Tree-distance and some other variants of evalb

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Abstract

Some alternatives to the standard evalb measures for parser evaluation are considered, principally the use of a *tree-distance* measure, which assigns a score to a *linearity* and *ancestry* respecting mapping between trees, in contrast to the evalb measures, which assign a score to a *span* preserving mapping. Analysis of the evalb measures suggests the other variants, concerning different normalisations, the portions of a tree compared and whether scores should be micro or macro averaged. The outputs of 6 parsing systems on Section 23 of the Penn Treebank were taken. It is shown that the ranking of the parsing systems varies as the alternative evaluation measures are used. For a fixed parsing system it is also shown that the ranking of parses from best-to-worst will vary according to whether the evalb or *tree-distance* measure is used. It is argued that the tree-distance measure ameliorates a problem that has been noted concerning over-penalisation of attachment errors.

1. Introduction

The PARSEVAL measures of parser performance (Black et al., 1991), as refined and implemented by the evalb program (Sekine and Collins, 1997; Collins, 1997) have become a widely adopted standard. Fundamentally this approach treats gold-standard and parser-generated trees $\mathcal{G}$ and $\mathcal{T}$, as *sets of labelled spans*, $\mathcal{G}^S$ and $\mathcal{T}^S$. The similarity of these sets is then quantified via precision and recall scores, often combined into a single $F1$ figure, itself equivalent (as shown below) to applying the standard *Dice* measure for quantifying the similarity of two sets.

Thus the evalb scoring projects trees into particular *sets* and applies *set* comparison measures. There is an alternative to this way of proceeding, which might be described as treating trees in their own right, rather than treating them via a projection into sets. That alternative is the *tree-distance* measure (K.Zhang and D.Shasha, 1989).

The tree-distance measure on two trees $\mathcal{G}$ and $\mathcal{T}$ may be arrived at by considering the *partial*, one-to-one mappings, $\sigma : \mathcal{G} \mapsto \mathcal{T}$, from the nodes of one tree to the nodes of the other. Given such a mapping, it is natural to identify the following sets of nodes

$$\begin{array}{rcl}\mathcal{D} & = & \{n \in \mathcal{G} : n \notin dom(\sigma)\} \\ \mathcal{I} & = & \{n \in \mathcal{T} : n \notin ran(\sigma)\} \\ \mathcal{S} & = & \{n \in \mathcal{G} : label(n) \neq label(\sigma(n))\} \\ \mathcal{M} & = & \{n \in \mathcal{G} : label(n) = label(\sigma(n))\}\end{array}$$

where $\mathcal{D}$, $\mathcal{I}$, $\mathcal{S}$ and $\mathcal{M}$ stand for *deleted*, *inserted*, *swapped* and *matched*. Based on these sets, a cost can be assigned to a mapping, with the standard arrangement setting this cost to be a sum of set sizes[1]: $D + I + S$. Amongst all possible mappings $\sigma : \mathcal{G} \mapsto \mathcal{T}$, the tree-distance measure considers only those mappings that

(T1) *preserve left-to-right order*
(T2) *preserve ancestry*

so one can also say that the mappings are required to be *homomorphisms* on the two dimensions of structure characteristic of a tree. Call a T1/T2-conformant mapping a T-mapping. The *tree-distance* between $\mathcal{G}$ and $\mathcal{T}$ can then be defined as the cost of the *least* costly T-mapping.

An example of a least-costly T-mapping between a pair of trees $\mathcal{G}$ and $\mathcal{T}$ is shown in Figure 1. Deleted nodes have < affixed to their label (and are red), inserted nodes have > prefixed (and are green), swapped nodes are shown linked with a dotted arrow (and are blue), and matched nodes are shown at the same height, with no linking arrow (and are black). The cost associated with this T-mapping is 4, from 1 deletion, 2 substitutions and 1 insertion.

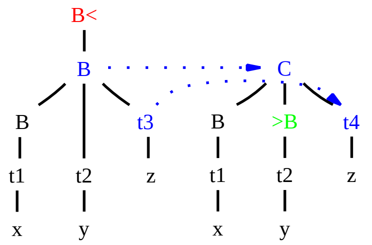


Figure 1: *a T-mapping*

There is an equivalent definition of tree-distance via the notion of an edit-script, being a sequence of edit operations on one tree, to derive a second tree, where the operations are deletion, insertion and re-labelling. See K.Zhang and D.Shasha (1989) or Bille (2005) for proofs that the costs of the least costly mapping and the least costly edit-script are identical, and for details of efficient algorithms for the computation of this measure.

Though tree-distance has been applied to question-answering and entailment recognition (Punyakanok et al., 2004; Kouylekov and Magnini, 2005; Emms, 2006a; Emms, 2006b) it has not been applied to parser evaluation. The main aim of the work reported below is to compare outcomes using tree-distance to the outcomes using the standard evalb measures.

Some further dimensions of contrast to the standard set-

[1] Using the roman version of a set's name to stand for its size, hence D for $|\mathcal{D}|$ etc. This arrangement effectively assigns a unit cost to each individual deletion, insertion or swap. There are applications of tree-distance in which the costs are parametrized according to the labels of the nodes (Punyakanok et al., 2004).

up will also be explored, to describe which some further definitions are required.

First of all we note how it is possible to subsume the `evalb` measures under the costed-mapping perspective that underlies the tree-distance measure. To begin with, the T1/T2 requirements on mappings should be replaced with the requirements that they

(E1) *preserve node labels*
(E2) *preserve lexical spans*

Call an E1/E2-conformant mapping from $\mathcal{G}$ to $\mathcal{T}$ an E-mapping. Note that E1/E2 make the choice of E-mapping practically deterministic – the exception being unary branches on which the same label recurs – quite unlike the set of possible T-mappings. For the same imaginary $\mathcal{G}/\mathcal{T}$ pair as considered in Figure 1., the corresponding E-mapping is shown in Figure 2. If we derive a cost from this E-mapping in the same way as for a T-mapping, the cost is 6, from 3 deletions and 3 insertions – from the `evalb`-perspective, the deletions are recall errors and the insertions are precision errors. We show now how the `evalb` quantities can be derived from an E-mapping.

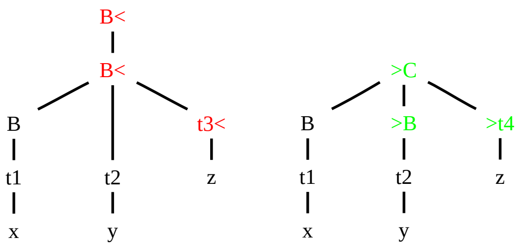


Figure 2: *an E-mapping*

First a technicality. Let the *roof* of a tree be the nodes which are not terminal or pre-terminal. The `evalb` labelled recall and precision quantities refer to the roof parts of the compared trees: pre-terminals are dealt with separately. We will use $\hat{}$ to signify the restriction to the *roof* part of trees. Given a (least-costly) E-mapping, Table 1., gives formulae defining the *labelled recall*, *labeled precision* of `evalb`, and their F1 combination[2].

labelled recall R *labelled precision P*	$\hat{M}/\hat{G}$ $\hat{M}/\hat{T}$
$F1$ $=$ *E Dice*	$2RP/(R+P)$ $= 2\hat{M}/(\hat{G}+\hat{T})$
E Jaccard	$\hat{M}/\vert(\hat{G}\cup\hat{T})\vert$ $= \hat{M}/(\hat{G}+\hat{T}-\hat{M})$

Table 1: *Scores definable from an E-mapping*

The second line concerning F1 gives an equivalent formula, which can be obtained when the formulae for R and P are substituted in:

$$\begin{aligned} F1 &= (2 \times \hat{M}/\hat{G} \times \hat{M}/\hat{T})/(\hat{M}/\hat{G} + \hat{M}/\hat{T}) \\ &= 2\hat{M} \times (1/\hat{G}\hat{T})/(1/\hat{G} + 1/\hat{T}) \\ &= 2\hat{M} \times (1/\hat{G}\hat{T})/((\hat{G}+\hat{T})/\hat{G}\hat{T}) \\ &= 2\hat{M}/(\hat{G}+\hat{T}) \end{aligned}$$

The result is the *Dice* formula for comparing 2 sets (van Rijsbergen, 1979). This quantifies the similarity by considering the size of their intersection (multiplied by 2) and normalises by the sum of their sizes; the multiplication by 2 is to ensure a quantity between 0 and 1, with 1 for identical sets.

Seeing the F1 score in this light invites the consideration of other normalizations of the match score, in particular by the size of the union $\hat{G} \cup \hat{T}$, giving the *Jaccard* score, formulae for which are given in the 4th row of Table 1. This Jaccard normalisation is another of the variants of the standard `evalb`-based scores that will be considered below.

As noted above, the `evalb` measures report labelled precision and recall confined to the *roof* part of trees. Another alternative which will be considered below is to apply the definitions with pre-terminals included, and this will be referred to as the *whole-tree* variant.

To fix ideas the following table takes the E-mapping shown in Figure 2 and gives the values for R, P, *E Dice*, and *E Jaccard* for the case of restriction to roof-trees

$\hat{G}$	$\hat{T}$	$\hat{D}$	$\hat{M}$	$\hat{I}$	R	P	E Dice	E Jacc
3	3	2	1	2	0.33	0.33	0.33	0.2

and the following table gives the corresponding values for the whole-tree variant where pre-terminals are included.

G-W	T-W	D	M-W	I	R	P	E Dice	E Jacc
6	6	3	3	3	0.5	0.5	0.5	0.33

All of the scores derivable from an E-mapping that were given Table 1. can be seen as different normalisations of the match-count $\hat{M}$. They can all also be seen as the inverses of similarly normalised 'cost-counting' measures, using the fact that under E1/E2, $\hat{M} = \hat{G} - \hat{D} = \hat{T} - \hat{I}$, and $|\hat{G} \cup \hat{T}| = \hat{G} + \hat{T} - \hat{M}$:

$$\begin{aligned} 1 - \hat{D}/\hat{G} &= (\hat{G} - \hat{D})/\hat{G} \\ &= \hat{M}/\hat{G} \\ 1 - \hat{I}/\hat{T} &= (\hat{T} - \hat{I})/\hat{T} \\ &= \hat{M}/\hat{T} \\ 1 - (\hat{D} + \hat{I})/(\hat{G} + \hat{T}) &= (\hat{G} + \hat{T} - (\hat{D} + \hat{I}))/(\hat{G} + \hat{T}) \\ &= ((\hat{G} - \hat{D}) + (\hat{T} - \hat{I}))/(\hat{G} + \hat{T}) \\ &= 2\hat{M}/(\hat{G} + \hat{T}) \\ 1 - (\hat{D} + \hat{I})/(\hat{G} \cup \hat{T}) &= (\hat{G} + \hat{T} - \hat{M} - (\hat{D} + \hat{I}))/(\hat{G} \cup \hat{T}) \\ &= ((\hat{G} - \hat{D}) + (\hat{T} - \hat{I}) - \hat{M})/(\hat{G} \cup \hat{T}) \\ &= M/(\hat{G} \cup \hat{T}) \end{aligned}$$

Taking up again the topic of tree-distance, this suggests that to undertake a comparision with `evalb`, we should consider corresponding normalisations of the tree-distance measure and then invert this into a similarity measure. Now

[2] $\hat{G}$ and $\hat{T}$ are used interchangeably in these formulae both for a set of nodes and its size.

tree-distance is a general measure for comparing trees, applicable to trees with different lexical yields, unlike the evalb scoring. In the above-defined recapitulation of the evalb score via an E-mapping, the lexical items are always mapped to each other in an E-mapping and do not contribute to the match count or to any set sizes in normalisations. In a least-cost T-mapping, from a gold to a test tree, lexical items predominantly are mapped to each other, though not exclusively. The normalisation should reflect this and diminish the significance of large numbers of word matches. Table 2 gives the Dice-style and Jaccard-style normalisations which will be used. If you take the worst-case T-mapping to be one where all of $\mathcal{G}$'s non-terminals are deleted, all of $\mathcal{T}$'s non-terminals are inserted, whilst all terminals are matched, both the Dice and Jaccard normalisations range between 0 and 1.

$TDice$	$1 - \frac{D+I+S}{(G-W)+(T-W)}$
$TJaccard$	$1 - \frac{D+I+S}{D+S+M+I-W}$

Table 2: *Scores definable from a T-mapping*

To illustrate, for the T-mapping shown in Figure 1., we obtain

G-W	T-W	D	S	M-W	I	T Dice	T Jacc
6	6	1	2	3	3	0.66	0.43

At this point a number of potential variants on the standard evalb scoring have been touched on: basing on T-mappings vs E-mappings, Dice vs Jaccard normalisations and (for E-mappings) whether or not to restrict to roof trees.

There is one final variation which will be considered. In the definitions given so far, scores have been defined for a single pair of trees. Extending this to a collection of pairs of trees, the *micro-averaging* approach simply averages the scores obtained on each tree pair. The standardly reported evalb scores are *macro*-averaged for a large collection, by summing the numerators and denominators over all tree-pairs, and then carrying out the divisions.

2. A priori considerations

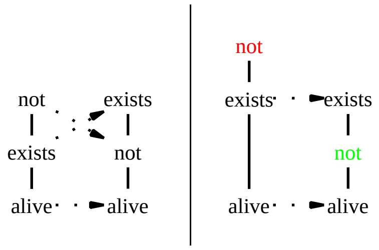
It is not the case that every E-mapping is a T-mapping. The span-preserving aspect of E-mappings is

E2: if (i,j) is in the mapping, then $span(i) = span(j)$

The ancestry-preserving aspect of T-mappings is

T2: if (i_1, j_1) and (i_2, j_2) are in the mapping, then $anc(i_1, i_2)$ iff $anc(j_1, j_2)$

The pictures below show a contrived a case where span preservation does not imply ancestry-preservation.



The left-hand picture shows an E-mapping. The 'exists' and 'not' nodes have the same span and are mapped to each other by the E-mapping, but have reversed ancestry relationships in the two trees, and so cannot be mapped to each other by a T-mapping. The cost associated with the E-mapping is 0, and correspondingly the evalb measures would score this pair of trees as perfectly matched. The right-hand picture shows a minimum cost T-mapping, where its respect for ancestry requires it to leave 'not' out of the mapping on either side, and so incurs a cost of 2.

This example involves unary branching, and a little analysis shows that unary-branching will be the hallmark of cases where an E-mapping is not a T-mapping.

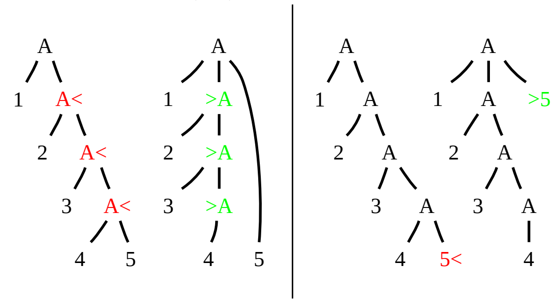
Suppose (i_1, j_1) and (i_2, j_2) are pairs in an E-mapping .

First of all, if $\neg anc(i_1, i_2)$ and $\neg anc(i_2, i_1)$, then $span(i_1)$ and $span(i_2)$ are disjoint, so by E2, $span(j_1)$ and $span(j_2)$ are disjoint, and $\neg anc(j_1, j_2)$ and $\neg anc(j_2, j_1)$.

Now suppose $anc(i_1, i_2)$. Then $span(i_2) \subseteq span(i_1)$. If $span(i_2) \subset span(i_1)$, then $span(j_2) \subset span(j_1)$ and $anc(j_1, j_2)$. However, if $span(i_2) = span(i_1)$ – which applies iff there is unary branching between i_1 and i_2 – then E2 guarantees $span(j_2) = span(j_1)$, from which it only follows that one or other of $anc(j_1, j_2)$ or $anc(j_2, j_1)$ holds.

A corollary of this is that when working with a tree (or roof of a tree) without unary branching, the E-mapping is a T-mapping, and because tree-distance chooses the least costly T-mapping, the cost of the E-mapping will be greater than or equal to the cost of the least costly T-mapping. Once costs are inverted to similarities, this means that in these cases one would expect an E-score to be *lower* than a corresponding T-score.

It has sometimes been noted that when a parser makes an attachment mistake, attaching high up a constituent which should have been attached low down, this implies span errors all along the path between the high and the low attachment sites (Bangalore et al., 1998). This is illustrated by the E-mapping to the left below, which incurs a cost of 6, and *E Dice* score of 0.25.



The T-mapping has the option to treat this situation differently, as shown in the right-hand picture. The T-

mapping is able to maps nodes to each other though they have different spans. For the nodes participating in the attachment error, the ancestry difference means they must be treated as deleted and inserted, and the T-mapping incurs a cost of 2, and *T Dice* score of 0.75.

3. Comparing Collins, Charniak and Petrov

For 6 different parsers we took the test parses produced on Section 23 of the Penn Treebank (Marcus et al., 1994) to see if the alternatives to the standard `evalb` scoring that were noted in section 1. give a different relative ordering of the parsers than that obtained by the standard `evalb` measures[3].

The parsers were the 3 models of Collins (2003), the maximum entropy inspired parser of Charniak (2000), and the 5 and 6 split-merge cycle versions of the parser of Petrov et al. (2006). In all the results reported below, E scores are derived from E-mappings and T scores are derived from T-mappings. For the software used to obtain the T-scores see Emms (2008).

Table 3 gives the E score outcomes, macro-averaged.

Parser	$\hat{D}$	$\hat{I}$	$\hat{T}$	E Dice	E Jac
Collins 1	5558	5408	44126	87.59	77.93
Collins 2	5292	5188	44172	88.15	78.81
Collins 3	5294	5188	44170	88.15	78.81
Petrov 5	4860	4525	43941	89.36	80.77
Charniak	4624	4460	44112	89.72	81.36
Petrov 6	4541	4409	44144	89.87	81.62

Table 3: *E scores, referring to the roof-only part of the tree*

The *E Dice* column, as argued above, is equivalent to the standard F1 of the `evalb`-defined R and P, and this equivalence can be verified from the $\hat{D}$, $\hat{I}$, and $\hat{T}$ columns, together with the fact that $\hat{G} = 44276$. The parsers are listed in order of increasing *E Dice* score (which coincides with the *E Jaccard* ordering), and Petrov et al. (2006) point out that on this basis, their parser beats those of Collins (2003) and Charniak (2000). However, on the web-site from which their parser may be downloaded they also note that the model reached after 6 split/merge iterations is 'overfitting the Wall Street Journal' and recommend use of the model reached after 5 split/merge iterations.

Evalb vs. Tree-distance

Parser	E Dice	E Jac	T Dice	T Jac
Collins 1	92.39	85.86	93.62	87.87
Collins 2	92.73	86.45	93.91	88.41
Collins 3	92.71	86.42	93.91	88.41
Petrov 5	93.37	87.58	94.50	89.47
Charniak	93.30	87.44	94.55	89.54
Petrov 6	93.61	87.99	94.72	89.87

Table 4: *E and T scores, whole tree, macro-averaged*

Table 4 gives the E and T scores, for whole trees, macro-averaged. The ordering of the parsers by T-scores is different to that by E-scores in this case, with T giving *Petrov 5* $<$ *Charniak* and E giving *Charniak* $<$ *Petrov 5*. The plot in Figure 3 shows this for the Dice normalisation. The effect persists with the Jaccard normalisation. Note that in line with expectation, the T scores are higher than the E scores.

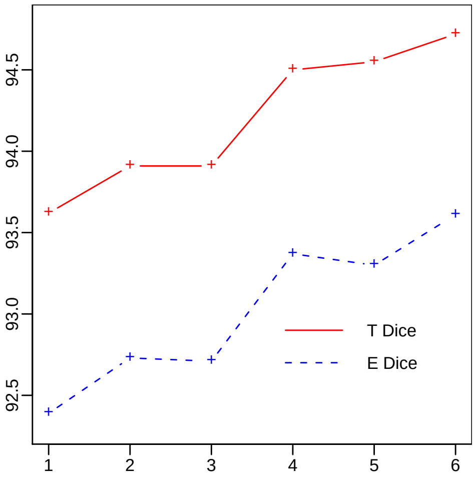


Figure 3: *E vs T whole tree macro averaged. On the x-axis 1-3 = Collins 1/2/3, 4 =* Petrov 5, *5 =* Charniak, *6 =* Petrov 6. *Same in later plots*

Whole vs. roof-trees

If the *E Dice* scores for whole trees (Table 4) and roof trees (Table 3) are compared, switching from whole trees to roof trees reverses the *Charniak* $<$ *Petrov 5* ordering. The plot in Figure 4 shows this. The effect persists with the Jaccard normalisation.

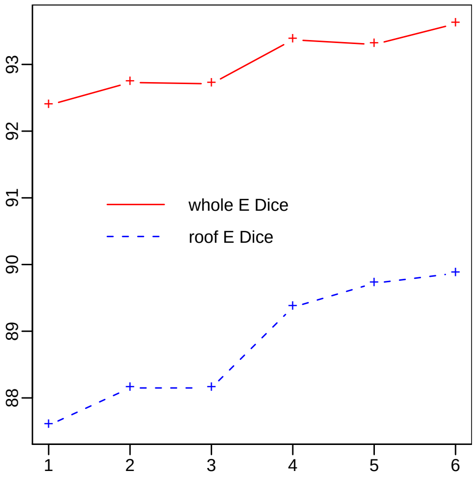


Figure 4: *Whole and Roof Tree, E Dice, macro-averaged*

Choice of normalisation

Thus far, varying between the Dice and Jaccard normalisations has not been shown to have any effect. The plots in Figure 5 and Figure 6 shows micro and macro averaged outcomes with the two normalisations. For the micro-averaged

[3] The scores refer to all sentences, not the length ≤ 40 subset, and the standard parameter settings was used, implying principally parse normalisations in which punctuation and nodes dominating traces are deleted.

E score, changing the normalisation from Dice to Jaccard changes the ranking of the parsers.

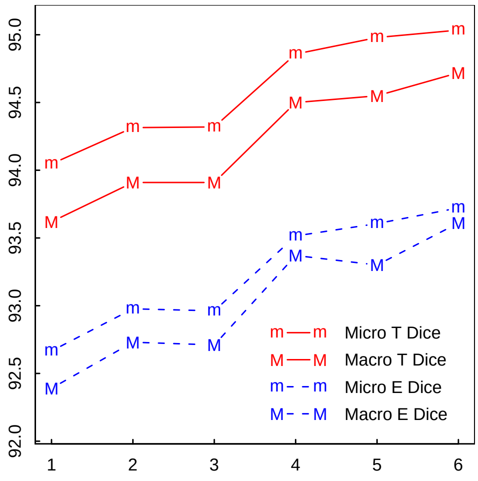


Figure 5: *Micro vs Macro averaging (whole tree, E/T, Dice norm)*

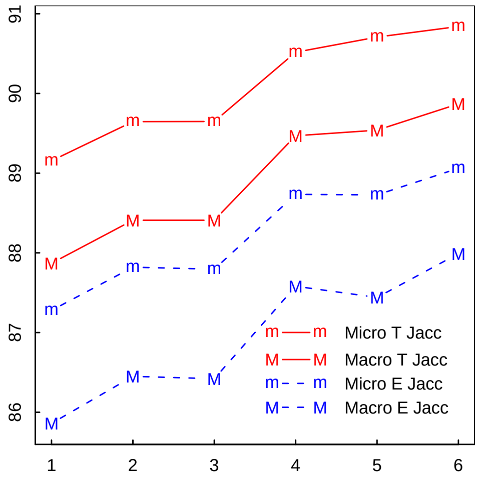


Figure 6: *Micro vs Macro averaging (whole tree, E/T, Jaccard norm)*

Micro vs. Macro averaging

Looking at the plots in Figure 5 and Figure 6, there is tendency for the micro-averaged scores to place *Charniak* farther ahead of *Petrov 5* then do the macro-averaged scores, and in the case of the *E Dice* measure (Figure 5) the switch from micro to macro-averaging switches the *Charniak* $>$ *Petrov 5* ordering.

Thus all of the dimensions of contrast to the standard `evalb` figures which defined in section 1. can lead to a differing ranking of the parsers investigated. None of the variants seem unnatural, so this ought to lead one to temper the importance attributed to the `evalb` ranking. The E vs T contrast is the most interesting of all, as the tree-distance measure seems particularly natural, being based on the mathematically natural notion of a homomorphism.

4. Comparing best-to-worst parse rankings

Besides comparing how the different measures rank parser*s*, we can also consider how they rank parse*s*.

The plot in Figure 7 plots E-score against T-score, with the Jaccard normalisation, for the *Petrov 5* parses. A smeared-out band results, indicating that more than one T-score can correspond to a single E-score, and vice-versa. A similar plot results with the other parsers, and other Dice normalisation. This is an indicator that the E and T scores will not produce the same ranking of parses. The *kendall-tau* measure (S.Siegel and N.J.Castellan, 1988) of the difference between the E and T rankings of parses was computed. This figure can be interpreted as how often, when a pair of parses is picked from one ranking, the pair will appear differently ordered in the other ranking. It comes out at 4-5%, for all the parsers, and with either normalisation.

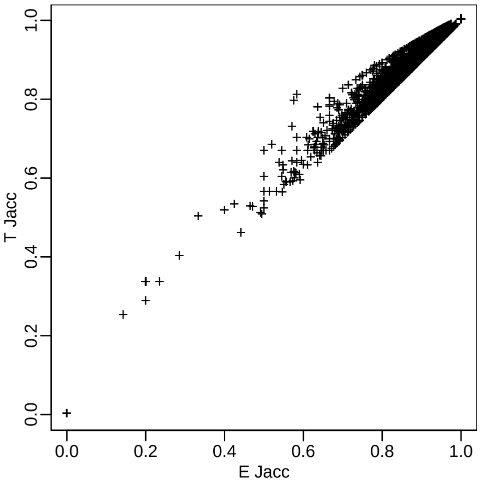


Figure 7: *T Jacc vs E Jacc.* Petrov 5 *parses in both cases*

The plot in Figure 8 plots the Jaccard and Dice normalisations of the E-scores against each other. This is closer to a single line, which is an indicator that varying the normalisation will not produce much change in the ranking of parses. When the kendall-tau measure of the difference between the Dice and Jaccard-normalised rankings of parses is computed it comes out 0.5% for the E-score, and 0.75% for the T-score.

Sentence 159 in the Section 23 test set was

> *Vincent Bajakian manager of the $ 1.8 billion Wellington Fund added to his positions in Bristol-Myers Squibb Woolworth and Dun & Bradstreet Friday*

and in the reference parse *Friday* is attached high as a daughter of the top-most vp-node, whereas in the *Petrov 5* parse it is attached low. This parse is ranked 504 places lower under the E scoring than under T, the largest rank difference amongst the 2416 trees. The first (resp. second) picture below shows its $\mathcal{G}$-to-$\mathcal{T}$ alignment for the E (resp. T) scorings. To save space some identical matched parts are elided as dots. This is a concrete case of the theoretical possibility mentioned at the end of section 2.

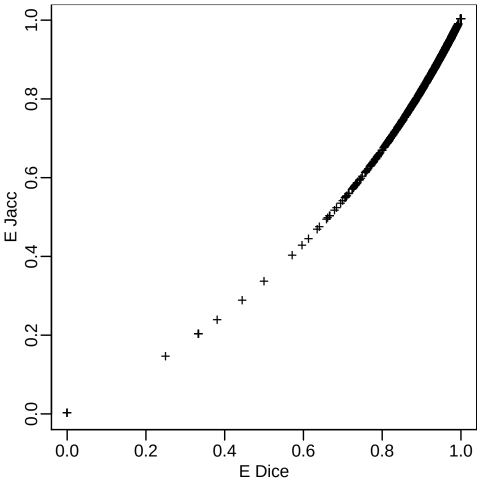
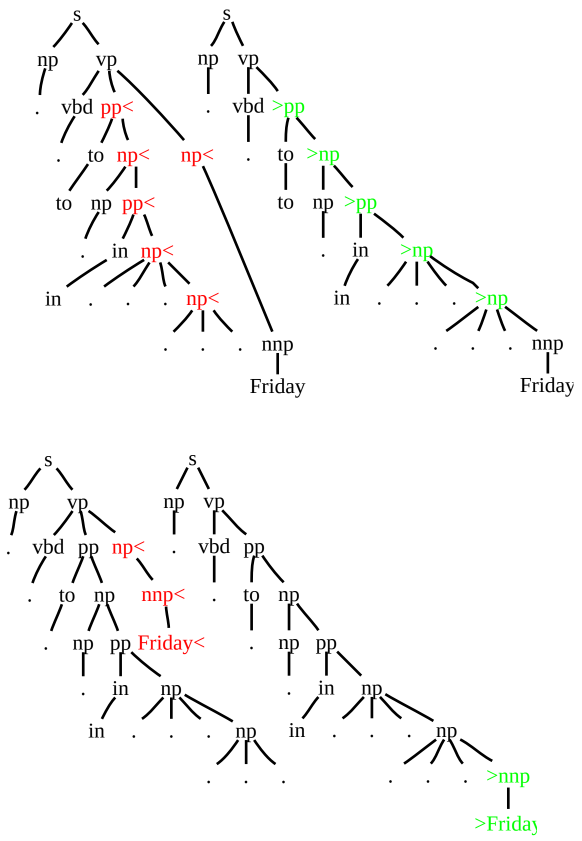


Figure 8: *E Dice vs E Jaccard.* Petrov 5 *parses in both cases*



5. Related and future work

The nearest related work is that of Roark (2002), who basically applies the linear edit distance (V.I.Levenshtein, 1966) to various linearisations of trees, rather than applying the 2 dimensional version of edit distance that we use here. He did not find a variation in the ranking of parsers that he considered, whereas we do. He essentially also considered only measures on *roof* trees. One aspect of his approach that it would be interesting to explore is an explicit modeling of movement, whereby an attachment error is recognised by a typical signature of paired deletions and insertions and re-costed. This is because although T-mappings can give a different analysis of attachment errors, allowing the sequence of nodes between the high and low attachment site to match, it still treats the mistakenly attached constituent as deleted and inserted, which is arguably too punitive.

Sampson and Babarczy (2003) contrast the `evalb` score with a *Leaf-Ancestor* (LA) score, which roughly maps a tree to the set of its root-to-leaf paths – which they term *lineages* – and then quantifies the similarity of two trees by the average linear edit distance between the lineages. It remains for future work to establish whether there is mathematical relationship between the leaf-anscestor and tree-distance score, and also whether, as with tree-distance, parsing systems come out differently ranked by this score than by the `evalb` score: the cited paper contrasts alternative rankings of parses rather than pars*ers*.

The results reported here refer exclusively to the Penn Treebank and it would be of interest to consider other treebanks, annotated in different styles, possibly extending the work of Rehbein and van Genabith (2007), who have contrasted `evalb` and LA scores on treebanks of German data, although the focus of that work seems to be more on comparing outcomes on two differently annotated treebanks of German data.

In the results reported here, the standard procedure was followed of normalising nodes which dominate traces out of the picture and it would also be of interest to look at outcomes where this is not done. It might be that there are more cases of span-preserving but ancestry-reversing E-mappings in this case.

6. Acknowledgements

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7. References

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