

**Title:**

**The global recurrence and variability of kinship terminology structure**

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**Abstract**

The extent to which kinship terminology varies between linguistic groups is a long-debated but unresolved social and linguistic puzzle. Contemporary research shows that a six-category typology is overly simplistic, but no alternative typologies have reached broad acceptance. This paper takes a data-driven solution to this problem. Using data from the recent release of Kinbank, a global database of 1,156 kinship terminology, I quantitatively review the global diversity of kinship terminology to derive a new and more granular typology of kinship terminology. In a two-part analysis, I begin by showing that kinship terminology structure is more diverse than is often assumed across three metrics. Firstly, more than six types are needed to represent the global diversity of kinship terminology. Secondly, typological categories are not equally variable. Some categories may only contain identically structured terminology. Others may contain languages that only share a single feature. Finally, different subsets of kin (e.g. cousins vs grandparents) show different levels of structural stability. In the second part of the analysis, I explore the global distribution of the new typological categories, identifying globally and locally recurring terminology structures. The recurrence of some types suggests that there are universal constraints to kinship terminology structure. My analysis demonstrates how data can carve this semantic domain at its joints to identify observed clusters of diversity.

## Main text

The divisions of diversity within kinship terminology typology have been endlessly debated with little agreement (Godelier 2012; Godelier, Trautmann, and Tjon Sie Fat 1998; Kronenfeld 2006; Leaf 2013; Read 2013). The persistence of typological debate surrounds how to divide the recurring structures in the global diversity of kinship terminology in a way that captures the key features of structural recurrence, acknowledges the extent of diversity (Kronenfeld 2006), and has some predictive value. The most prevalent kinship terminology typology collapses diversity into six types, derived from a set of theoretically identified rules (Godelier 2012; Murdock 1949). The six types describe some key features of global kinship terminology diversity, but the generalness of the categories has made the classification of particular languages awkward (Kronenfeld 2006). Recent research has also shown that the existing typology presumes a symmetry between generations that is not supported (Passmore et al. 2021), and the typology's relationship to social structure only has regional support (Passmore and Jordan 2020). This paper will use a bottom-up, data-driven approach to carve this semantic domain at its joints to identify key and observed clusters of diversity. These findings will be of interest to linguists interested in semantic typology, and anthropologists who are interested in kinship system diversity.

Although contemporary research has called for new typologies (Kronenfeld 2006; Read 2013), the six-category typology is still widely used (Cronk et al. 2018; Stone 2014). The original labels of this typology are no longer suitable, so I use the descriptive titles: Lineal (equivalent to *Eskimo*), Bifurcate merging (equivalent to *Iroquois*, *Omaha*, *Crow*), generational (*Hawaiian*), and bifurcate collateral (*Sudanese*) (Godelier 2012). The categories of this typology are derived from the presence or absence of two rules, collaterality, and bifurcation (Lowie 1928). Two further categories are often included when we include

common variations of intergenerational skewing (when kinterms are used across generations). The six-category division of diversity does capture broad categorizations of global diversity, in particular, describing the ways some kinterms extend across genealogical boundaries (although it is not comprehensive). Lineal types delineate nuclear kin from extended family (*brother* vs *cousin* in English), Bifurcate merging types distinguish cross-relatives (parents opposite-sex siblings) from parallel (parents' same-sex siblings), generational types group all generational relatives together, and bifurcate collateral splits everyone apart. These classifications draw our attention to particular features of kinship terminology, but variability can occur across several other dimensions, such as relative age, gender of the speaker, or relative gender of the speaker (e.g. Nerlove & Romney, 1967a).

The recurrence of kinship terminology structure in unrelated languages (Murdock 1949; 1970; Nerlove and Romney 1967a) occurs at a rate much higher than is seen in other linguistic (grammar) or cultural (music) domains. The recurring structure presents almost like a designed system, for which scholars have long desired an explanation (Levinson 2010). Key theories propose that kinship terminology recurs because of cognitive constraints (Kemp and Regier 2012), or because of the constraints of social organization (Murdock 1949). Cognitive models propose that a culturally-defined communicative need trades off a cognitive demand for simple communication, which constrains the extent of kinship terminology diversity (Kemp and Regier 2012). Models of social structure suggest that structural social norms surrounding marriage, descent, and residence patterns, determine the cultural definitions of family and therefore the structure of kinship terminology (Murdock 1949). These approaches offer explanations for why kinship recurs, to build more direct causal models that relate language structure to external factors, we need to have a robust grasp of kinship terminology diversity and the recurring patterns.

76  
77 A typology will always underestimate kinship terminology diversity since its goal is to  
78 reduce diversity into broad descriptive categories. With specific regard to the comparative  
79 analysis of kinship terminology, we often ignore two dimensions of variation: first is within  
80 type variation, and the second is the culturally internal meaning of kinship. The data-driven  
81 approach I will describe in this paper offers new and quantitative approaches to  
82 understanding within-type variation in typological analysis. It is important, however, to  
83 acknowledge that typological analyses are unlikely to capture the importance of kinship  
84 terminology as culturally internal systems (e.g. (Carsten 2003; McKinnon and Silverman  
85 2005)). In any form of comparative analysis, it is difficult to define any concept (in this case,  
86 like "brother") in a way that it can be operationalized such that it is independent of language  
87 and culture (Evans 2020). This may lead to doubts about what typology can reveal.  
88 Nevertheless, the questions raised by patterns of similarity in kinship terminology between  
89 unrelated languages are too prevalent to have occurred by chance. One approach to minimize  
90 the impact of culturally-internal differences is to maximize the amount of comparable  
91 information and build a typology from the bottom-up, rather than the theoretically driven  
92 model the existing typology derives from. The evidence tells us that the existing typology  
93 relies too heavily on simplification to accurately represent global diversity, or to be useful in  
94 contemporary theoretical and empirical analysis. The goal of this paper is to shift the focus to  
95 include more variability.

96  
97 Although the study of kinship terminology is extensive (Kemp, Xu, and Regier 2018;  
98 Kronenfeld 2006; Murdock 1970; Read 2013; Whiting et al. 1988), global typological  
99 analysis has never been performed at the most granular level – the kinterm. Instead of  
100 persisting with the awkwardness of a proscriptive typology, this paper utilizes the recent

101 release of 1,156 kinship terminology, and 183,282 kinterms within the database Kinbank  
102 (Passmore et al. In Review) to generate a novel typology for kinship terminology that  
103 captures the observed diversity across a global sample of languages. The analysis of  
104 terminological diversity at the level of the kinterm allows us to observe diversity in a state  
105 that is reflective of the continuous reality that linguistic diversity often exists in, rather than  
106 using typological generalisations.

107

108 The Kinbank dataset covers speakers for 96% of the territories covered in Ethnologue, and at  
109 least 20% of every continent. Increasingly the granularity of the analyses, and using bottom-  
110 up analytical approaches, we can cut kinship terminology diversity at its joints. Through this  
111 approach, we can identify the key divisions across the large sample of observed terminology,  
112 rather than retrospectively applying languages to existing poorly fitting categories. The data-  
113 driven approach also lets us explore the global and local recurrence of the new types; the  
114 heterogeneous variability across kinship terminology categories; and propose a possible  
115 model of constrained change to explain the unequal frequency of kinship terminology  
116 structures.

117

118

## **The usefulness of deriving typology from a continuous morphospace**

At the most fundamental level, a typology is a set of categories describing known or theoretical diversity (Song 2018). Although categories are often the outcome of typology, the process of building typology is an overview of diversity, identifying which features of kinship terminology covary, and placing categories of systems together for further analyses (Round and Corbett 2020; Song 2018). In kinship terminology, further analysis might entail: identifying changing structural patterns across time and space (e.g. Passmore & Jordan, 2020), or identifying functional relationships to behavioral domains (Cronk et al. 2018).

In this analysis, I build a new typology using a morphospacial approach to delineate categories from the extensive Kinbank sample and use these to build a new typology. A morphospacial approach is the projection of observed diversity (languages) of kinship terminology on a continuous mathematical space, also known as a bottom-up or data-driven approach to typology. The continuous and multi-dimensional nature of this space means we can visually and algorithmically carve up the complex structures of kinship terminology while minimizing the amount of variation we abstract away from the analysis. Morphospacial approaches have already been successfully used to analyze diversity in biological (e.g. Pigot et al., 2020), linguistic (e.g. Hua, Meakins, Algy, & Bromham, 2021), and cross-cultural contexts (e.g. Kapitány, Kavanagh, & Whitehouse, 2020), to identify the principal dimensions of diversity. The continuous nature of the space not only allows the division of diversity but also allows the measurement of variability within each category. Oftentimes, typological categorization can often imply all languages within a category are identical, even though this is not true. A morphospacial approach allows us to measure how much variation typological categories contain. Creating categories that accommodate “fuzziness” allows the typology to group languages under general structural principles while acknowledging the

144 notion that terminology might not all be exactly alike. For example, the most common sibling  
145 terminology has four kinterms: elder brother, elder sister, younger brother, and younger  
146 sister. The Siouan language Hidatsa mostly shows this pattern, except with special terms for  
147 an elder opposite-sex sibling, making the language very similar to, but not identical the  
148 typological category (Morgan 1871). Building a typology using observed data means the  
149 categories of kinship terminology are closer to the observed patterns of diversity, cutting  
150 diversity at the joints and creating categories that most languages will fit into.

151

152 Carving diversity at the joints is a common goal for large-scale cultural analysis, but the  
153 incredible cross-cultural structure in kinship terminology, compared to other cultural  
154 phenomena, offers this semantic domain as a prime example of data-driven typological  
155 analysis. For example: within Kinbank cousin and sibling kinship terminology contain half as  
156 many structures as languages, 259 unique organizations from 506 languages. In a dataset of  
157 5,242 songs and 719 societies, there are only two identically coded songs, and 99% of  
158 languages from a sample of 2,430 languages have a unique grammar (Skirgård et al. 2022).

159 The structure of kinship terminology makes it ripe for quantitative typological analyses. With  
160 the release of Kinbank, we are now in a position to re-evaluate global terminological  
161 diversity and typology. Since the development of the extant typology, research on kinship  
162 terminology has developed more and new knowledge on the construction of terminology  
163 systems (e.g. Jones, 2010; Read, 2013). With the breadth and digitization of the Kinbank  
164 sample, we can develop a quantitative approach to identify clusters of similar terminology  
165 which will be the building blocks of a new typology that can feed into the ongoing debates.  
166 The representativeness of the Kinbank datasets allows the reassessment of the assumptions  
167 made and categories used to ensure existing typology accurately reflects the current  
168 understanding of the field.

169

## 170 **Methods: Building a pipeline to identify kinship terminology structure and variation**

171 To build a typology for kinship terminology from empirical data I employ a five-stage  
172 pipeline to quantify and compare kinship terminology structure, using the newly released  
173 Kinbank database (Figure 1). This is referred to as the kinspace pipeline from here on. First, I  
174 describe the dataset, then I describe each step of the pipeline.

175

176 The Kinbank database contains a global sample of 1,156 kinship terminology, and 183,282  
177 kinterms (Passmore et al. In Review). The Kinbank dataset is structured around two key  
178 properties, the kin category, and the kinterm. The kin category is a grid of genealogical  
179 relatives (with distinctions for the gender of the speaker) used to establish a language-  
180 independent yardstick for cross-linguistic comparison (Evans 2010; 2020; Passmore et al. In  
181 Review). The kinterm is the word (or form) applied to a particular kin category in a particular  
182 language.

183

### 184 **Steps 1 & 2: The structure of one kinship terminology.**

185 To represent kinship terminology structure, I build a numerical vector from a defined set of  
186 kin categories, which I call a *structural vector* (Figure 1). A structural vector compares the  
187 kinterm for each kin category to every other category, labeling a comparison with a “1” if  
188 words are the same between categories or a “0” if they are different. For example, figure 1  
189 shows the structural vector process for three kin categories, meB (male speaker's elder  
190 brother), meZ (male speaker's elder sister), and myB (male speaker's younger brother). The  
191 categories have the English kinterms *brother*, *sister*, and *brother* respectively. meB and meZ  
192 have different kinterms and English, meaning when compared we code a zero. Both meB and  
193 myB have the kinterm *brother* in English, so when these kin categories are compared, a “1” is



coded. The total number of comparisons depends on the set of kin categories being compared. The binary representation of a kinship terminology reconstructs the structure of kinterms for any language but will ignore any linguistic information within the terms themselves. The similarity of forms may provide additional information to the structure of a typology, but here I focus on structural diversity (See *Discussion*). After creating a structural vector for all languages, they are concatenated into a single structural matrix (Step 2; Figure 1).

### **Steps 3 & 4: Calculating kinship terminology similarity.**

The third step of the kinspace pipeline quantifies the distance between pairs of languages. The distance between languages is measured through a distance metric called Jaccard's distance. First, I calculate Jaccard's *similarity*, defined as the number of co-occurring features divided by the total number of features. Jaccard's similarity gives a value between 0 and 1, with values closer to 1 indicating more similarity. To convert the similarity measure to a distance, the similarity score is subtracted from one. Step 2 and 3 in Figure 1 provides a visual explanation of Jaccard's distance between English and Bontok. There are three comparisons in Step 2, which are indicated as shapes for visual purposes but are the same comparisons used in the previous step. Bontok has a single sibling term for all kin categories, unlike English which has two terms divided by gender. This means that when comparing meB to meZ, Bontok is coded as a "1", and English as a "0" (circle). When comparing meB to myB (hexagon), both English and Bontok use the same kinterm for both kin categories, so they are both coded as one. meZ and myB have different kinterms in English, but again they are the same in Bontok (square). In this example, English and Bontok have one feature the same, from a total of three features, resulting in a Jaccard similarity of 0.3, and a Jaccard's distance of 0.7. It is important to note that this distance measure ignores features that are absent in both languages. Within kinship terminology, many categories are unlikely to occur.

219 Some categories are theorized to never occur, like the rule of collaterality (Héritier 1981), and  
220 some do not occur simply because there are so many possibilities. Regardless of the reason,  
221 co-absent features are considerably more common than co-occurring features. Because of  
222 their frequency, including co-absent features in the similarity calculation inflates the level of  
223 similarity to a level where it is difficult to distinguish differences between different kinship  
224 terminology structures – hence, they are excluded. After each pairwise calculation is made,  
225 the distances are placed in a distance matrix (Step 4).

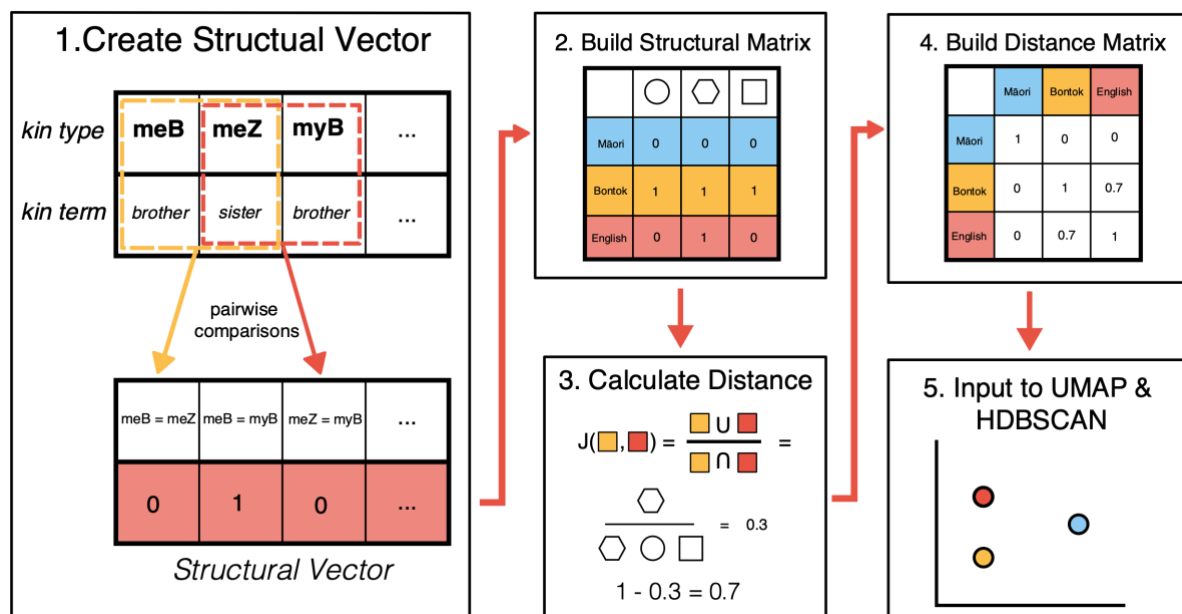
226

### 227 **Step 5: Identifying and visualizing clusters.**

228 The final step of the kinspace pipeline is to identify clusters of kinship terminology and to  
229 visualize kinship terminology diversity (Step 5). The similarity matrix is the input for the  
230 clustering algorithm, called hierarchical density-based clustering of applications with noise  
231 (HDBSCAN; (McInnes, Healy, and Astels 2017)). Unlike most existing clustering algorithms  
232 (e.g., K-means), HDBSCAN uses a measure of density within the morphospace to  
233 automatically identify the total number of clusters and calculate the probability of each data  
234 point existing within each cluster (or identify a language as an outlier). This approach  
235 minimizes human input (such as specifying the number of clusters), but also creates 'fuzzy'  
236 categories through probabilistic assignment, which is more reflective of the continuous reality  
237 in which kinship terminology (and many cultural phenomena) exist. Having assigned  
238 languages to clusters, I calculate the inverse Simpson's index (ISI), *post hoc*. ISI measures  
239 whether a cluster contains many language families (scores close to one) or very few language  
240 families (scores close to zero), relative to the size of the category. This measure tells us  
241 whether a particular cluster is a result of a specific linguistic lineage or recurs across the  
242 world. A supplementary algorithm, UMAP, projects the multi-dimensional kinship  
243 morphospace into two dimensions allowing the visualization of observed diversity. In the

UMAP projections, the important metric is the distance between points in space, rather than the interpretability of the X and Y axes (See Figure 2a for an example).

In summary, the kinspace pipeline first builds binary structural vectors of kinship terminology. Jaccard's distance calculates the similarity between all languages for some subset of kin categories. The Jaccard's distance matrix is passed to HDSCAN to probabilistically identify clusters of kinship terminology. The same distance metric is also passed to UMAP to project the multi-dimensional space into two dimensions for visualization.



**Figure 1:** A visualization of the pipeline used in this paper. Step 1 calculates the structural vector of each kinship terminology, which is concatenated in Step 2 as a structural matrix. Step 3 calculates the pairwise distances between all languages in the structural matrix, which are contained in Step 4 as a distance matrix. Step 5 sees the constructed data as an input matrix in the HDBSCAN and UMAP algorithms.

**Proof of concept: A morphological approach reproduces robust sibling typology.**

A typology of sibling kin types typically considers eight kin categories: elder brother, younger brother, elder sister, younger sister, and then for each, whether the speaker is male or female. These eight categories can be organized into 4,140 possible different combinations<sup>1</sup>, but two independent analyses of sibling typologies show that there are only around 12 types (Murdock 1968; Nerlove and Romney 1967b). The typology initially proposed by Nerlove and Romney categorized 96% of their 245-language sample, making this subset of kinship terminology typology the most complete and robust typology within the domain. I apply the kinspace pipeline to Kinbank sibling data to reproduce this typology as a proof of concept.

In Kinbank there are 864 languages with a complete set of sibling terms. Applying the kinspace pipeline to siblings returns 15 clusters, twelve categories align to the original typology, with three additional categories identified. Figure 2a shows the output of the kinspace pipeline, where each point is a language, and languages are colored by their algorithmically assigned clusters. To reiterate, the important dimension of the UMAP projection is the distance between points (like a geographical map), rather than the distance along the axes. Clusters are labeled in order of frequency, using the alphabet. Grey-colored languages are outliers. Figure 2a highlights the advantages of a morphospacial approach to kinship terminology diversity, and to accommodating cultural variation in general, by representing the extent of diversity visually and continuously. The continuous space allows further inspection of typological decisions and an understanding of when typological categories are supported and where they are weak. It shows where outliers lie relative to the observed population and the uninhabited areas of diversity can direct us toward unlikely terminological structures.

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<sup>1</sup> This is the eighth Bell number,  $B_8$

285

286 The kinspace pipeline aligns languages with the Nerlove and Romney categories around 81%  
287 of the time (adjusted Rand index 0.81). I attribute differences between the Nerlove &  
288 Romney and kinspace categories are attributed to failures in the existing typology, rather than  
289 the kinspace pipeline. The three additional categories occur because Nerlove and Romney  
290 lump "derivative" or "reversed" types into single categories, which the kinspace pipeline  
291 separates. For example, type 3 from the Nerlove & Romney typology (terms for elder  
292 brother, younger brother, and a single sister term) groups the mirrored structure (terms for  
293 elder sister, younger sister, and a single brother term) into one category, which the kinspace  
294 pipeline separates into two categories. There are five other instances of lumped categories  
295 within the Nerlove and Romney typology, of which the kinspace pipeline identifies three.  
296 Although these types were previously identified, they were not typologically separated due to  
297 their infrequency. If we are interested in how typology might elucidate other patterns of  
298 behavior, the separation of mirrored types is an important step in the analysis of kinship  
299 terminology diversity. Of the 864 languages 94% can be categorized as one of the 15 types,  
300 with 51 languages identified as outliers. The outlier detection component of this pipeline is an  
301 interesting area for future research but will not be explored further here.

302

303 The frequency of each sibling type is similar in both the Nerlove and Romney and Kinbank  
304 datasets (Figure 2b). Replicating the frequency of types across two independent samples  
305 suggests that there are robust systematic reasons for the recurrence of sibling terminology.  
306 However, the differences in frequency patterns could be misleading due to the relatedness of  
307 languages (Bromham 2022). Briefly, if two languages are thought to be close descendants of  
308 an ancestral language, the likelihood that they both contain the same kinship system is higher  
309 than chance. This means that languages are not independent of each other, and counts will

310 inflate the importance of types that exist amongst highly related languages. Using ISI scores  
311 to account for language family relatedness shows that the most globally prevalent type is also  
312 found in most families (type A; *See supplementary materials*). The most frequent system  
313 differentiates siblings on gender and age (elder brother, younger brother, elder sister, younger  
314 sister; cluster A or Nerlove and Romney type 6; ISI = 0.92). The most regionally restricted  
315 type, L or Nerlove and Romney type 8 are almost exclusively found in Austronesian  
316 languages within Papunesia, with a lone Tupian language presenting the same structure (ISI =  
317 0.14). This category contains three kinterms: a male speaking to their sister, a woman  
318 speaking to their brother, and speaking to a same-sex sibling (Table S2).

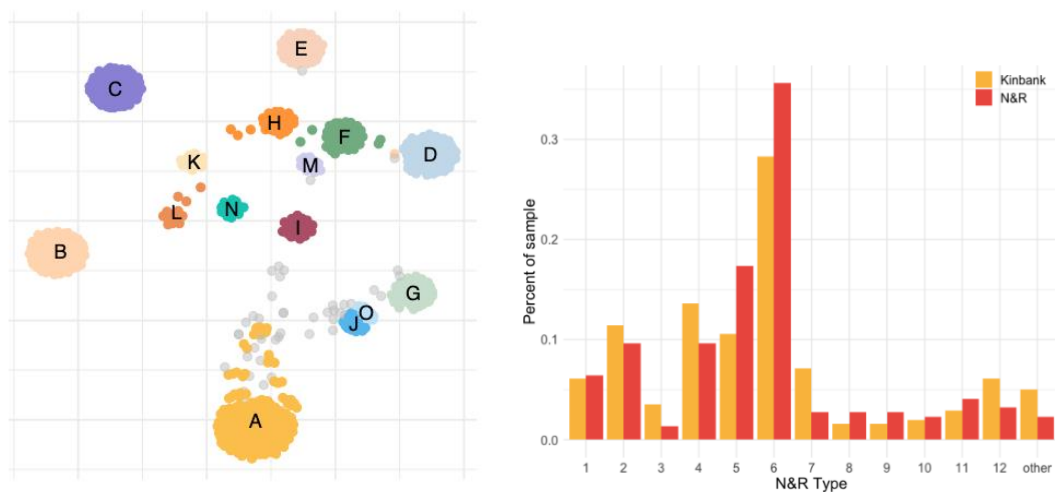
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320 The reproduction and improvement of the sibling typology provide evidence for how the  
321 kinspace pipeline can elucidate a more robust typology of kinship terminology. By creating  
322 types based solely on structural properties, I parse three additional categories from observed  
323 terminology. Although these had been previously identified, the data-driven approach  
324 highlights the importance of diversity over simplicity in typology by forcing the division of  
325 reciprocal organizations. By introducing the Inverse Simpsons Index as a measure of cross-  
326 cultural validity, I also add further understanding to the pervasiveness of structures in a  
327 global sample. The ISI presents an opportunity to understand when a type is likely to have  
328 arisen through independent innovations, and when it is the result of a particular cultural  
329 niche.

330

331 Having shown that the kinspace pipeline can return expected results within siblings, I apply  
332 the kinspace pipeline to four other kinterm subsets following existing divisions in the  
333 literature (Murdock 1970). They are cousins and siblings, parents and parents' siblings,  
334 grandparents, and finally, children and niblings (siblings' children). This pipeline provides us

with the cluster's descriptions, frequencies, validity, and diversity statistics described above for each subset (Table 1). Traditionally, kinship terminology has been treated as a single coherent system, but recent research has shown that intergenerational terminology harmony is relatively low (Passmore et al. 2021). By analyzing generational subsets of kinship terminology separately, we can compare and contrast how the structure varies in different parts of kinship terminology. This generational approach notably ignores the analyses of inter-generational kinship terms, also known as skewing. It is possible that the kinspace pipeline could be applied to explore diversity in these areas, but this would require a level of attention the current paper does not have sufficient space for.



**Figure 2: A)** A UMAP projection of the sibling structural diversity. Each dot indicates a language, and the distance between dots indicates similarity. Letters and colors indicate clusters identified by HDBSCAN. The letters align with a description of the category in the supplementary tables. **B)** Proportion of the 12 sibling types from the Nerlove and Romney (1967) and Kinbank samples.

**Morphospace clusters show more categories needed to capture diversity.**

Across all subsets, the kinspace pipeline suggests many more types than are perceived in wider literature (e.g. Cronk et al., 2018; Stone, 2014). The kinspace pipeline reveals 17 cousin clusters, 14 clusters for parents' and parents' siblings, 8 grandparent clusters, and 19 sibling clusters (Table 1). Descriptions of the types within each subset can be found in the supplementary tables.

An important typological question is how much does this additional variation matter when analyzing global patterns? Some theorists have already proposed that it is safe to abstract some variation to understand the general principles guiding kinship terminology (Kronenfeld 2006). However, the generalizations only make sense in the light of diversity. Without establishing the extent of diversity before abstraction, it is impossible to know where simplification is useful, and when it is ignoring important variation (Evans and Levinson 2009). The morphological approach used in the kinspace pipeline allows us to assess the validity of categories by analyzing the variation in terminological structure within a subset of kin terms, and by analyzing the variation within identified clusters. In the next sections, I explore the type-internal and between-generation variability alongside the post hoc ISI measure of global vs local recurrence to understand which structures of kinship terminology recur over the world and compare the stability of the new categories.



**Table 1:** Summary of the number of each kinterm subset showing: The number of languages analyzed, the number of unique structures in that subset, the number of clusters suggested by HDBSCAN, the average silhouette score for that subset, and the number of theoretical possibilities for that subset.

Subset	Languages	Unique Types	N Clusters	Silhouette	Theoretical categories
Siblings	864	87	15	0.95	4,140
G <sup>0</sup>	506	259	17	0.22	1.57 x 1,035
G <sup>+1</sup>	728	91	14	0.73	5.17 x 1,013
G <sup>+2</sup>	887	13	8	0.97	15
G <sup>-1</sup>	604	179	19	0.73	5.17 x 1,013

### Cousins are the least structured subset of kinterms.

Variability within types is often ignored in the development of a typology. By using a morphospacial approach to typology, the pressure to exclude within-type variation is partially mitigated. Analyzing the variation also creates a new dimension of typological analysis. Generational analyses of kinship terminology create two dimensions of variability: variation within generations of kin and variation within each typological category. Measurement of within-type variability improves our understanding of real-world diversity in two ways. First, it makes it clear that languages are not literal representations of the languages in the categories they are placed in. Second, it quantifies the rigidity of any particular category. I measure variability on these levels by applying post hoc statistics of cluster validity and cluster tightness. To measure cluster validity, I use silhouette scores. Silhouette scores measure whether a language is closer to the center of a cluster different from the one they were allocated. We can aggregate this measure within a cluster to identify how well-defined a

category is. A score close to one indicates a well-defined category, a score close to minus one indicates an invalid category, and a score close to zero indicates a poorly defined category. The average score within a generation provides us with a comparable measure of structure between subsets, and the average score for a type does the same for a particular category. In some instances, silhouette scores can be misleading, such as when there are very close, but separate clusters. In these instances, I use cluster tightness. Cluster tightness is a similar metric, which measures the average distance between all within a cluster. A value close to zero indicates a tight cluster.

Cousins and siblings (i.e., analyzing all cousins and siblings simultaneously) are the least structured kin subset of those analyzed, with an average silhouette score of 0.2 (table 1). Comparatively, grandparents and siblings show the most structure (Silhouette score for grandparents = 0.88; Silhouette score for siblings 0.85), followed by niblings (0.66) and parents and parents' siblings (0.63). Cousins and siblings contain more combinatorial possibilities than other subsets. For example, the set of 40 cousins and sibling kin types have  $1.57 \times 1,035$  possible organizations, whereas the set of 16 sibling terms only has 4,140 possibilities, and a set of four grandparent terms only have 15 possible organizations. However, parents and parents' siblings, and children and niblings have similarly high numbers of theoretical organizations but maintain more structure than observed in cousins.

This paper does not quantitatively explore why cousins are more variable than any other subset, but mixed evidence suggests cousin organization is under more external co-selection (e.g. pressures from changes in social structure) than other subsets of kinship terminology, which aligns with this finding (Racz, Passmore, and Jordan 2020; Trautmann 1981). However, there is also evidence contrary to this claim (Sheard et al. 2020). Similarly, changes

in Indo-European kinterms has been found to be faster in cousin terms, over parental or sibling terms (Racz et al. 2019). For example, a dramatic reduction in the population size of the Kuikuru (Brazil) meant that cross-cousin marriage practices were no longer feasible, resulting in a terminology change from having bifurcate collateral distinctions in cousins to a generational system (Dole 1969).

#### **Cousin terminology containing crossness contains more variation.**

A common implication for kinship terminology typology is that each category within the typology is equally variable. This is widely considered to be not true but has not been quantifiable. Here, I explore the variability within each cousin cluster (Figure 3, Table 2), although similar explorations could be performed for each generational subset. Within cousin terminology, there are clusters of terminology that contain very little variation, and some which contain a lot of variation (Figure 3). The low-variability clusters tend to be variations of a lineal or generational type, and the clusters with lots of variation tend to contain bifurcate merging or bifurcate collateral features. There are nine Lineal variations found by the clustering algorithm, which all have a distinction between siblings and cousins, but have different ways of organizing those relatives. For example, Cluster A has a single term for all children of parents' siblings, a term for an elder sibling, and a term for a younger sibling. Cluster N on the other hand has a term for parents' siblings' children who are older, and one for those who are younger, a term for elder brother, a term for elder sister, and a term for a younger sibling. Similar variations are seen in the other Lineal clusters. Across all lineal types, however, most languages are identically structured, seen in the low average distance scores and the high counts of identical structures in table 2.

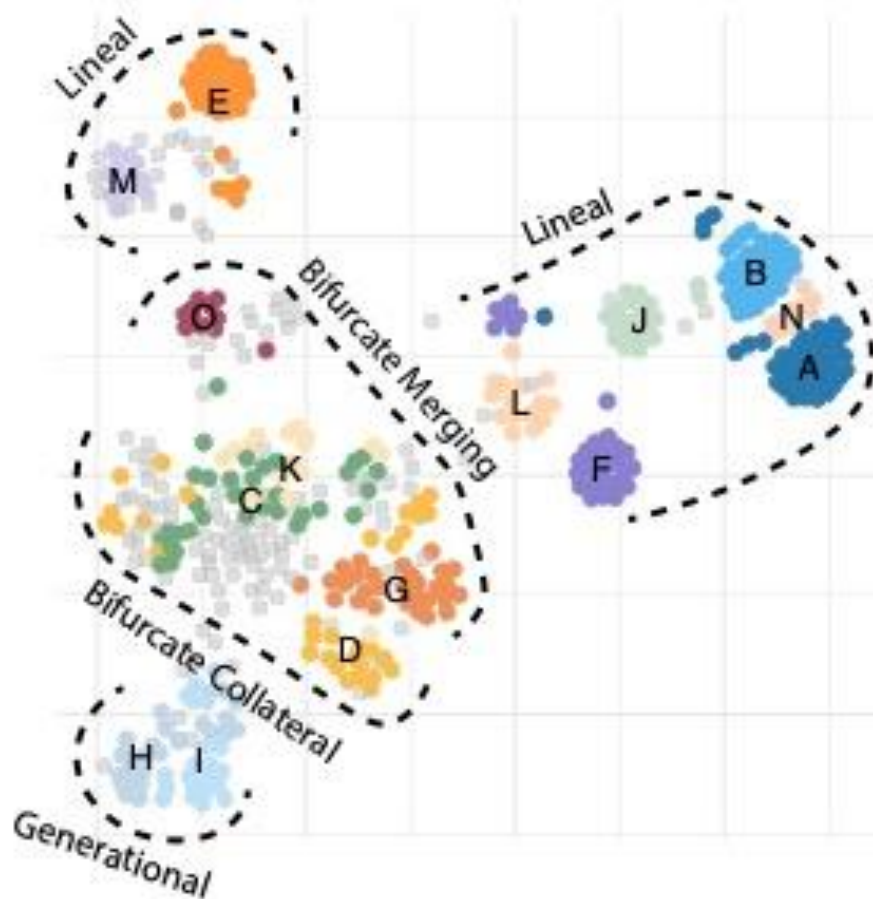
445 Bifurcate merging and bifurcate collateral terminology are defined by their variants of  
446 crossness. In the case of cousins, crossness is when the children of your parent's siblings are  
447 distinguished depending on whether they are your parent's same, or opposite-gendered  
448 siblings. For example, the father and the father's sister are opposite genders to each other, and  
449 therefore the children of the father's sister are crossed. Bifurcate merging types separate cross  
450 cousins from other relatives in that generation but merge siblings and parallel cousins.

451 Bifurcate collateral types divide this generation into categories for siblings, parallel cousins,  
452 and cross-cousins. The kinspace pipeline identifies three different crossed clusters: G, K, and  
453 O. Within this space is also the C cluster, which contains distinct terms for each relative, and  
454 cluster D which is classed as a lineal type, however, both appear to be poorly defined  
455 categories. Clusters G, K, and O are more variable, compared to the tightly defined lineal  
456 clusters (e.g., A or B). K is the second most variable cluster with a within-cluster distance of  
457 27% less than the average distance of this space. G has a within-cluster distance of 45% less.  
458 For comparisons, Cluster A, B, and N have within-cluster distances of 93%, 96%, and 100%  
459 less than the average distance. Languages within each of clusters A, B, and N are almost  
460 structurally identical.

461

462 Using cluster distance measures, alongside visualizations of the continuous kinship space, I  
463 have shown that all clusters are not equally variable (Figure 3). This finding illuminates a  
464 tension in typological analysis: the use of categories to define a fluid space. Sometimes  
465 typology can cut observed diversity into identifiable divisions (for example between the  
466 clusters A, B, and N), but in other situations, the divisions are less clear (as amongst the  
467 crossed-types). Understanding the variability of types is a feature of bottom-up data-driven  
468 analysis and places us in a position to parse what variation we are interested in and what  
469 variation can be ignored. I have shown that there are more types of lineal organization than

are commonly acknowledged, but also that lineal types show significant constraints. Why different organizations are more flexible, and how that might relate to internal or external co-selection is an important area for future research.



**Figure 3:** Projection of cousin and sibling terminology, colored by clusters. Lettered labels are the centroid of each cluster. Dotted lines indicate general boundaries between types and are labeled by existing terminology (Godelier, 2012).

479 **Table 2:** Cousin and sibling clusters. Cluster labels link to Figure 3. Columns show the  
480 cluster label from the pervading broad typology (Broad Category), the number of languages  
481 in that cluster (N Languages), the number of languages with identical structure (Modal  
482 Count), and finally, the Inverse Simpson's index as a measure of within-cluster diversity  
483 (Diversity).

Cluster	Broad Category	N Languages	Modal Count	Diversity	Silhouette	Av. Distance
A	Lineal	46	37	0.45	-0.63	0.04
B	Lineal	39	33	0.92	-0.34	0.02
C	Descriptive	33	7	0.83	-0.07	0.64
D	Lineal	32	3	0.84	0.25	0.47
E	Lineal	32	25	0.45	-0.2	0.09
F	Lineal	31	24	0.19	-0.53	0.10
G	Bifurcate merging	29	3	0.33	0.42	0.37
H	Generational	24	6	0.16	0.34	0.33
I	Generational	21	10	0.43	0.61	0.26
J	Lineal	20	18	0.76	0.96	0.00
K	Bifurcate merging	17	2	0.69	0.24	0.48
L	Lineal	15	4	0.68	-0.39	0.06
M	Lineal	14	12	0.46	0.87	0.02
N	Lineal	11	10	0.78	1	0.00
O	Bifurcate collateral	10	3	0.62	0.86	0.15
Outlier	-	132	-	-	-0.27	0.79

484

## **Kinship terminology balances constraint with diversity**

The focal message of this paper is that kinship terminology is more varied than the existing typology presents and that by using a data-driven approach, we can incorporate this variation to develop a new typology. But typology is only possible in kinship terminology because of the prevalence of recurring structures seen across the world. The least structured subset of kinterms, cousins and siblings, contains half as many structures as languages, 259 unique organizations from 506 languages. This gives a ratio of 1.95 languages per unique structure. Nibling organizations have a ratio of 3.4 (179 structures from 604 languages), parents and parents' siblings' organizations have a ratio of 8 (91 from 728), and siblings have a ratio of 9.9 (87 from 864). Grandparents can be organized in 4,140 possible ways accounting for gender and sex of speaker distinctions, however, since the gender of the speaker is never observed in the dataset there are only 15 possibilities, of which we observe 13 across 887 languages, a ratio of 68. Typology is useful in the analyses of kinship terminology because there is a significant structure to divide. There are many possible ways to organize kinship terminology, but we only observe a small subset.

The ratio of counts points out that kinship terminology contains more structure than other domains. Within each subset, however, types do not recur with the same frequency. This may be because some areas of the globe are sampled more than others. Comparing diversity scores controls for that imbalance to identify which structures recur globally and which recur locally (Table 2 for cousin type diversity). Within all subsets, diversity scores range between 0.1 (very few language families relative to the frequency) to around 0.9 (lots of language families relative to the frequency). Figure 5 shows the proportion of languages within a particular cluster against the diversity score for that cluster. In each cluster there tends to be one type that is more frequent than any other. The most frequent type is also found in many places

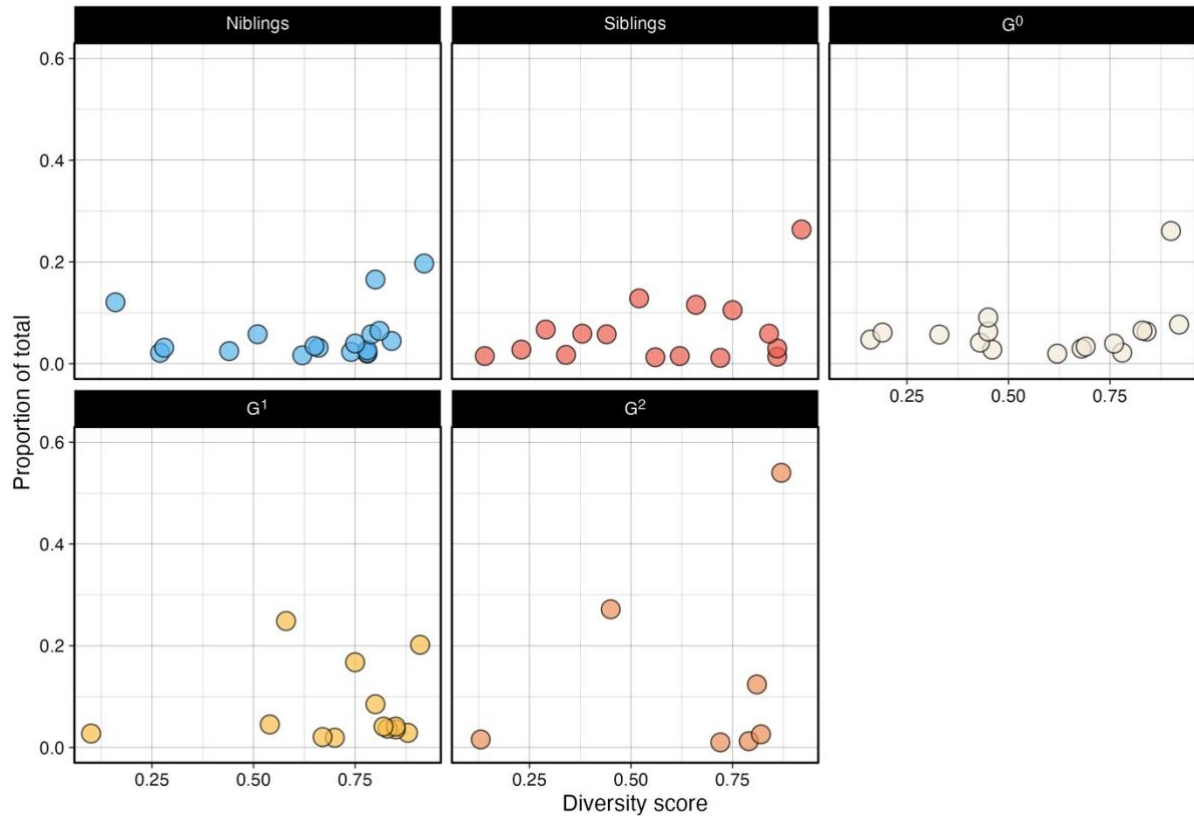
across the globe (i.e., has a high diversity score). There is no apparent relationship between frequency and diversity, however. Some structures show local distributions, and others are found almost everywhere. The recurrence and frequency of some types around the world suggest there are some statistically universal constraints to kinship terminology (Savage et al. 2015), but the appearance of localized types means that these organizations are likely not determined by their environment, but may be guided by them.

Kinship terminology have been shown to balance simplicity and informativeness (Kemp and Regier 2012). The balance of these opposing forces explains why we don't observe many of the theoretically possible kinship terminologies but leaves open why some types occur around the world and others do not (Figure 5). A simple conclusion might be that across the globe some kinship systems are more common. Identical kinship systems will need to convey the same kinship information, and therefore means some kinship terminologies are more common. However, this assumes the relationship between kinship terminology and kinship systems contains a one-to-one relationship, which research has shown is unlikely (Passmore and Jordan 2020).

An alternative explanation is that kinship terminology is constructed from a set of statistically universal rules which in combination create a subset of structural possibilities from a large theoretically possible space (Jones 2010a). The rules are combined in different orders to convey kinship information, but different orders can result in a convergent structure, implying a difference in meaning (Wierzbicka 1987). For example, Algonquin (Algic language family, Canada) and Yandruwandha (Pama-Nyungan, Australia) have identical structures when comparing kinterms for parents and parents' siblings. Both languages have five kinterms for the 20 parent and parents' siblings' kin categories: terms representing the



categories father, father's brother, father's sister, mother and mother's sister, and mother's brother. The geographic distance between these societies suggests that their similarity is not a result of inherited systems, but from convergence in structure.



**Figure 5:** The proportion of languages within each cluster as a total of all languages, by subset. Circles are sized by diversity scores. More frequent types are often diverse, but not more so than less frequent types.

### Types can be connected through minimal change, but it does not constrain recurrence.

To prove that the recurrence of kinship terminology could be the result of convergent evolution, I show in this section that all the types identified through the clustering process can be connected through minimal rule changes, creating a network of change. To build this network, I leverage existing generative models of kinship terminology. Generative approaches to kinship terminology are a popular tool for understanding structure (Greenberg

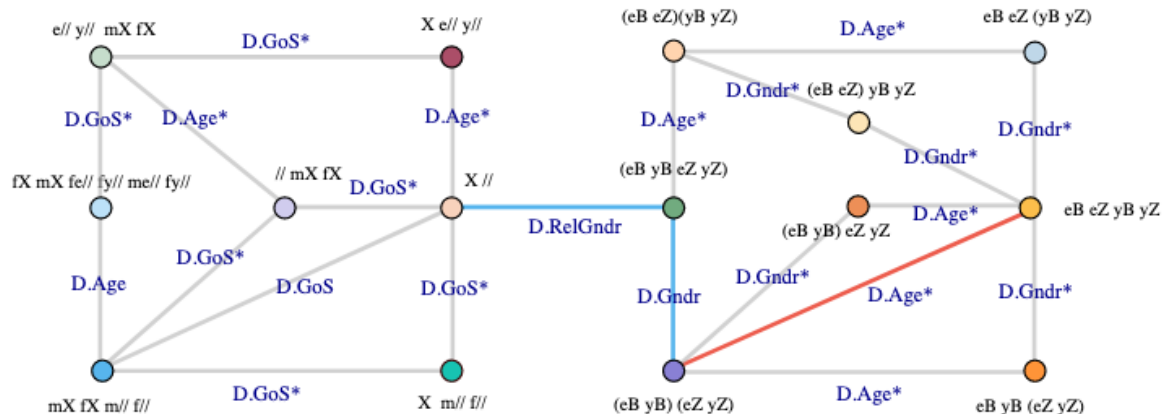
1949; Hage 1997; Jones 2003a; 2003b; 2010a; Read 2013). As a general description, the theories present some subset of rules or equations, that can be combined under a set of conditions to generate a set of possible kinship terminology structures. Often, the rules that are applied have some form of universality, whether that be a set of *primitives* (Greenberg 1949), a universal set of faithfulness constraints (Jones 2010a), or a formalized system of kinship algebra (Read 2013). These theoretical and rule-based representations of kinship terminology might not explain how humans think about kinship (Levinson 2010), but they are useful tools for understanding diversity and change. In the past, these generative approaches have been manually applied to small datasets to establish their relevance, however, datasets like Kinbank mean there is an opportunity to study these rules at a term-based level without precluding which dimensions or primitives are most important.

560

Each generative approach has costs and benefits to help our understanding of kinship terminology. For simplicity, I focus on the Optimality theory from here on (Jones 2010a; Smolensky and Prince 1993). Optimality theory presumes that there are some set of universal faithfulness constraints that are applied in rank order (or left unused) to generate a kinship terminology organization for the communicative need of a society (Jones 2010b). For example, we can generate all types in the sibling typology above by applying and permuting four rules: *Distinguish Gender*, *Distinguish Gender of Speaker*, *Distinguish Relative Gender*, and *Distinguish Relative Age*. The most common type, a system of four terms based on gender distinctions and relative age distinctions, could be derived from applying the *Distinguish Gender rules* and *Distinguish relative age rules*, in any order, to create the four kinterm categories. An organization where relative age exists in male siblings, but not female siblings can only be achieved by applying rules in a specific order. First, terms must be separated via a *gender distinction*, then applying the *relative age* rule is applied to male

siblings only. The application of Optimality theory to kinship terminology was presented as a framework that could generate diversity, but by using the description of the rule we can utilize this model to understand evolutionary models of change.

Although a generative approach looks to explain terminological diversity, kinship terminology is also not randomly sampled from a space of possibilities. Rather, they are constrained by the histories of the languages and cultures from which they originate (Jordan and Dunn 2010; Sheard and Jordan 2020). The temporal constraints on kinship structure mean that not all structural changes in kinship terminology are equally likely to occur. For example, it is unlikely that a system that distinguishes siblings by relative sex (a term for same-sex sibling and a term for opposite-sex sibling) will spontaneously change to distinctions based on gender and relative age (separate terms for elder brother, younger brother, elder sister, and younger sister). From an optimality theory point of view, a change between these two systems requires the order of rules to be completely reshuffled. A more parsimonious model would be that small changes are most likely. The smallest changes occur in the lowest-ranking rules. Using this assumption, we can create a network of minimal change by identifying which types change into other types with a minimal change in rules. A minimal change network is displayed for siblings in figure 5. Figure 5 shows that a change from a system of gendered sibling terms to a single term for each genealogical category (red line), requires the addition or subtraction of the rule *Distinguish Age*. To change from the same gendered sibling system to a relative gender system requires at least two rule changes (blue lines): a loss of the *Distinguish Gender* relative age, to a system containing one sibling term for all siblings, and the addition of the rule *Distinguish relative gender*.

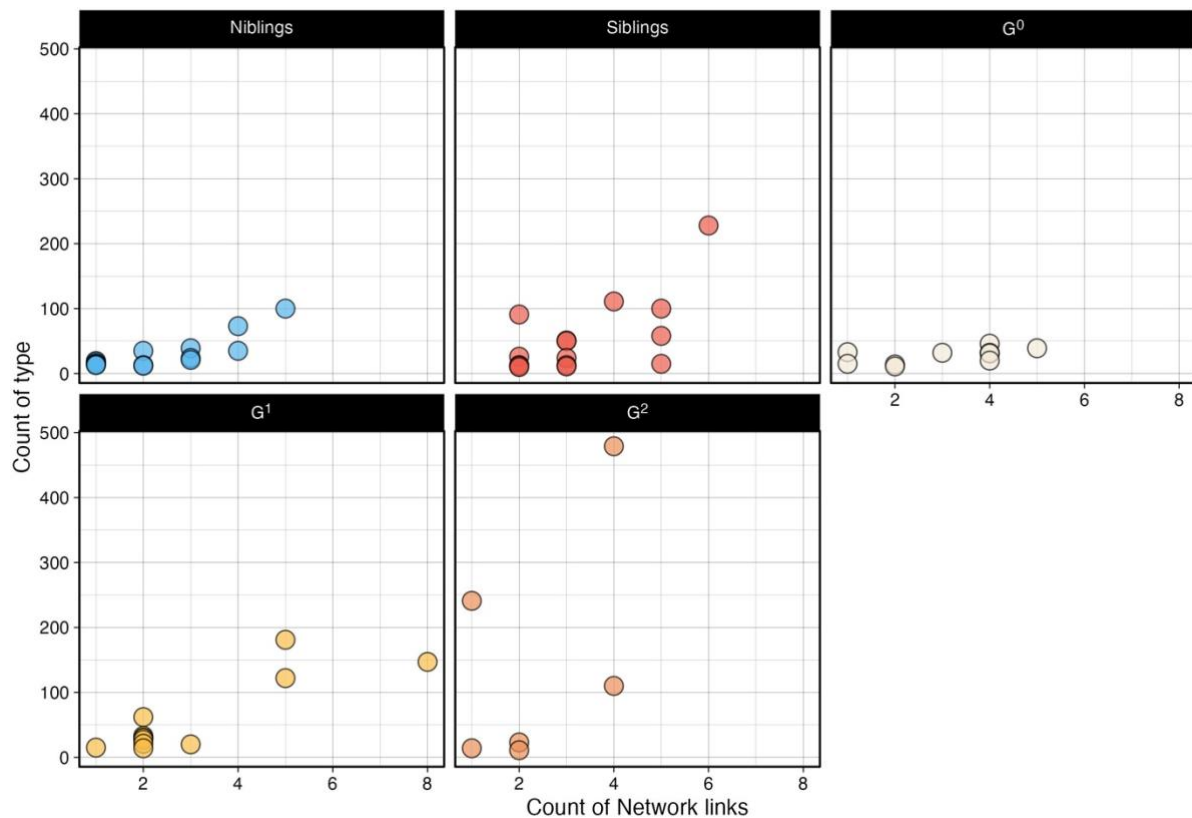


**Figure 5:** Network of minimal change within the sibling typology. Each node is an organization and is described using the kin notation described in table S1. Each edge is labeled with a full or partial (\*) rule change. *D* is short for distinguish, followed by either GoS (Gender of the speaker), Age, RelGndr (Relative Gender), or Gndr (Gender).

The most notable outcome of this network is that some structures have more connections than others. For example, there are five ways to move into the elder brother, younger brother, elder sister, and younger sister sibling organization (Figure 5: yellow, middle right-hand side). But only two ways to move into a system with words for elder brother, younger brother, and a single sister term (Figure 5: orange, bottom right). It is also notable that the most connected nodes are often also the most frequent (Figure 6). A Bayesian simple linear model between the frequency of each type, and the number of network links, with random slopes for the kin subset, suggests there that every additional link in the network will result in around 20 more occurrences of that type.

However, as stated above, raw count correlations can be misleading on account of the relatedness of languages. Equally, the number of edges is a crude measure of the influence within a network. It is also necessary to account for the importance of neighbors. That is, if a node and its neighbors are well connected, that node is likely to contain a shorter distance on

average to all other nodes. If a node is well connected and its neighbors are not, then the node will have a comparably lower connection to the network as a whole. Building the same models but using measures of diversity to account for linguistic history (figure 5), and *strength* as a measure of network connectedness, shows no relationship between the recurrence of a type around the world and its position in a network. So, although raw counts support the network relationship, this is likely driven by the oversampling of some terminology structures. When we control for sample bias, the effect is considerably weaker, offering little support for this model of constraint.



**Figure 6:** Scatterplots showing the raw relationship between the frequency of a particular typological category against the number of network links that type has. Each graph shows the relationships for a subset of kin categories. Each dot is a category from the data-driven typology.

633

## 634 **Discussion**

635 This paper presents the largest comparison of kinship terminology to date (1,109 languages).  
636 It reveals through quantitative analysis, structured variability within categories of existing  
637 typology. The returned clusters are not the result of comparing minutiae, but present  
638 identifiable differences in kinship terminology structure. Although the diversity of types from  
639 the clustering analysis is higher than the existing typology, the quantitative approach shows  
640 that the integrity of different kin subsets is also variable. Siblings and cousins show a high  
641 level of systematicity, with few languages containing structures outside the identified  
642 clusters. Cousins on the other hand are considerably more variable. The existing hypothesis  
643 suggests that cousin terminology is more prone to the impact of external social influence  
644 (Guillon and Mace 2016; Murdock 1949; Whiting et al. 1988). Research on the relationship  
645 between kinship terminology and behavior found only regional relationships but concluded  
646 this may be due to an insufficient typology (Passmore and Jordan 2020). Using the clusters  
647 and structural vectors presented in this paper allowed for a more granular categorization of  
648 diversity which future research can leverage to create new knowledge on the diversity and  
649 evolution of kinship terminology.

650

651 This paper also reveals that some identified categories are more variable than others. This  
652 was particularly the case within cousin organizations. Lineal cousin organizations were more  
653 strictly defined than cousin organizations that contained crossness, which was highly  
654 variable. The study of crossness has been a long-term focus of anthropological study because  
655 of its implications on contemporary and historical social organization, with specific regard to  
656 cousin marriage (Tjon Sie Fat 1994; Trautmann 1981; Trautmann and Whiteley 2012). The  
657 analysis of variability in cousin terminology points out that although theoretically derived

658 crossness models show how particular structures might emerge (Tjon Sie Fat 1994), observed  
659 crossed terminologies have complex and often unique patterns. Identifying the extent of  
660 diversity within crossed systems raises the question of how generalizable crossed systems can  
661 be. The kinterm-focused database Kinbank will be useful in identifying whether we can parse  
662 key features of crossed systems from the cultural nuances observed when quantifying their  
663 diversity.

664

665 The paper has shown that kinship terminology is more diverse than existing typology might  
666 suggest, it is also likely an underestimate of kinship terminology diversity. Kinbank is built  
667 on a grid of genealogical distance, which creates a language-independent yardstick to aid in  
668 comparative analysis. I use this grid to make comparisons of structure, but there are ignored  
669 subtleties when only considering structure. For example, English and Spanish sibling  
670 terminology are structurally identical, but the Spanish terms for brother and sister (*hermano*  
671 and *hermana*) are morphologically much more similar than their English counterparts.

672 Exploratory analyses performed during this paper found that using form similarity created too  
673 much variability to parse a coherent story, but this type of analysis is worth exploring in the  
674 future. A historically important aspect of kinship terminology has been the presence of  
675 intergenerational skewing or intergenerational kinterms. This paper focused on generational  
676 divisions, following earlier categorizations (Murdock 1970). There have been attempts at  
677 applying this approach to intergenerational structures (see (Passmore 2020)), but the  
678 importance of the generational patterns deserves more central attention than can be provided  
679 here and should be the focus of future Kinbank work.

680

681 A more fundamental loss of diversity occurs through the language-external measure of  
682 kinship terminology, which ignores much of the language-internal variation (Read 2013;

Wierzbicka 2016). The key language-internal dimensions that could be informative in a comparative instance are the breadth of kinterms (Barnard 1978), the meaning of kinterms (Danziger 1993), and within-language variability of kinship terminology (Marley 2020). The persistent tension between comparative and language-internal measures makes it difficult to see how we can unite these two approaches, but they both provide valuable insights into our knowledge of the systems of kinship (Evans 2020).

## **Conclusion**

Ultimately, this paper attempts to shine a light on kinship terminology diversity, a domain of anthropology that inhabits both the most general and particular of methodologies. By approaching terminology diversity from the bottom up, I hope to strike a balance between these poles. Moving forward, the recategorization of terminology presented here can inspire more work on kinship terminology and what it can tell us about kinship organization, and its relationship to human diversity, and help us understand the role of kinship organization in the tales of human pasts.



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865 Please cite Passmore et al. (In Review) if using the Kinbank dataset.