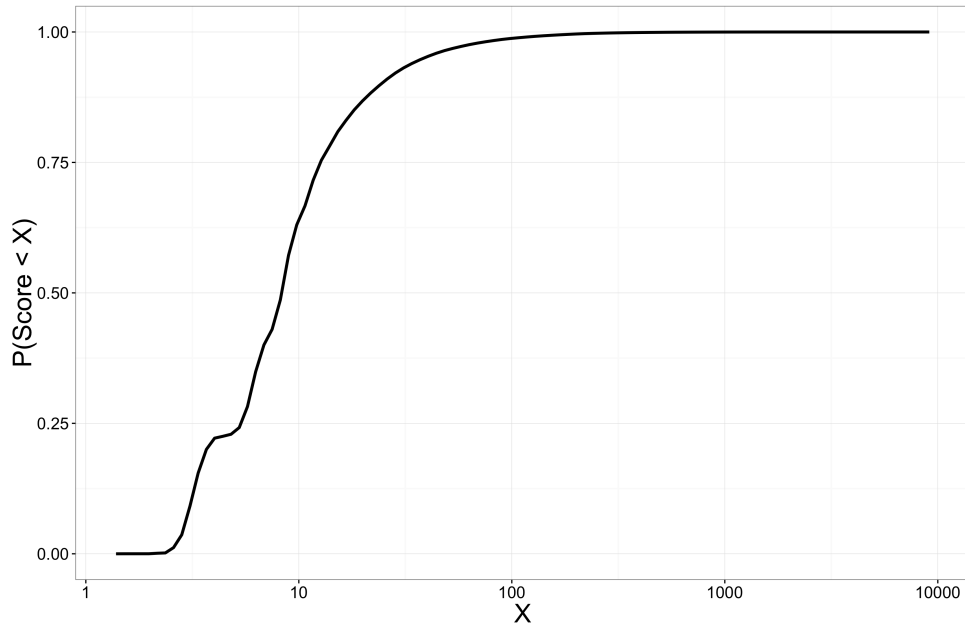


Figure 3: Cumulative frequency distribution of the dyad level alignment scores. The x-axis represents the dyad level alignment score on the  $\log_{10}$  scale.



## 4.4 Boiler Plate Removal

Boiler plate can be procedural language like headers, section titles, common phrases or topic specific phrases such as definitions of legal terms, tax brackets, etc. [Wilkerson et al. \(2015\)](#) rely on human coders to identify alignment text that is boiler plate, and then use a machine learning algorithm to extrapolate to all alignments based on the bag-of-words features. We also rely on an automatic classifier, but we propose a novel approach for generating training data without relying on human coders. We use the fact that boiler plate language is highly repetitive within-states. Furthermore, language that is passed several times within the same state is likely to be not substantively relevant. Using these facts allows us to accumulate a large amount of labeled data which we use to train a machine learning classifier to automatically weed out boiler plate from our alignments. In addition to the text itself, we use the position in the text as a feature in the classification task.

## 5 Evaluation of Validity

We use three strategies in order to assess the validity of text reuse as a measure of policy equivalence. First, we evaluate whether there is a disproportionately high number of alignments between bills on the same policy area. Second, we analyze how well the bill similarity aggregated to the state level corresponds with policy diffusion networks identified in previous research ([Desmarais et al., 2015](#)). And third, we study the relationship between the ideological distance between the sponsors of bills and the alignment scores between those bills. If substantive policy content, and importantly, the same ideological direction of the provisions is detected by the alignment algorithm, we will expect an inverse relationship between these two measures.

## 5.1 NCSL Tables

In our first validation exercise, we consider whether high alignment scores provide a reliable signal of similar policy proposals. To build a ground truth data set in terms of policy proposal, we rely on thematic tables published by the National Council of State Legislatures (NCSL).<sup>4</sup> We collected a sample of these tables with the following procedure:

1. Collect all urls returned by the bing search query: "site:ncsl.org "legislation.aspx""<sup>5</sup>
2. Sample 50 urls
3. Select bills that fulfill these three conditions:
  - (a) The website is a NCSL table
  - (b) The table refers (at least in part) to legislation introduced in 2011 or later.
  - (c) The table contains less than 100 individual bills.
4. Scrape all information from these tables

Condition a) is necessary, since some of the urls returned by the web query refer to blog entries or to protected websites that require NCSL membership. The rationale behind condition b) is to maximize the number of bills we can match to our database (see Figure 2). We additionally constrain the number of bills per table to be below 100, in order to assure, that the topic of the table is not too broad. We chose 100 since this number would correspond roughly to two bills per state (often there is a house and a senate bill in each state for a particular policy). The web query from step 1 returned 266 urls. From the 50 sampled urls 22 fulfilled the three criteria. From these 22 tables we constructed a dataset of 950 bills, of which we could match 704 to our bill database. For all bill pairs that we do not have alignment scores for (i.e. the bills did not get matched by the pre-selection algorithm) we assume a score of 0<sup>6</sup>.

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<sup>4</sup>[www.ncsl.org](http://www.ncsl.org)

<sup>5</sup>We used the bing websearch API to collect the urls.

<sup>6</sup>If a bill is not selected in the pre-selection step, this means that there are basically no matching sequences in this dyad.

Figure 4 displays the performance of the alignment score in predicting if two bills are in the same NCSL table. We present precision—the proportion of bill pairs with a given alignment score that exceed the threshold on the  $x$ -axis that are in the same NCSL table, and recall—the proportion of same-NCSL-table pairs that exceed a given alignment score threshold. We see generally high precision—over 80% with moderate (higher than 50) to high alignment scores (about 3% of bill-dyad alignment scores fall into this category). When alignment scores are very high (over 100) we see extremely high precision (1% of bill-dyad alignment scores fall into this category). Recall is generally low, but that is expected for our case, as (1) the introduction of similar policies in bills in two different states is a rare event, and relatedly, (2) the appearance of two bills in the same NCSL table is a rare event ( $3 * 10^{-4}\%$  in the current analysis); and classifier recall is notoriously low in rare event data (Weiss and Hirsh, 2000)—even commonly approaching zero, as in our case (Weiss, 2004). Our results suggest that the presence of a large alignment score between bills is an effective indicator of policy similarity.

## 5.2 Diffusion networks and Text re-use

To evaluate whether text re-use corresponds to the transfer of policy, we test whether the presence of a diffusion network tie between two states is a predictor of text reuse. We use the policy diffusion networks inferred in Desmarais et al. (2015). The diffusion networks were inferred using policy adoption sequences, and the network inference algorithm developed by Gomez Rodriguez et al. (2010). A tie from state  $i$  to state  $j$  in the diffusion network indicates that state  $j$  has frequently emulated state  $i$ ’s policies in the preceding thirty-five years. To calculate an aggregate alignment score for each state-pair we calculate the sum of the natural logs of the alignment scores associated with each pair of bills across the two states. We use the log since a handful of large alignment scores lead to extreme outliers on the original scales. The “Diffusion Ties” variable indicates the presence of a

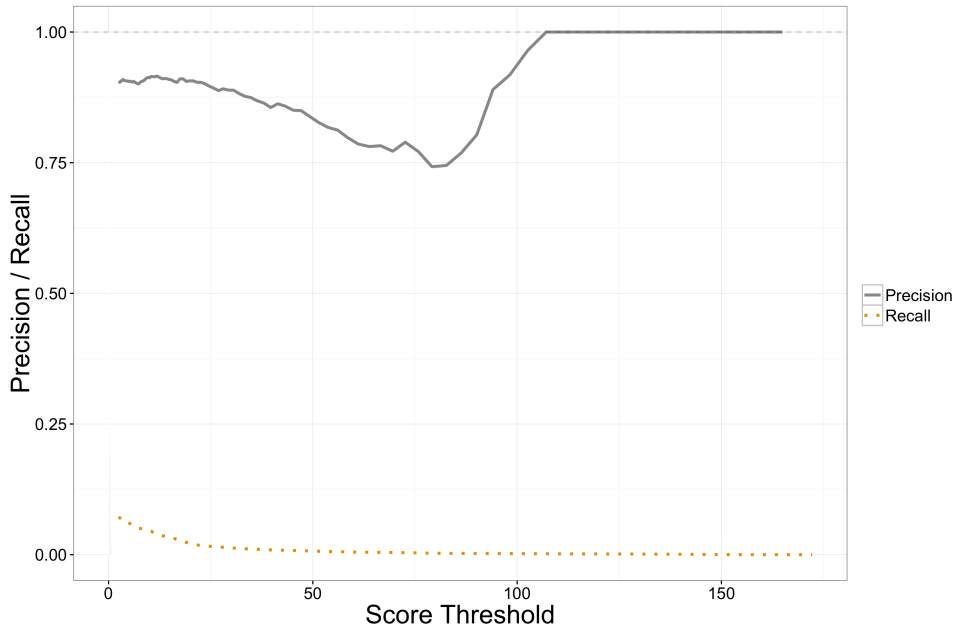


Figure 4: Precision-Recall curve for classifying two bills being in the same ncs1 table by thresholding the bill-dyad alignment score. The x axis displays the threshold, the y axis represents precision and recall. The shaded area in the background displays the frequency distribution of the alignment scores. Note that the figure does not include alignments with score exactly 0.

diffusion edge between states in the 2008 diffusion network, as measured by [Desmarais et al. \(2015\)](#). The diffusion network in 2008 is inferred using policy adoptions in the 35 years preceding (and excluding) 2008. There is one observation in the analysis for each of the 1,225 unique state-pairs. Since this is dyadic data, we use a matrix permutation method, quadratic assignment procedure, to calculate  $p$ -values ([Krackhardt, 1988](#)). As a robustness check, we run the model with both the identity and log link.<sup>7</sup>

	Identity Link		Log Link	
	Coefficient	p-value	Coefficient	p-value
Intercept	-6760712.2229	0.0048	8.2122	0.0000
Diffusion Tie	498466.2990	0.0496	0.2683	0.0968
Coverage	2199070.8445	0.0000	1.4324	0.0000

Table 2: Predicting number of alignments in legislation across states with diffusion ties. Coefficients calculated with OLS regression.  $p$ -values based on 5,000 QAP permutations.

<sup>7</sup>The  $p$ -values were calculated using 5,000 random matrix permutations.

Results of the dyadic regression are presented in Table 2. In both specifications there is a positive relationship between the number of diffusion ties and the number of alignments. The relationship is statistically significant at the 0.05 level with the identity link and at the 0.10 level with the log link. Furthermore, the magnitudes of the relationships are substantively significant. With the identity link, the presence of a diffusion tie leads to a 0.25 standard deviation increase in the expected aggregate alignment score. Based on the log link, the addition of a diffusion tie corresponds to a 30% increase in the expected aggregated alignment score.<sup>8</sup> These results offer further evidence of the validity of quantifying text re-use as a measure of policy similarity, as the aggregate volume of text re-use between states is positively associated with previously-identified diffusion ties between states.

### 5.3 Ideological Distance of Aligned Bills

In the previous two validity tests, we focused mainly on the policy domain aspect of policy similarity, rather than ideological similarity. In the third and final validity test we ask whether we observe a greater volume of text reuse between bills introduced by legislators who are ideologically similar. For calculating ideological distance, we rely on latent ideology scores measured by (Shor and McCarty, 2011). The data set contains scores for 20,738 legislators from 50 state legislatures. The `openstates` API, which we can match to our bills data, contains data and identifiers on 12,000 legislators. Of these, we were able to uniquely match about 8,000 legislators to their records in the ideal point data. This allowed us to obtain ideal points for the sponsors of 58% of bills and  $48 \times 10^6$  (38%) pairs of bills. In order to assess the validity of text reuse as a measure of substantive policy overlap, we expect the quality of the alignments to be inversely correlated to the distance between the bills sponsors' ideal points. The ideal points are located on a common scale across all states, the distance between sponsors from different

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<sup>8</sup>Calculated as  $100 \times [\exp(0.2683) - 1] = 30.77$

states is therefore meaningful.

In the following sections we present several analyses to assess this correlation. When we are generating the alignments the bills are split up into sections. We generate an alignment score for a bill dyad by first taking the logarithm and then summing over all section dyads of the bill dyad. The ideal point of the bill is derived from the ideal point of the primary bill sponsor. For bills with several primary sponsors we use the average of those sponsors' ideal points to obtain a single measure. Figure 6 displays the distribution of ideological distance and log-alignment score for the roughly 50 million dyads in the dataset. Each dot is a hexagonal tile, the color of the tile represents the number of dyads in that area. Two major observations can be made in this plot. First, the vast majority of alignment scores are close to zero. Second, the triangular shape of the distribution indicates the high precision - low recall character of the alignment score discussed above: few bills exhibit meaningful policy overlap with other bills, but in the region of lower ideological distance we observe a greater occurrence of positive outliers, which arise from significant policy overlap.

In order to investigate this pattern more closely, we additionally provide lines for quantile regressions in the Figure 6. Figure 7 displays more details about these regression. Figure 5 displays the distribution without the quantile regression lines. Confidence intervals are calculated by resampling bills, which represents an implementation of the clustered nonparametric bootstrap proposed by [Harden \(2011\)](#). We see that there is no relationship between the ideological similarity of bill sponsors and the median alignment scores between bills. However, as the quantile we model increases—especially above the 90th percentile, we see that the relationship grows strong and negative in magnitude, and is statistically significant. These results both validate the use of text reuse as a measure of policy similarity, and reinforce the high precision and low recall nature of text reuse as a measure of policy similarity.

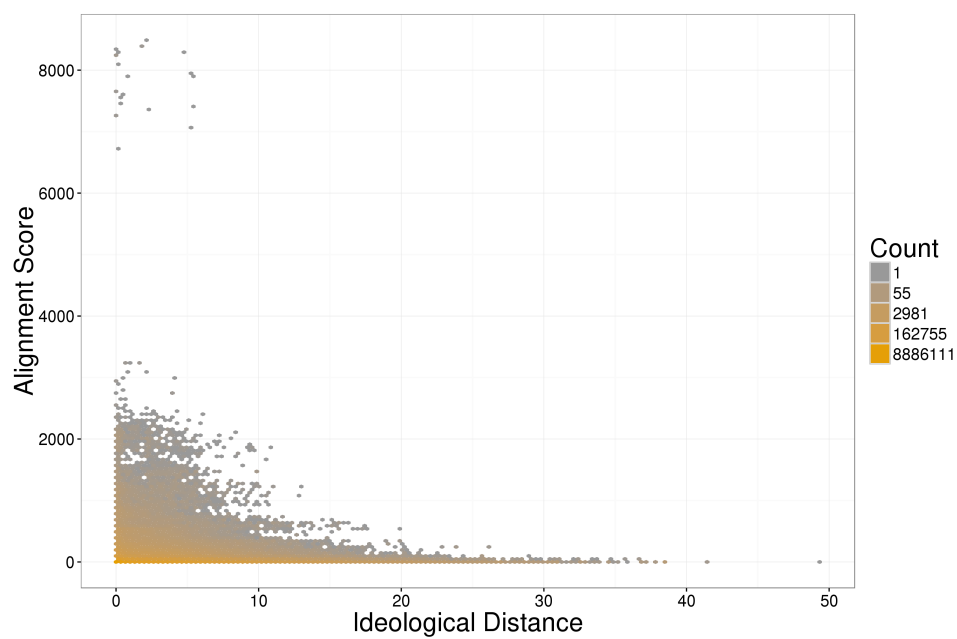


Figure 5: Hexbin plot of alignment score and ideological distance of all 50 million bill dyads.

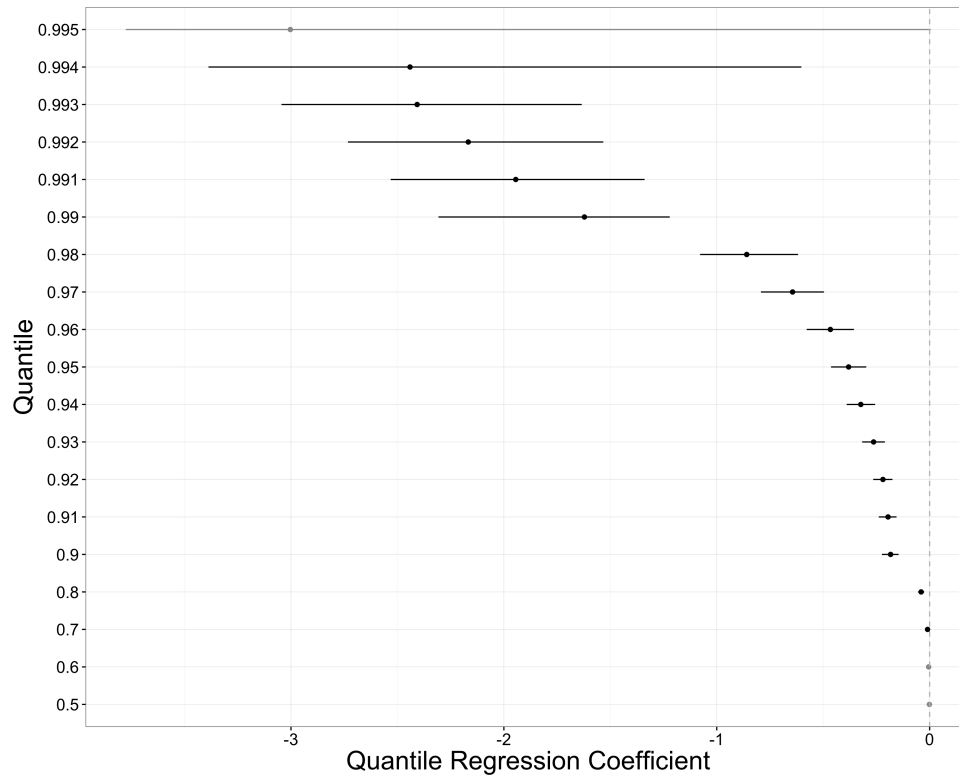


Figure 6: Coefficients of quantile regression for alignment score on ideological distance. Dots indicate the point estimate. Horizontal bar represent 95% confidence intervals obtained via the clustered bootstrap, [using 500 iterations]. Note that the x-axis is not in a natural scale



## 6 Conclusion

Scholarship on public policy and legislative politics relies heavily on measuring the content of legislation, especially with a relative or comparative approach. Manual comparison of bills is prohibitively time consuming when it comes to covering a large proportion of legislation introduced in one or more legislatures. We show that the automated detection of similar text strings in bills provides an effective approach to comparing bill contents. The log alignment scores serve as a highly valid summary measure of the similarity of two bills. We show high validity of this measure in three complimentary tests. First, it correlates with the presence of a diffusion tie inferred from patterns of policy diffusion. Second, it correlates with the ideological similarity between bill sponsors. Third, it exhibits extremely high precision in predicting whether two bills are listed in the NCSL policy area tables. We demonstrate the potential for using this data to test new or unexplored hypotheses on lawmaking in the states by testing whether bill text similarity correlates with campaign contributions to US state legislators.

The log alignment scores we derive provide a resource for scholars to test hypotheses of the causes and consequences of the introduction and adoption of similar policies—a measure which crosses different policy areas, states, and time. Where and when do similar policies cross state borders? Which legislators introduce similar legislation? Does lobbying by pressure groups result in the adoption of similar policies across states? Do similar patterns of campaign contributions to legislators predict similar policies in proposed legislation? Questions such as these can be directly investigated using the policy similarity measures we introduce.

A consistent result in our analysis is that the measure of policy similarity based on text reuse is high precision and low recall. As such, in future research we advise scholars to focus on upper quantiles of the distribution of alignments, especially when considering

measurements at the bill-level. This can be done through the use of quantile regression, or through thresholding on high alignment scores (e.g., 50+) to indicate the presence of highly similar policy proposals in legislation.

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# Appendix

*Sketch for a proof that SW alignment is globally optimal*

Notation  $F_i$  is the alignment of size  $i$  with  $i = 1, 2, \dots, (n + k - 1)$ .  $S(F_i)$  is the score of the alignment.

First show that the score in each cell is optimal:

1. There are three options for  $F_1$  (Gap in  $\mathcal{A}$ , Gap in  $\mathcal{B}$ , . This alignment is optimal when  $S(F_1)$  is maximized
2. Every alignment's score  $S(F_i)$  with  $i > 1$  when maximized, is composed of the score of the 'one-shorter' alignment  $S(F_{i-1})$  and the score of the  $i$ -th element. If not the score could be increased by choosing a different  $F_{i-1}$  that has a higher score.
3. The dp matrix contains all possible alignments. Since every cell is optimal, the highest score in the dp matrix must be globally optimal