Phylogenetic simulations over constraint-based grammar formalisms

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Quantifying genetic distance

- Linguistic phylogeny attempts to estimate the evolutionary history of languages
- Traditional methods use cognate sets as comparanda
- Recent work on the efficacy of grammatical parameters
  - Dunn et al. (2005)
  - Longobardi & Guardiano (2009) successfully used syntactic parameters in a computational phylogeny of 23 Indo-European and 6 non-Indo-European languages
  - Eden (2013) used phonological stress parameters on the same languages and further demonstrated that weighted phonotactic constraints can be utilized as well

Optimality Theory

- In Optimality Theory (OT), input-output relations are determined by interaction of conflicting violable constraints.
- Example constraints:
  - NoCoda: codas are prohibited
  - Max: deletion is prohibited ("*maximise output*")
- Possible grammars using these constraints:
  - Grammar 1: NoCoda ≫ Max
    /pat/ ⟶ [pa] (*i.e., delete to avoid codas*)
  - Grammar 2: Max ≫ NoCoda
    /pat/ ⟶ [pat] (*i.e., retain codas, no deletion*)
- Constraint rankings are directed acyclic graphs (DAGs)
- OT diverges from Eden's (2013) constraint implementation:
  - Assumes a universal constraint set Con
  - Allows constraints to be unranked

Constraint pair pseudo-parameters

- For each pair of constraints, C_1, C_2, we define a dominance relation R following Antilla and Cho (1998):

$$R(C_1, C_2) = \begin{cases} 1 & \text{if } C_1 \gg C_2 \\ 0 & \text{otherwise} \end{cases}$$

- R(NoCoda, Max) conveys whether a language deletes codas ($R = 1$) or retains them ($R = 0$)
- Some R values are less meaningful
  - e.g., R(NoCoda, Max-Voice) cannot be set directly, as these two constraints do not directly conflict. (Max-Voice prohibits the deletion of voice features.)
- Pseudo-parameters have a numeric advantage over traditional parameters:
  - n parameters yields only n points of comparison
  - A set of n constraints yields $\sim n^2$ pseudo-parameters

Constraint ranking | Domination matrix | Pseudo-parameters

$C_1 \gg C_2 \gg C_3 \longrightarrow$

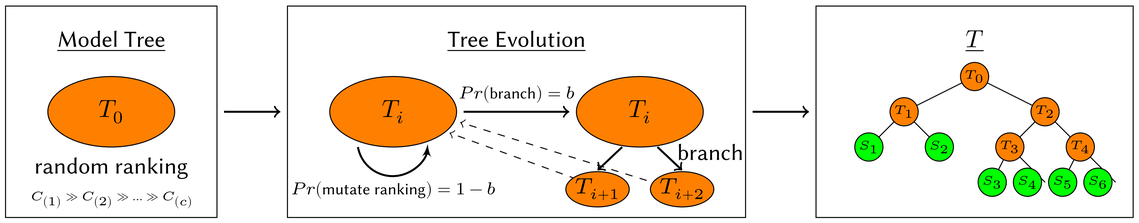
	C_1	C_2	C_3
C_1	0	1	1
C_2	0	0	1
C_3	0	0	0

$\longrightarrow$ $R(C_1,C_1)=0$, $R(C_1,C_2)=1$, $R(C_1,C_3)=1$, $R(C_2,C_1)=0$, $R(C_2,C_2)=0$, $R(C_2,C_3)=1$, $R(C_3,C_1)=0$, $R(C_3,C_2)=0$, $R(C_3,C_3)=0$

Methodology

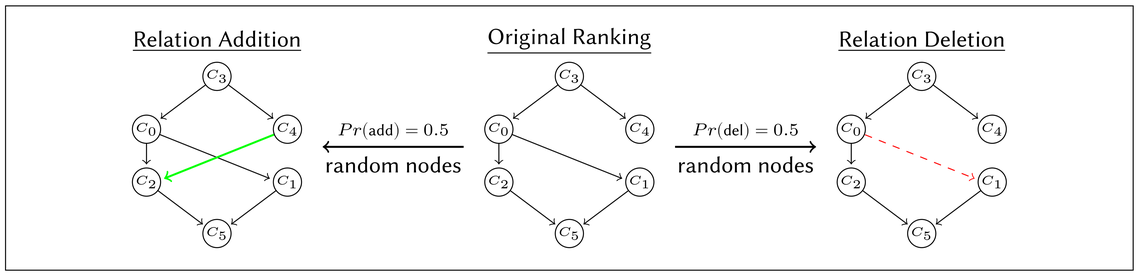
Gold standard tree

- Simulations follow the procedure described by Nichols and Warnow (2008)
- Parameters vary with respect to the number of constraints c, the size of the set of leaf nodes S, and the branching probability b
- T evolves until it reaches a minimum number of leaf nodes



Ranking mutation

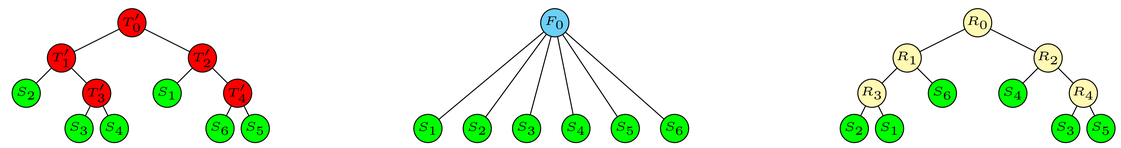
- Constraint rankings are represented with directed acyclic graphs (DAGs)
- Mutation either adds an edge in the DAG or removes an edge
- The mutated source and target nodes are chosen randomly



Test trees

- Constraint rankings of languages in the set of leaves S are decomposed into pseudo-parameter vectors
- The test tree T' is produced by hierarchically clustering S, using Euclidean distance over the pseudo-parameter vectors
- T' is compared against two baseline trees

Test tree from clustering (T') | Flat tree baseline (BF) | Random tree baseline (BR)

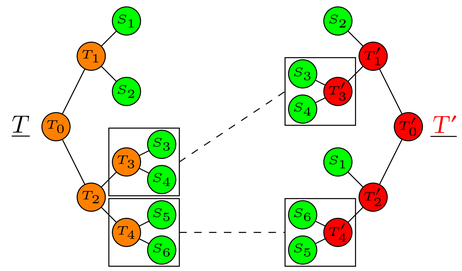


Evaluation

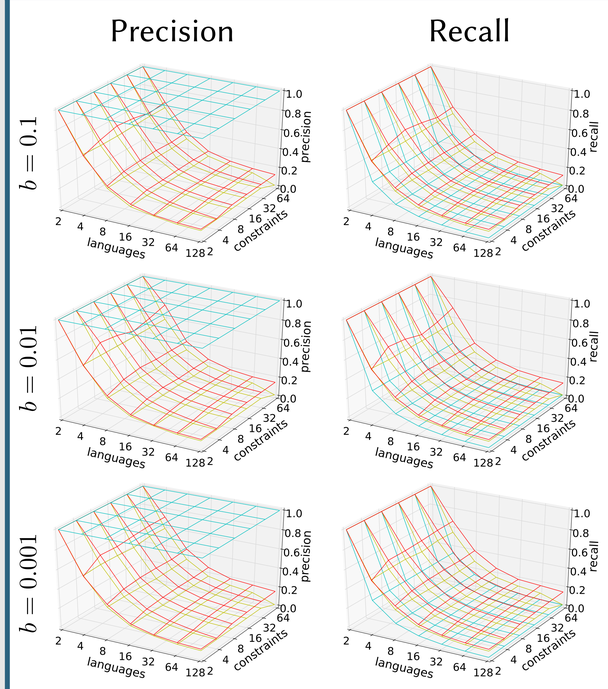
- Unlabeled precision and recall was calculated between T and the three test trees T', BF, BR
- Two internal nodes are considered matching if they dominate the same set of leaves
- We consider an experiment successful when T' is more accurate than the baseline trees

$$\text{Precision} = \frac{\text{\# matching nodes}}{\text{\# nodes in test tree}} = \frac{|\{T'_3, T'_4\}|}{|\{T'_0, T'_1, T'_2, T'_3, T'_4\}|} = \frac{2}{5}$$

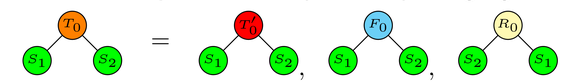
$$\text{Recall} = \frac{\text{\# matching nodes}}{\text{\# nodes in gold tree}} = \frac{|\{T'_3, T'_4\}|}{|\{T_0, T_1, T_2, T_3, T_4\}|} = \frac{2}{5}$$



Results



- Our method (T') outperforms flat (BF) and random (BR) baseline trees in most conditions
- All 3 trees have perfect accuracy with only 2 languages:



- BF always has perfect precision because it only contains the root node
- The accuracy of T' increases as the number of constraints increases, because the number of comparisons increases
- T' is more accurate with lower branching probabilities, as changes accumulate and propagate through subtrees
- The accuracies of all three trees decrease as the number of languages increase. This follows from the number of available hypotheses: the number of internal nodes is on the order of the number of leaves

Future Directions

- Extend this approach to real language data, e.g., language families with extensive phonological work
- Stress data is particularly propitious
  - Large attested typology (e.g., the StressTyp2 database)
  - There are about 14 core constraints (Kager, 1999)
  - Compare constraint-based phylogeny directly with Eden's (2013) parameter approach
- Certain linguistic changes are more likely to occur than others (e.g. from phonetic pressures). Enriching our system with these biases should improve its performance over real language data