Technical Report

Alignment-Based Learner

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Reference Guide[1]

Jeroen Geertzen
jg532 [at] cam.ac.uk

Research Centre for English & Applied Linguistics
Faculty of English Building
University of Cambridge
9 West Road, CB3 9DP Cambridge
United Kingdom

Menno M. van Zaanen
mvzaanen [at] uvt.nl

Department of Communication and Information Sciences
Faculty of Humanities
Tilburg University
P.O. Box 90153, 5000 LE Tilburg
The Netherlands

[1] This document is available from:
http://www.uvt.nl/~menno/research/software/abl/

Contents

Preface

Alignment-Based Learning (ABL) is a symbolic grammar inference framework that has successfully been applied for several unsupervised machine learning tasks in Natural Language Processing (NLP). Given sequences of symbols only, a system that implements ABL induces structure by aligning and comparing the input sequences. As a result, the input sequences are augmented with the induced structure.

The first phase in ABL, *alignment learning*, builds a search space of possible structures, called *hypotheses*, by comparing the sequences and clustering subsequences that share similar context. In the second phase, *selection learning*, the most probable combination of hypothesized structures are selected in an Expectation-Maximization search.

We believe the implementation of ABL presented here will be beneficial for further explorations in applying alignment-based grammar inference and will turn out to be useful for unsupervised machine learning research in NLP and other areas.

This document is structured as follows. In the first chapter, the terms of the license are given to which you are allowed to use this ABL implementation. In the subsequent chapters, instructions are given how to install the package on your computer (Chapter 2) and how to run the software and run experiments (Chapter 3). The instructions are accompanied with examples for inducing natural language syntax. This document ends with a global description of how the C++ source code is organized to support extensions and modifications.

We would appreciate it if you would send bug reports, ideas for extensions, extensions that could be included in future releases, as well as comments and feedback on this manual, to `mvzaanen@uvt.nl`.

Chapter 1

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    Menno van Zaanen
    Department of Communication and Information Sciences
    Faculty of Humanities
    Tilburg University
    P.O. Box 90153
    NL-5000 LE Tilburg
    The Netherlands

Chapter 2

Installation

The ABL software package can be found at
`http://ilk.uvt.nl/~menno/research/software/abl/`

Before downloading the file `abl-1.2.tar.gz`, send an email to `mvzaanen@uvt.nl` indicating that you would like to register and are going to download the ABL package. The file is a gzipped tar archive that contains the ABL software package, the license, and documentation.

To install the package on your UNIX based system system, issue the following command from the command line prompt (`>`)

```
> tar xvzf abl-1.2.tar.gz
```

As a result, a directory `abl-1.2` will be created. Enter this directory and compile the software, assuming that you have autoconf and automake on your system

```
> cd abl-1.2/
> ./configure
> make
> make install
```

If the process was successful, three new commands are available: `abl_align`, `abl_cluster`, and `abl_select`. Additionally, within the directory `abl-1.2`, a `doc/` directory has been created with a postscript version of this document. If `make install` failed, the programs are still available within the `src` directory.

The software is now ready to be used. For each program, help can be printed on the command line by using it with the switch `-h`. For any questions on compiling, installing, or using the software, please send a message to `mvzaanen@uvt.nl`.

Chapter 3

Software usage

This chapter shows how to use the Alignment-Based Learning (ABL) software package by discussing the steps in the grammar induction process, the commands to be issued, how to select specific algorithms and metrics by setting the right parameters, and other practical issues. The instructions are exemplified by simple natural language examples.

3.1 Using ABL

Alignment-based learning (van Zaanen, 2002) is a two phase algorithm with different possible instantiations. In the first phase, called *alignment learning*, sequences of symbols (in our examples sentences of words) are compared to find possible constituents (hypotheses). Directly after alignment learning, it is required to cluster hypothesized constituents with similar context together. We will refer to this step as *clustering*. In the second phase, called *selection learning*, the most probable combination of hypotheses are selected to be the induced constituents.

3.1.1 Alignment learning

Let us consider the following example-corpus of plain text sentences with one sentence per line in a file called `ex01.txt`

```
she is smart
she is tired
```

To perform alignment learning on this file, we can give the following command on the command line prompt

```
> abl_align -a wm -p u -i ex01.txt -o ex01.txt.aligned
```

The `-i` parameter and `-o` parameter specify input and output files respectively. With the `-a` parameter, the alignment algorithm or method is selected[1]. In this case, by providing `wm` we use unbiased string edit distance (Wagner and Fischer, 1974). With the `-p` parameter we select which part of the sentence

[1] See Section 4 for an overview and explanation of all alignment methods.

to consider as possible constituents, which is usually the unequal parts (`-p u`). The resulting output[2], for each sentence will be the sentence itself followed by one or more hypotheses. The sentence and hypotheses are separated by the string `@@@`. The content of the `ex01.txt.aligned` file is

```
she is smart @@@ (0,3,[0])(2,3,[1])
she is tired @@@ (2,3,[1])(0,3,[0])
```

As can be observed in the output, an hypothesis or constituent is formatted in the following way

```
(A,B,[C])
```

where non-terminal `C` spans from position `A` in the sentence to position `B` in the sentence. In this example, `C` consists of only one number. In more complex cases, `C` may be a list of numbers, separated by commas. The output in file `ex01.txt.aligned` can also be visualized as follows

(she is (smart)$_1$)$_0$
(she is (tired)$_1$)$_0$

Those parts that are unequal in both sentences are grouped into the same equivalence class. In the remainder of this document we will use the parenthesized representation instead of the ABL representation for the sake of easy visualization.

3.1.2 Clustering

The string edit distance based algorithms in the alignment learning phase work by pairwise comparison of sentences in the corpus. As a result of these comparisons, hypotheses can have multiple non-terminals that all share the same context. What is needed is a *clustering* step that clusters these same-context-non-terminals to a single non-terminal. E.g. when we apply alignment learning on the following input of file `ex02.txt`

```
she works well
she sings well
she listens well
```

we will obtain the following structure

(she (works)$_{1,2}$ well)$_0$
(she (sings)$_{1,3}$ well)$_0$
(she (listens)$_{2,3}$ well)$_0$

In this output the hypotheses with non-terminals 1,2 and 1,3 and 2,3 share the same context. We can cluster all non-terminals that share the same context with the following command

```
> abl_cluster -i ex01.txt.aligned -o ex01.txt.clustered
```

in which the `-i` and `-o` parameter specify input and output files respectively. After clustering, the resulting file, `ex01.txt.clustered`, will have the following content

[2] In ABL format.

(she (works)$_1$ well)$_0$
(she (sings)$_1$ well)$_0$
(she (listens)$_1$ well)$_0$

3.1.3 Selection learning

The set of hypotheses that are generated during alignment learning contain hypotheses that are unlikely to be correct constituents. We assume that the underlying grammar that is to be induced is context-free, which implies that overlapping constituents are unacceptable. In the selection learning phase, the most probable combination of hypotheses from all hypotheses that are generated by the alignment learning phase is selected according to a specific metric.

Let us consider the following sentences in `ex03.txt`

```
she runs from CBD to Bondi
he drives from CBD to Bondi
he walks terribly slow
```

The resulting output after alignment learning and clustering (in `ex03.txt.clustered`) is as follows

((she runs)$_1$ from CBD to Bondi)$_0$
((1 he (2 drives)$_1$ from CBD to Bondi)$_2$)$_0$
(he (walks terribly slow)$_2$)$_0$

The underlined words indicate those parts that are shared context. As can be observed, the hypotheses with non-terminal types 1 and 2 are overlapping in the second sentence. We can apply selection learning on file `ex03.txt.clustered` by issuing the following command

```
> abl_select -s b -i ex03.txt.clustered -o ex03.txt.selected
```

in which the `-i` and `-o` parameter specify input and output files respectively. With the `-s` parameter, we can specify the selection method[3]. After we have applied selection learning, the resulting output in `ex03.txt.selected` contains for each sentence constituents that are not overlapping

((she runs)$_1$ from CBD to Bondi)$_0$
((1 he drives)$_1$ from CBD to Bondi)$_0$
(he (walks terribly slow)$_2$)$_0$

As can be observed in sentence two, hypothesis two is discarded as a constituent.

When using a large corpus as input on machines that are low on internal memory, the switch `-m` can be used to preserve memory use at the cost of execution speed.

[3]See Section 5 for an overview and explanation of all alignment methods.

3.2 Practical issues

3.2.1 Using pipes

All three programs, `abl_align`, `abl_cluster`, and `abl_select` are able to both read/write from files and read/write to standard input and standard output. The latter possibility allows these programs nicely to be put in sequence by using pipes. For example, the following command

```
> abl_align -a wm -p u | abl_cluster | abl_select -s b
```

allows users to type input sentences on standard input (close with CTRL-d) after which the induced structure is printed on the standard output. Likewise, the following commands

```
> cat in.txt | abl_align -a wm -p u | abl_cluster \
> | abl_select -s b > out.txt
```

applies ABL on file `in.txt` and saves the induced structure in file `out.txt`. To get to know exactly what is generated in each step, we can use the `-v` or `--verbose` switch on each program, which writes status information to the terminal, in addition to the data to the file `out.txt`. E.g.

```
abl_align      :  # sentences loaded            :  61
abl_align      :  # hypotheses generated        :  520
abl_align      :  # seconds execution time      :  0.02
abl_cluster    :  # sentences loaded            :  61
abl_cluster    :  # hypotheses loaded           :  520
abl_cluster    :  # unique non-terminals input  :  1058
abl_cluster    :  # unique non-terminals output :  145
abl_cluster    :  # hypotheses clustered        :  913 (0.86)
abl_cluster    :  # seconds execution time      :  0.03
abl_select     :  # sentences loaded            :  61
abl_select     :  # hypotheses loaded           :  520
abl_select     :  # hypotheses selected         :  361
abl_select     :  # seconds execution time      :  0.02
```

3.2.2 Supported character sets

The ABL software supports the use of 7-bit (ASCII) and 8-bit (extended ASCII, ISO-8859) ASCII characters. There is no *special* support for handling Unicode characters. Words in sentences can contain any character from these encodings, except for spaces (word delimiters), newlines (sentence delimiters), or the string `@@@` (sentence-hypotheses delimiter).

3.2.3 Empty hypotheses

By default, the alignment-learning phase may generate so called *empty hypotheses*: hypotheses that do not span any word. Consider for example

```
(she is (very)_1 ill)_0
(she is ()_1 ill)_0
```

in which hypothesis with non-terminal type 1 in the second sentence is empty. Depending on the task ABL is used in, it might not be desired to have empty spans being generated. In these cases, use the `-e` switch on `abl_align`. Taking the sentences from the previous example, the output of

```
> abl_align -a wm -p u -e
```

would be

```
(she is (very)_1 ill)_0
(she is ill)_0
```

Chapter 4

Alignment learning methods

This version of the ABL implementation supports seven alignment learning methods: three edit distance based methods and four suffix tree based methods. For a corpus of n sentences, the algorithmic complexity of the edit distance based methods generally is $O(n^2)$, whereas the algorithmic complexity of the suffix tree based methods generally is $O(n)$. However, the alignments obtained by edit distance based methods seem to be better biased towards natural language syntax (see Geertzen and van Zaanen (2004)).

Each method available for alignment learning will be explained briefly in the following sections. For more details about the edit distance based methods and the suffix tree based methods, see van Zaanen (2002) and Geertzen (2003) respectively.

4.1 Edit distance based methods

Edit distance based methods that can be specified when using the command `abl_align` are: *default* (`-a wm`), *biased* (`-a wb`), and *all* (`-a a`). These alignment methods are all based on the edit distance algorithm (Wagner and Fischer, 1974). This algorithm finds the minimum edit cost to transform one sentence into the other based on a predefined cost function. This function assigns a cost to each of the edit operations: insertion, deletion and substitution.

4.1.1 default

The first method, which is called *default*, uses a cost function that makes the algorithm find the longest common subsequences in two sentences. The longest common subsequences divide words in the sentences into groups of words that can be found in both sentences or only in one of the two sentences. Based on this information, hypotheses are generated (taking equal, unequal or both types of word groups as hypotheses).

4.1.2 biased

Using the longest common subsequence to find the unequal parts of the sentences does not always result in the preferred hypotheses. Consider the following sentences

```
...from Central Business District to Bondi
...from Bondi to Central Business District
```

When aligning these sentences using *default* alignment gives us the following output

```
...from ()1 Central Business District ( to Bondi )2
...from (Bondi to)1 Central Business District ()2
```

which is syntactically undesirable. The preferred syntactical structure emerges when, instead of getting the longest common subsequences, we prefer to link the word `to`, which would result in the following alignment

```
...from (Central Business District)1 to (Bondi)2
...from (Bondi)1 to (Central Business District)2
```

To let the system have a preference to link `to` instead of `Central Business District` can be accomplished by biasing the cost function towards linking words that have similar relative offsets in the sentence. This alignment learning method is called *biased*.

4.1.3 all

It may be the case that the biased method does not find the correct alignment. A third method tries to solve this problem by introducing all possible alignments to find hypotheses, making the assumption that during selection learning, the correct hypotheses will emerge as constituents. This alignment learning method is called *all*. Note that this method introduces considerably more hypotheses (including many overlapping ones) and puts a higher load on the selection learning phases.

4.2 Suffix tree based methods

Suffix tree based methods that can be specified when using the command `abl_align` are: *suffix tree 1* (`-a st1`), *suffix tree 2* (`-a st2`), *suffix tree 3* (`-a st3`), and *suffix tree 4* (`-a st4a`). These alignment methods are all based on building a generalized suffix tree (GST) of the corpus and combining structural information of common suffixes and prefixes.

4.2.1 st1

The location in the GST where one edge branches into multiple edges marks the position in the sentences involved where hypotheses can start. Since it is less obvious where the hypotheses should end, we assume for `st1` the pair of brackets to close at the end of the sentences. The hypotheses generated by this algorithm for the next three sentences are indicated with brackets

(she (is walking away ()$_2$)$_1$)$_0$
(she (was walking)$_1$)$_0$
(she (runs away ()$_2$)$_1$)$_0$

4.2.2 st2

To find distinct words followed with joint words (e.g. away in the first and third sentence in the previous section), we can construct a generalized prefix tree (GPT). By analyzing the GPT similarly to the GST in st1, we are able to place closing brackets. Since the opening brackets cannot be read from the GPT we assume prefix hypotheses to start at the beginning of the sentence.

This results in

((()$_1$ she is)$_2$ walking)$_3$ away)$_0$
(()$_1$ she was)$_2$ walking)$_0$
(()$_1$ she runs)$_2$ away)$_0$

4.2.3 st3

The method st3 combines the alignments of st1 and st2, such that the hypotheses generated by this algorithm for the three sentences look as follows

($_0$($_3$($_2$($_1$)$_1$ she ($_1$is)$_2$ walking)$_3$ away ($_2$)$_2$)$_1$)$_0$
($_0$($_2$($_1$)$_1$ she ($_1$was)$_2$ walking)$_1$)$_0$
($_0$($_3$($_1$)$_1$ she ($_1$runs)$_3$ away ($_2$)$_2$)$_1$)$_0$

4.2.4 st4

To capture hypotheses that start somewhere in the sentence and stop somewhere later in the sentence as well, we introduce st4, which uses both GPT and GST but additionally matches opening and closing brackets, such that the hypotheses generated by this algorithm for the three sentences look as follows

($_0$($_1$($_2$($_3$)$_3$ she ($_4$($_5$($_6$is)$_6$)$_2$ walking)$_5$)$_1$ away ($_8$)$_8$)$_4$)$_0$
($_0$($_1$($_2$)$_2$ she ($_3$($_4$was)$_4$)$_1$ walking)$_3$)$_0$
($_0$($_1$($_2$)$_2$ she ($_3$($_2$runs)$_2$)$_1$ away ($_6$)$_6$)$_3$)$_0$

Chapter 5

Selection learning methods

This version of the ABL implementation supports three basic selection learning methods that can be specified when using the command `abl_select`: *first* (`-s f`), *leaf* (`-s l`), and *branch* (`-s b`).

When using one of the probabilistic selection learning methods (leaf or branch), it may be possible that several combinations of hypotheses have the same probability (after computing the combined probability). The system then selects one of these combinations at random.

5.1 first

The first method, *first*, is a non-probabilistic method that builds upon the assumption that a hypothesis that is learned earlier is always correct. This means that newly learned hypotheses that overlap with older ones are considered to be incorrect, and thus should be removed.

5.2 leaf

The method *leaf* computes the probability of a hypothesis by counting the number of times the particular words of the hypothesis have occurred in the learned text as a hypothesis, divided by the total number of hypotheses.

5.3 branch

In addition to only consider the words of the sentence delimited by the hypothesis as in the method *leaf*, this model computes the probability based the words of the hypothesis and its non-terminal type label.

Chapter 6

Data formats and command-line options

6.1 Data formats

All ABL programs assume a single sentence (possibly augmented with hypotheses and constituents) to be on single line. As a result, input for alignment learning could look as follows

```
she is smart
she is tired
```

The output of `abl_align` and the input and output of `abl_cluster` and `abl_select` are expected to be in *ABL format*. For each line is specified

- *the plain sentence*, consisting of 1 or more words;
- followed by a *separator string*: `@@@`;
- followed by one of more *constituents*. A constituent is formatted in the following way

  `(A,B,[C])`

  where non-terminal(s) `C` spans from position `A` in the sentence to position `B` in the sentence and `A`, `B`, and `C` are integers. `C` may also be a list of integers separated by commas.

For instance

```
she is smart @@@ (0,3,[0])(2,3,[1])
she is tired @@@ (2,3,[1])(0,3,[0])
```

The two sentences in ABL format can also be visualized as follows

(she is (smart)$_1$)$_0$
(she is (tired)$_1$)$_0$

6.2 Command-line options

Parameters to structure learning with ABL can be specified on the command-line. Typing for any of the ABL programs the argument `-h` will provide you with an overview of possible parameters to specify. An elaborated overview of all possible parameters is presented in this section.

Parameters that each program in the package have in common are the following

`-i`	`--input=FILE`	Name of the input file. When this parameter is omitted, input is expected on STDIN.
`-o`	`--output=FILE`	Name of the output file. When this parameter is omitted, output will be given on STDOUT.
`-h`	`--help`	Prints the usage of the program on STDERR.
`-d`	`--debug`	Prints information about internal processes useful for debugging purposes.
`-v`	`--verbose`	Show details about the processing that might be interesting to the user, such as execution time and statistics.
`-V`	`--version`	Shows version of the program and subsequently exits.

6.2.1 `abl_align`

The program for the alignment learning phase, `abl_align`, has the following *specific* parameters

`-a`	`--align`	The method to use for alignment learning. The available methods are: - wagner_min, wm: wagner_fisher edit distance with default gamma (see Section 4.1.1) - wagner_biased, wb: wagner_fisher edit distance with biased gamma (see Section 4.1.2) - all, aa, a: all possible alignments (see Section 4.1.3) - left, l: only produce left branching trees. - right, r: only produce right branching trees. - both, b: produce left and right branching trees. - suffix_tree_1, st1: suffix tree based alignment, method 1 (see Section 4.2.1) - suffix_tree_2, st2: suffix tree based alignment, method 2 (see Section 4.2.2) - suffix_tree_3, st3: suffix tree based alignment, method 3 (see Section 4.2.3) - suffix_tree_4, st4: suffix tree based alignment, method 4 (see Section 4.2.4)
`-p`	`--part`	Part of the sentences that should be used as hypotheses. (defaults to unequal) - equal, e: equal parts - unequal, u: unequal parts - both, b: equal and unequal parts
`-s`	`--seed`	Seed (for the both alignment type)

`-t`	`--time`	Number of seconds between each checkpoint
`-c`	`--check`	prefix of checkpoint files (default is abl_align)
`-e`	`--excl_empty`	Do not generate hypotheses that span 0 words (see Section 3.2.3)
`-n`	`--nomerge`	Do not try to merge hypotheses (see Section 7.2)
`-x`	`--exhaustive`	Compare exhaustively each possible sentence pair (see Section 7.1)

6.2.2 `abl_cluster`

The program for clustering non-terminals, `abl_cluster`, has no *specific* parameters.

6.2.3 `abl_select`

The program for the selection learning phase, `abl_select`, has the following *specific* parameters

`-s`	`--select`	The selection method: - first, f: earlier learned constituents are correct (see Section 5.1) - leaf, l: terms selection method (see Section 5.2) - branch, b; const selection method (see Section 5.3)

Chapter 7

Optimizing ABL usage

Depending on the characteristics of the training data, several options in alignment learning and selection learning make it possible to reduce the execution time of the algorithm. In the following two sections, the effects of several options are discussed.

7.1 Edit-distance based: exhaustive or smart?

When using *edit distance* based alignment learning, each sentence in the training data can be compared in pairwise fashion with each other sentence in the training data

Algorithm 1 pairwise comparison of all sentences in training data.

Require: S : ordered set of training sentences
  for all sentence $s_i \in S$ **do**
    for all sentence $s_j \in S$ where $j > i$ **do**
      compare(s_i,s_j)
    end for
  end for

Execution of Algorithm 1 results in $N(N-1)/2$ pairwise comparisons. Because comparing sentences that have no words in common will never result in hypothesis generation, the number of pairwise comparisons can be reduced

When comparing Algorithm 1 with Algorithm 2 in terms of runtime complexity, we can see that in Algorithm 2 reduction of the number of pairwise comparisons is achieved at the cost of indexing and listing sentences to compare with, two preprocessing steps which are both linear in corpus size. The program `abl_align` uses Algorithm 2 by default. However, there are two reasons why Algorithm 1 might be better used instead

small training set If the training set is relatively small, or the sentences in the training set have little overlap, the cost of considering twice all sentences in the set does not outweigh the advantage of fewer comparison steps.

conservative memory usage When conservative computer memory usage is

Algorithm 2 smart comparison of all sentences in training data.

Require: S : set of training sentences
Require: s_i : i-th sentence
  for all sentence $s_i \in S$ **do**
    index_words(s_i)
  end for
  for all sentence $s_i \in S$ **do**
    make_compare_list(s_i)
  end for
  for all sentence $s_i \in$ compare_list(s_i) **do**
    for all sentence $s_j \in S$ where $j > i$ **do**
      compare(s_i,s_j)
    end for
  end for

important, not creating the compare lists for the sentences reduces memory usage.

The second algorithm can be selected by specifying the switch `-x` or `--exhaustive` for `abl_align`. To give an indication of the difference in execution time between both algorithms and hence which method applies best for which case, let us consider the results of alignment learning on 6,797 sentences of the OVIS corpus (Strik et al., 1997) and 44,424 sentences of the WSJ corpus (Marcus et al., 1993).

Table 7.1: Number of compares for both algorithms on two corpora

	OVIS	WSJ
# sentences	6,797	44,323
# comparisons Algorithm 1	23,096,206	982,242,003
# comparisons Algorithm 2	6,240,829	749,019,471
Algorithm 2 / Algorithm 1	0.11	0.76

For the OVIS sentences, almost 90% of pairwise comparisons turned out to be unnecessary. For the WSJ, despite having longer and more complicated sentences, there is 24% that could be avoided. To give insight in *when* comparing all sentence pairs can be useful, let us look to the execution speed as function of the time for both algorithms (Figure 7.1, left).

For the OVIS sentences Algorithm 2 turns out to be the most efficient already right from the beginning. This has also been confirmed for larger natural language corpora such as the WSJ, where we can conclude the same. This makes switch `-x` only favorable when we need to be conservative in computer memory usage.

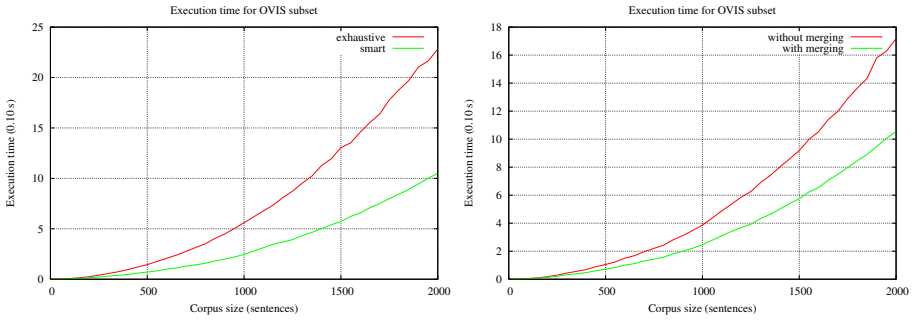


Figure 7.1: Execution time for 2000 sentences OVIS.

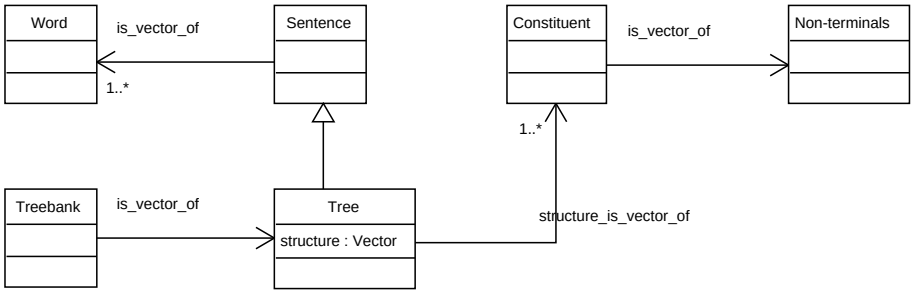
7.2 Generating all hypotheses or projecting on existing hypotheses

By default, hypotheses that are about to be introduced for a sentence pair are compared with already found hypotheses for this sentence pair and merged when they span the same words. This requires more steps in computation, but gets compensated by quite smaller data structures to store the generated hypothesis in. This optimization at the cost of memory can be switched of with the `-n` or `--nomerge` switch. The difference in execution time between merging and not merging is expressed in the right graph in Figure 7.1. From the graph we can observe that for the OVIS corpus execution time decreases considerably when attempting to merge hypotheses.

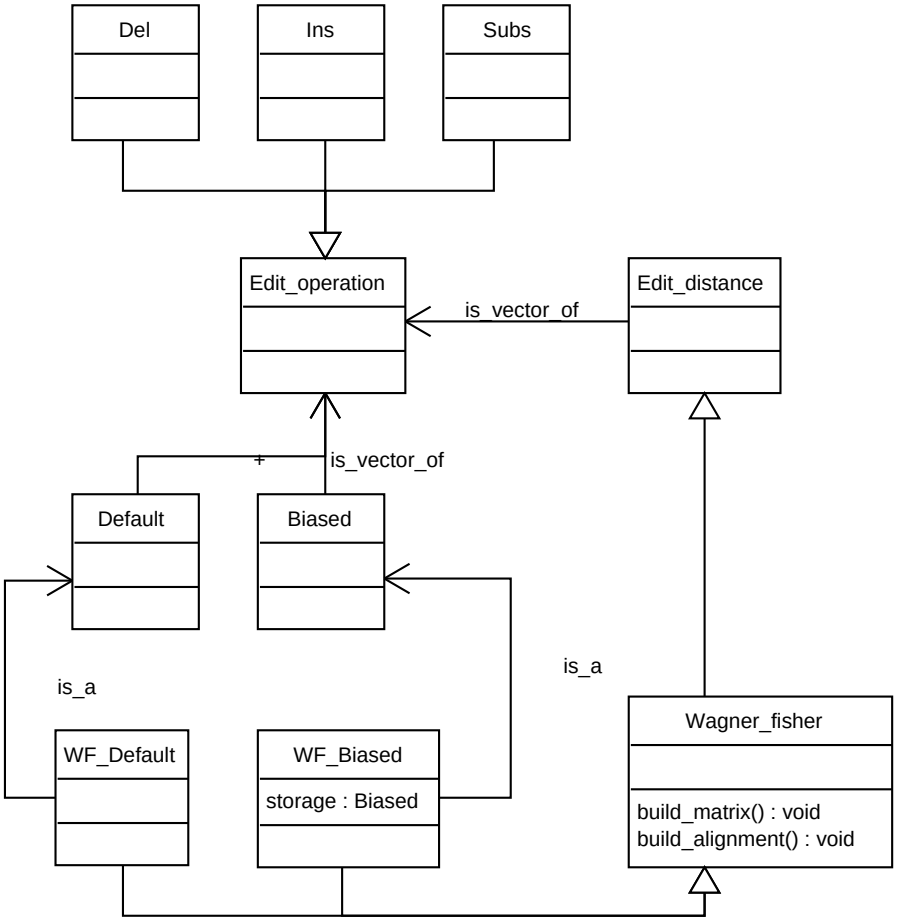
Chapter 8

Source code organization

The main classes in the source code are organized as follows. Classes that support reading/writing and operating on treebanks



Classes that support edit distance based alignment methods


Del
Ins
Subs
Edit_operation
is_vector_of
Edit_distance
+
is_vector_of
Default
Biased
is_a
is_a
Wagner_fisher
WF_Default
WF_Biased
storage : Biased
build_matrix() : void
build_alignment() : void

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