Constructing a Family Tree of Ten Indo-European Languages with Delexicalized Cross-linguistic Transfer Patterns

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Abstract

It is reasonable to hypothesize that the divergence patterns formulated by historical linguists and typologists reflect constraints on human languages, and are thus consistent with Second Language Acquisition (SLA) in a certain way. In this paper, we validate this hypothesis on ten Indo-European languages. We formalize the delexicalized transfer as interpretable tree-to-string and tree-to-tree patterns which can be automatically induced from web data by applying neural syntactic parsing and grammar induction technologies. This allows us to quantitatively probe cross-linguistic transfer and extend inquiries of SLA. We extend existing works which utilize mixed features and support the agreement between delexicalized cross-linguistic transfer and the phylogenetic structure resulting from the historical-comparative paradigm.

1 Introduction

The traditional historical classification of Indo-European languages generally focuses on diachronic language change, based on the cross-lingual patterns of lexical entities and of sound laws connecting cognate words (Clackson, 2007). Recently, several preliminary works suggest the coherence between such classification and derived results with various combinations of linguistic features extracted from non-native (L2) texts [Nagata and Whittaker, 2013; Nagata, 2014; Berzak et al., 2014; Rabinovich et al., 2018]. They demonstrate the hypothesis that cross-linguistic transfer, which refers to the application of learners’ knowledge of one language to the use of another as shown in Figure 1, is so strong that we can reveal the language family relationships preserved in L2 texts. The limitation is that they all use mixed features across lexical, syntactic and semantic dimensions. In view of the fact that cognates across languages provide credible genealogical clues, it is not clear to what extent does a single factor reflect the influence from traditional phylogenetic language groups.

Previous works (Dunn et al., 2005; Murawaki, 2015) have investigated the role of syntactic structures in phylogeny prediction, especially from the perspective of modern generative theory (Longobardi and Guardiano, 2009). In this paper, we concentrate on the cross-lingually transferred delexicalized feature and aim to find out whether it can work as effectively as lexical information such as cognates.

![Figure 1](image_url)

**Figure 1:** Example of cross-linguistic transfer. The L2 English phrase is written by a French native speaker and it preserves linguistic features from L1 French, which results in the crossing of VB and ADVP in Figure 2(c).

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¹Henceforth, non-native data and its corrected version are referred to as L2 and L1, respectively.
²This is different from the widely-known cross-lingual transfer learning in the NLP community which broadly means adapting models from resource-rich languages to resource-poor languages.
Based on parallel L2-L1 data, we design two interpretable structures: tree-to-string and tree-to-tree patterns, as illustrated in Figure 2. Such patterns can be automatically induced from large-scale data by means of state-of-the-art neural syntactic parsing and grammar induction technologies. In particular, tree-to-string patterns are derived in the framework of Synchronous Tree-Substitution Grammar (STSG; Zhang et al. (2006)), while tree-to-tree patterns are generated by a novel tree alignment algorithm. Then we build a large language-pattern matrix, with which we can probe cross-linguistic transfer in a quantitative manner and assist the study of second language acquisition (SLA). Experiments on ten representative Indo-European languages, show that with the delexicalized patterns we can reproduce the exact phylogenetic structure resulting from the historical-comparative paradigm.

![Diagrams of tree-to-string and tree-to-tree patterns](https://example.com/diagrams.png)

Figure 2: Examples of cross-lingual transfer patterns summarized as tree-to-string (red box) and tree-to-tree (blue box) patterns. The top and bottom trees correspond to the syntactic analysis for L2-English and their corrected sentences respectively. $x_0$, $x_1$, and $x_2$ represent constituent tokens, among which the dashed lines refer to word alignment. (a) depicts a top-ranking pattern for all native languages and (b)–(d) show remarkably frequent patterns related to language-specific properties of different native languages: (b) reflects the heavy use of noun-noun compound in Mandarin Chinese; (c) reflects the different word orders in English and French related to adverbal adjuncts; (d) reflects the different word orders in English and Arabic related to Modal words.

## 2 Inducing Delexicalized Cross-lingual Transfer Patterns

We define two kinds of syntactically motivated structures (tree-to-string and tree-to-tree patterns) to measure the inherent transfer, as illustrated in Figure 2. Both of them intuitively show structural language variances, largely word order errors. Based on reliable syntactic analysis for aligned parallel data, we can generate such patterns with grammar induction technologies.

### 2.1 Inducing Tree-to-string Patterns with STSG

Tree-substitution grammar (TSG) defines the model of deriving parse trees with a rewriting system and has been proved effective to capture native language signals (Swanson and Charniak, 2013). Here we propose to utilize Synchronous TSG (STSG) which describes the process of gathering tree-to-string fragments from aligned hierarchical (L2 trees) and flat structures (L1 strings). We derive such patterns with a modified GHKM algorithm (Galley et al., 2004). In particular, reordering across all levels of a parse tree makes it possible to capture the divergence of word orders. Note that we only keep reordering rules and exclude patterns containing any lexical information.

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3 The alignment between L2 and L1 tokens is calculated with BerkeleyAligner [https://code.google.com/archive/p/berkeleyaligner/].
2.2 Inducing Tree-to-tree Patterns with Tree Alignment Algorithm

We design a novel alignment algorithm to induce tree-to-tree patterns which can provide richer structural information. Let $T_1$ and $T_2$ denote the constituent trees for L1 and L2 sentences respectively. For each subtree $T^k_2$ in $T_2$, suppose that it corresponds to the span $[w^b_2, w^e_2]$ in the L2 sentence and the indexes of their mapped tokens in the L1 sentence are $p^b_1, ..., p^e_1$. $T^k_2$ is regarded as anchor iff there exist $i$ and $j$, satisfying the following conditions:

$$b \leq i < j \leq e, p^i_1 > p^j_1.$$

These anchors indicate token-level reordering where our algorithm starts. Their aligned trees in $T_1$ are defined as the minimum subtree which covers $p^b_1, ..., p^e_1$. Then we can extract a tree-to-tree pattern by removing lexical information. To avoid repeated extraction, we carry out the algorithm in a bottom-up recursion and record the visited subtrees during the process. With this algorithm, we can induce the minimalist pattern set for each sentence pair efficiently.

3 Experiment

3.1 Data

Following Mizumoto et al. (2011), we extract a large volume of L2-L1 sentence pairs by mining the revision logs of authors who are learning English on Lang-8. The initial sentences written by learners can be regarded as L2 texts, while the sentences corrected by native speakers can be regarded as L1 texts. After careful data cleansing, we build a corpus of 6,791,165 parallel sentence pairs from writers of 96 different native languages, and the corpus covers a wide variety of topics and genres. We keep 21 languages each of which has at least 10,000 sentence pairs in the corpus for pattern analysis and 10 of them are in the Indo-European language family which we use as our experimental data.

| Feature                  | Purity Score | Leaf-pair Distance |
|--------------------------|--------------|--------------------|
| Word Pairs               | 100          | 8.11               |
| CFG Rules                | 70.74        | 11.40              |
| Tree-to-string Patterns  | 100          | 6.42               |
| Tree-to-tree Patterns    | 100          | 7.82               |

Table 1: Evaluation results of clustered trees based on different features.

3.2 Tailoring Parser to L2

L2 texts exhibit many distinguishing features compared to their L1 counterparts, but almost all existing parsers are fine-tuned on L1s. We propose to tailor parsing models to L2 by incrementally enhancing the standard parser with learner data. We choose the Berkeley Neural Parser (Kitaev et al., 2018) which incorporates self-attention layers (Kitaev and Klein, 2018) and BERT word representations (Devlin et al., 2018). The original training data consists of trees from WSJ 02-21 sections of Penn TreeBank (PTB; Marcus et al. (1993)). L2 trees are extracted from two learner English treebanks, i.e., Konan-JIEM and ICNALE (Nagata and Sakaguchi, 2016). We extract 3390, 1000 and 800 L2 trees from these two treebanks in proportion as the supplementary-training, development and test sets respectively.

Parsing results are displayed in Figure 3. The overall trend indicates that expanding training data can bring about a positive, but limited effect. The best-performing model can achieve an $F_1$ score of 93.11%, which shows that the tailored parser can produce relatively reliable syntactic trees for L2 English sentences.

*https://lang-8.com/*
3.3 Hierarchical Clustering

To facilitate further retrieval and calculation, we build a large language-pattern matrix with dimensions of $N_p \times N_l$, where $N_p$ and $N_l$ refer to the total numbers of extracted patterns and native languages respectively, and utilize principal component analysis (PCA) to reduce dimensionality. Based on the matrix, we obtain a square matrix with dimensions of $N_l \times N_l$ by calculating the Euclidean distance between any two languages. Then we use hierarchical clustering (Müllner, 2011; Müllner and others, 2013) to produce the dendrogram.

3.4 Evaluation

Several methodologies have been proposed for evaluating phylogenetic trees (Robinson and Foulds, 1981; Kuhner and Felsenstein, 1994; Heller and Ghahramani, 2005; Teh et al., 2008; Rabinovich et al., 2017). We choose purity score (Heller and Ghahramani, 2005) and leaf-pair distance (Rabinovich et al., 2017) as our evaluation metric. The first method finds the smallest subtree containing leaves with the same discrete class and the purity is 100% iff all leaves in each class are contained in some pure subtree. The second method calculates the average length of shortest paths in terms of any two leaves. A smaller distance represents higher structural similarity.

3.5 Result and Analysis

We reconstruct the family tree for 10 Indo-European languages. To compare with other features, we also implement clustering based on aligned word pairs and CFG rules extracted from non-native texts. The produced dendrograms are shown in Figure 4 and numerical results are displayed in Table 1. We can see that simple CFG rules are not enough but delexicalized patterns can work as effectively as lexical information when predicting phylogenetic relationships.

We rank all the tree-string fragments by frequency in terms of each native language. Statistical analysis of patterns renders interesting structures which are consistent with typical linguistic phenomena in certain languages, as shown in Figure 2. Analyzing frequent cases of induced patterns, we find that they reveal the information about how the delexicalized knowledge of native languages is transferred into the second language, which can benefit the understanding of interlanguage and second language acquisition (SLA).

4 Conclusion

In this paper, we investigate to what extent does a single delexicalized feature reflect the influence from traditional phylogenetic language groups. In particular, we design two kinds of interpretable patterns

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5Germanic (German), Indic (Hindi), Iranian (Persian), Romance (Spanish, Italian, French, Brazilian Portuguese), Slavic (Russian, Polish, Ukrainian)
and induce them from parallel data with grammar induction technologies. The produced family tree of 10 Indo-European languages match well with the phylogenetic structure resulting from historical-comparative paradigm. It suggests the coherence between genetic relationships and delexicalized cross-linguistic transfer, and more experiments need to be implemented in future research.

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