

Querying the Semantic Web with Natural Language

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1 A Brief Introduction to the Semantic Web

The semantic web (as invisioned by Tim Berners-Lee et al.) is an extention of the internet which provides more structure to the vast chaos of data on the net. The goal has always been for the semantic web to become a means for AI agents to share information and reasoning [4]. The world wide web has it's foundation in HTML/CSS/JS documents and HTTP requests. Similarly, the semantic web is rooted in RDF/OWL documents and SPARQL queries.

RDF documents are XML pages which describe object types (classes), and instances of those types. They can also document relations between objects hierarchically or compositionally. RDF documents are quite expressive, in and of themselves.

Then there are OWL ontologies which are RDF documents for describing relations between RDF entities [1]. OWL is more technically specified in such a way that it allows for further automated reasoning over RDF data stores. RDF may make the semantic web expressive, but OWL allows it to be intellegent.

To unlock the power behind the semantic web, there needs to be a way for people to interface with it and ask questions about stored (or reasoned) information. One of the main interfaces is called SPARQL. SPARQL is a query language that is used to ask questions about semantic data [2]. The main benefit to this type of interface is that it allows users to ask complex, exact questions. The main drawback is that, being a formal query language, SPARQL has a steep learning curve and is only accessible to expert users.

The system I propose in this work attempts to make the semantic web more accessible by allowing users to ask questions in natural language. That is, plain English. The actual implementation of this tool handels only a small range of questions, but it does demonstrate promissing possibilities.

2 Converting Natural Language Questions into SPARQL Queries

Since SPARQL is already a well-worn tool for navigating the semantic web, it make sence to leverage it. This system we have built recieves natural language questions such as, "What author has writen both high fantasy and science fiction?" Then the system produces a SPARQL query which asks the same question. The end goal is to allow general users to achieve the same level of sophistication as expert users using English rather than SPARQL.

Work by Kaufmann and Bernstein [13] indicates that users have a clear

preference for even limited natural language interfaces when compared to keyword or query language interfaces. Other recent works [9, 11, 12] have shown that simple natural language questions can be translated based on known sentence structure using (among other things) NER, named-entity recognition.

These systems are limited - they generally only handle simple, direct questions. A recent publication by Sharef et al. [20] outlines obstacles in developing full natural language interfaces for the semantic web. That paper notes a particular difficulty with parsing what we call ‘multifaceted’ questions - questions with multiple variables, constraints, or operations. This is the precise gap which this work attempts to bridge.

The foundations of both compiler design and natural language processing have significant overlap [6, 18]. However, in practice, there has not been much synergy between the two disciplines [3, 10, 18]. I believe cooperation between these astranged fields is necessary to move forward in either.

Our approach was to build a “natural language compiler” of sorts. That is, to approach the problem of converting natural language questions into SPARQL queries just as one might convert Java source code into byte code. The problems are, of course, an order of magnitude apart in complexity. So our only aim was only to parse a limited range of natural language questions. But in that range of questions, we intend to show that multifaceted questions can be handled on a limited basis.

2.1 Named Entity Recognition

Different types of named objects are recognized as part of the parsing process. Since the names are matched during parsing, the NER is greatly improved by context. Still, this matching requires a bit of preprocessing.

Statistical character models are constructed from the output of queries for all objects of a certain type in the target RDF database. These models are used to recognize arbitrary tokens (or combinations of tokens) within the parser’s grammar.

These models allow for probabilistic recognition of the input strings in $O(1)$ time (at least, in relation to the number of objects in the RDF database). They recognize variations on the names (typos, variations, etc.) within some user-defined bound.

2.2 Parsing

TODO: Insert General Introduction to Top-Down Parsing

This system uses a custom parser which has been implemented especially for this project. One of the contributions of this work is the unique implementation of this parser. The parser automatically handles left recursion and a few other hiccups which usually give top-down parsers trouble. However, the parse trees (which the parser outputs) retain the original structure of the initial grammar. This is accomplished by reversing the transformation required to remove left recursion (etc.).

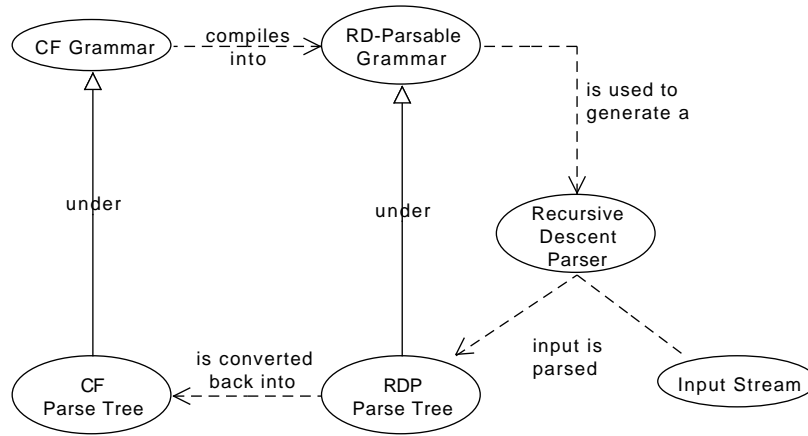


Figure 1: A high level overview of the parsing process.

The grammar generated to handle the natural language questions is composed of rules which handle each type of question. The ‘type’ of question is vague: it is largely a matter of design preference. The broader the scope of a ‘type’, the harder it will be to develop a grammar which recognizes that question. But the narrower the types, the more types will need to be implemented to cover the same range of questions.

Grammar rules are defined for each question, then compiled into a single unified grammar (see figure 2) with left recursion and other such nuisances automatically ‘compiled’ into the grammar. Again, that is to be discussed in a later section.

Given a natural language question, the parser then produces a number of parse trees and selects the “best” (most probable) interpretation. That interpretation

```

Grammar:
0) S -> bibliography_request
1) bibliography_request -> 'WHAT' 'BOOKS' 'HAS' 'author' 'WROTE'
2) S -> author_search
3) author_search -> 'WHO' 'HAVE_WRITEN' BOOK_DESCRIPTION
4) author_search -> 'WHICH' 'AUTHOR' 'HAVE_WRITEN' BOOK_DESCRIPTION
5) BOOK_DESCRIPTION -> 'BOTH' BOOK_DESCRIPTION 'AND' BOOK_DESCRIPTION _BOOK_DESCRIPTION0
6) _BOOK_DESCRIPTION0 -> 'AND' BOOK_DESCRIPTION _BOOK_DESCRIPTION0
7) _0 -> ε
8) _0 -> 'BOOKS'
9) _BOOK_DESCRIPTION0 -> ε
10) BOOK_DESCRIPTION -> 'genre' _0 _BOOK_DESCRIPTION0

```

Figure 2: Grammar

```

Question:
Which writers have published both high fantasy and science fiction?

Best Interpretation:
S
  author_search
    'WHICH':['WHICH']
    'AUTHOR':writers
    'HAVE_WRITEN'
    'HAVE':['HAVE']
    'WROTE':published
  BOOK_DESCRIPTION
    'BOTH':['BOTH']
    BOOK_DESCRIPTION
      GENRE_DESCRIPTION
        'genre':['HIGH', 'FANTASY']: 4.475702
    'AND':['AND']
    BOOK_DESCRIPTION
      GENRE_DESCRIPTION
        'genre':['SCIENCE', 'FICTION']: 4.602974

```

Figure 3: Input and Parse Tree

2.3 Resolution

After parsing, specific instances of named entities need to be ‘resolved’ to corresponding RDF entities. Natural language names (like “John Smith”) are mapped to RDF URIs (like “http://sbc.net/smith394”) in a semi-automated process. This boils down to searching a database of names with a good fuzzy string matching algorithm and falling back on the user to select the appropriate name when there is no obvious best match.

A lot of work went into selecting the best fuzzy matching algorithm for natural language names. Though Levenshtein’s ‘edit distance’ metric is a

good

2.4 Compilation

Compiling SPARQL queries from the resolved parse trees is the last step. For each type of question, there will be a separate unit which generates SPARQL queries. There might be a more elegant way to handle this problem, but this seems like an extensible (if tedious to implement) solution. Generation is often just a matter of fitting RDF URIs into hard-coded templates.

```
SPARQL:
PREFIX dbpprop:<http://dbpedia.org/property/>
PREFIX dbp:<http://dbpedia.org/resource/>
PREFIX dbpowl:<http://dbpedia.org/ontology/>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>
SELECT ?author ?name
WHERE{
    ?author a dbpowl:Writer;
        rdfs:label ?name.

    ?book0 a dbpowl:Book;
        dbpowl:author ?author;
        dbpprop:genre <http://dbpedia.org/resource/High_fantasy>.

    ?book1 a dbpowl:Book;
        dbpowl:author ?author;
        dbpprop:genre <http://dbpedia.org/resource/Science_fiction>.

    FILTER langMatches( lang(?name), "EN" ).
}
GROUP BY ?author
```

Figure 4: SPARQL Output

3 Software Architecture

This architecture is aimed at handling complex questions in a narrow domain. It does more than named entity recognition - it actually considers the full syntax of the language and processes natural language questions much like a compiler might process source code. It uses top-down parsing to generate a parse tree for the input question then compiles SPARQL queries

from that parse tree. This section will explain the design of the system at the highest level.

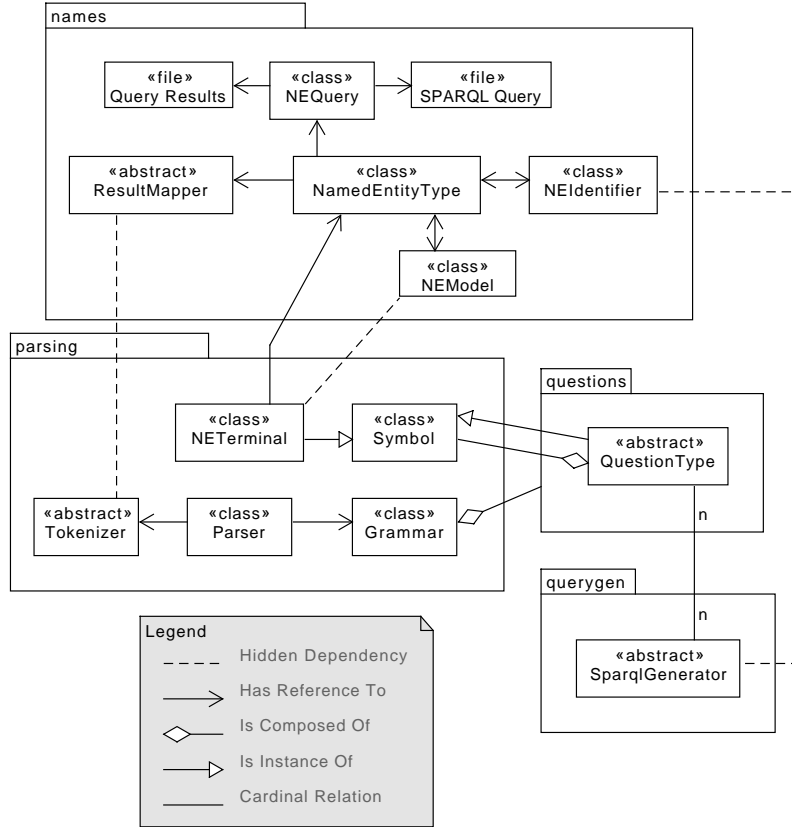


Figure 5: Architecture

One of the goals of this project was to develop a highly extensible architecture. There wasn't enough time to cover the breadth of questions one would hope for in a mature product - such being the nature of research. But I felt it was important to create a practical working system that could handle a wide range of questions if more time was dedicated towards that end.

To make the system extensible, it was important to decouple the various components as much as possible. Still - language processing is a naturally interdependent process with many overlapping concerns. For instance, parsing seems to be an independent problem from named entity recognition (NER),

but to achieve better parsing results it was necessary to integrate NER into the parser so that semantic context could inform the NER.

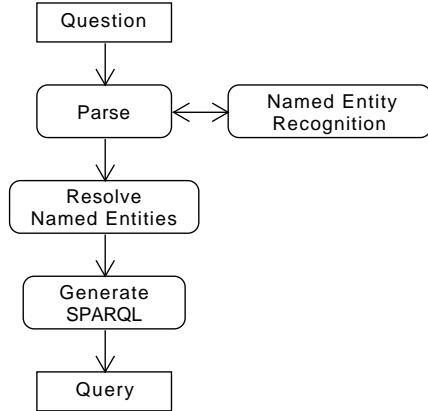


Figure 6: Process

Another design concern was the accessibility of the SPARQL endpoint. It would be ideal if the endpoint was always accessible, would accept an unlimited number of queries, and would always respond quickly. But in practice, none of those ideals are true. As such, the results of certain queries (necessary for developing NER models and URI resolution) are cached into local files. The tradeoff is that data in the cache can stagnate. That problem is mitigated by simply flushing the cached results periodically.

4 Resolving User Input Names to RDF Entities

Matching natural language names to RDF entities is essential to evaluating natural language questions over RDF databases. This poses several problems: names can be misspelled (e.g. "Swartsenegger" for the label "Schwarzenegger"), may be reordered (e.g. "John Smith" for the label "Smith, John"), or the name may be abbreviated (e.g. "R.L. Stine" for the label "Robert Lawrence Stine"). That's not to mention the small problem posed by people who have changed their name entirely, sometimes multiple times (e.g. "The artist formerly known as 'The artist formerly known as Prince'"). And despite all of these convolutions, a natural language system will need to recognize and match these arbitrary instances with the often-sparse naming information present in RDF data.

My approach to this problem was to find a string distance function which was robust to these changes and use that to simply find the best match name in $O(n)$ time. Since the names are narrowed down by context (using the parser), this was an acceptable solution: we don't need to iterate over every single label in the RDF set, just those which belong to the particular type of object the user is asking about.

There are a surplus of string comparison functions to choose from [8]. For my particular application, I have used a variation on the *Jaccard index*. It is robust to misspellings and reorderings, with the added benefit of being quite efficient. The Jaccard index is used in datamining for efficiently comparing long documents, but it is comparable to other more complex methods of name comparison [8] and anecdotal evidence suggests it will work well here.

Another problem is resolving multiple close names (or even exactly the same name) to a single entity. I took a simplistic approach (just asking the user) but I will also discuss other more sophisticated possibilities for further research.

4.1 Name Standardization and Enumeration

Before jumping into the specifics of the name comparison algorithm, there are a few trivialities to deal with. Names with abbreviations, punctuation, and names with multiple parts can all trip up comparison algorithms.

One standardization method I used was to remove punctuation and change all letters to upper case. There may be a few edge cases where "John O'neal" isn't the same as "John Oneal", but the mistake is acceptable the majority of the time. And such names are so close that they would trigger the system to prompt the user for confirmation anyways.

Names with multiple parts, like "John Jacob Jingleheimer Schmidt", need to be matched by partial variation like "Schmidt", "Mr. Schmidt", and "John Schmidt". Using a sufficiently robust string comparison function, these variations will often still match the full, multi-part name better than other multi-part names. But that's a dubious assumption to rely upon - it's best to tokenize the name and include the different partial variations as other names linked with the entity. As part of my own system, I simply included the first and last names as variations on the name, excluding the middle name(s).

4.2 Jaccard Index

The Jaccard index is a measure of how similar two sets are to each other. This is useful in a whole host of applications [5], as you might imagine. In this application, using the Jaccard index on fragments of strings yields a very robust string comparison function.

Let A and B be sets or multisets, then the Jaccard index $J(A, B)$ is defined [8, 17]:

$$J(A, B) = \frac{|A \cap B|}{|A \cup B|}$$

Or if both sets are empty, $J(A, B) = 1$. For comparing strings, the sets might be of characters (e.g. 'HELLO' $\mapsto \{E, H, L, O\}$), of tokens (e.g. 'JOHN H SMITH' $\mapsto \{'JOHN', 'H', 'SMITH'\}$), or in this case, *n-grams*.

These n-grams (also known as 'k-grams' or 'shingles' [17]) are all unbroken substrings of length n of a given string. So the 3-grams of the string 'anabasis' are {'ana', 'nab', 'aba', 'bas', 'asi', 'sis'}.

In this application, n-grams were constructed to include imaginary pre and post string characters (represented here as '^' and '\$' respectively). So, for instance, the 3-grams of 'cat' are then {'^c', '^ca', 'cat', 'at\$', 't\$\$'}.

This gives significance to the beginning and end of a string when using the Jaccard index with the n-grams.

For a distance function, one can use:

$$d(s_1, s_2) = 1 - J(ngrams(s_1), ngrams(s_2))$$

This doesn't produce a true metric space for the strings (since two different strings can have exactly the same n-grams), but it does satisfy the triangle inequality [5] and is always non-negative. As such, one could conceivably construct an M-tree [7] to improve lookup speed. That hasn't been necessary in this research, but then again, this domain might be smaller than one might experience in practice.

4.2.1 Comparison with Levenshtein (Edit) Distance

Levenshtein distance (also known as 'edit distance') is a more common fuzzy string comparison algorithm than the Jaccard index. Its ubiquity might be due to a simple happenstance: the algorithm for calculating edit distance is a favorite example in algorithm design courses for demonstrating dynamic programming. But its popularity is by no means a guarantee that it is the best choice, as I'll demonstrate.

Levenshtein distance is define as [16] the minimum number of 'edits' (additions, deletions, or swaps) that must occur before one string matches another. But these are only single-character edits, and so the algorithm doesn't handle large displacements of parts of the name with any sort of grace. This is best demonstrated by example; see figure 8.

```
Levenshtein:
14 'global kirstein investing' 'kirstein global investing'
13 'global kirstein investing' 'scherl global investing'
7 'kirstein global investing' 'scherl global investing'

Jaccard w/3-grams:
0.3125 'global kirstein investing' 'kirstein global investing'
0.594594594595 'global kirstein investing' 'scherl global investing'
0.514285714286 'kirstein global investing' 'scherl global investing'
```

Figure 7: Bad Levenstein Name Matching

Using levenshtein distance to match 'closest' strings, word inversions would be considered bulk deletions and insertions. The Jaccard index handles this better because inverting whole words still preserves the ngrams within those words even if it breaks the joining ngrams between the words.

Admittedly, the Jaccard index is less forgiving of small typos. A single character edit breaks n n-grams. So, for short single word names, levenshtein distance is probably the preferred metric.

4.2.2 Information Content Sensitive Jaccard Index

The Jaccard index by itself is a fairly good way to compare names. But it would be better if the algorithm also noticed things like how 'unusual' certain name patterns were. "Tom Smith" might be closer to "John Smith" than "Tom" based purely on their Jaccard index, but any reasonable person would pick "Tom Smith" and "Tom" to be the closer names because "Smith" is such a common surname.

In more technical terms, the part of the string "Smith" should recieve less 'weight' in the comparison function because it conveys less information.

Consider the more general form of the Jaccard index [5]:

$$J(\vec{x}, \vec{y}) = \frac{\sum_i \min(x_i, y_i)}{\sum_i \max(x_i, y_i)}$$

Where \vec{x} and \vec{y} are large dimensional vectors rather than sets. To help relate it back to the original form, imagine that \vec{x} and \vec{y} are lists of counts of all

the possible things that could be in the two sets (or multisets) A and B .

$$\begin{aligned} x_i &= \text{count}(e_i; A) \\ e_i &\in \{A \cup B\} \end{aligned}$$

Now if we want to consider the amount of information each little portion of the string contains, we can calculate it using the equation layed down by Shannon [19]. Namely, that the self information of an event is the log of the inverse of the probability that event occuring. In this case, the 'event' is the occurence of a certain n-gram in the string.

$$\begin{aligned} I(e_i) &= \log \left(\frac{1}{P(e_i)} \right) \\ &= -\log(P(e_i)) \end{aligned}$$

To determine this probability, we can look at the frequency of the n-gram in a large sample set of names. We need to index those names anyways, as part of the named entity recognition proces. With a large set, we can get pretty close to a true approximation of the probability of an n-gram occuring in a general population of those names:

$$P(e_i) \approx \frac{\text{count}(e_i; N) + 1}{|N| + 2}$$

Where N is the multiset containing the union of all the n-grams of all the names. Then, we can weight the vectors x and y such that we have an information sensitive comparision function: $\hat{J}(x, y)$:

$$\begin{aligned} \hat{J}(\vec{x}, \vec{y}) &= \frac{\sum_i \min(x_i I(e_i), y_i I(e_i))}{\sum_i \max(x_i I(e_i), y_i I(e_i))} \\ &= J(\vec{x} \cdot \vec{I}, \vec{y} \cdot \vec{I}) \\ \vec{I} &= \langle I(e_1), I(e_2), \dots, I(e_n) \rangle \end{aligned}$$

The above example shows this comparison in action. In the top comparision, without considering information content, the closest pair of names is "tom smith" and "john smith". But after indexing the sample names, we can calculate comparisons that do consider the information content. Then we can see that the closer names are "tom smith" and "tom".

```

Without Info:
0.647058823529 'tom smith' 'john smith'
0.769230769231 'tom smith' 'tom'
1.0 'john smith' 'tom'

Sample Set:
adam smith
bob smith
carl smith
dale jones
ernest kirstein

With Info:
0.729636835639 'tom smith' 'john smith'
0.723483108499 'tom smith' 'tom'
1.0 'john smith' 'tom'

```

Figure 8: Information Sensitive Name Matching

4.3 Ambiguity

What should the system do when the user inputs a name which is close to the names of several entities by the chosen name comparison function? The easiest solution would be to simply ask the user which of the possible entities they meant. But this isn't always a great solution; what if you're asking about a cornicopia of names? Sure, it might be out of scope for this particular system to resolve questions such as "Which of the actors in 'my_data_file.txt' have been in movies together?" But that's certainly within the realm of possibilities for some future work.

One approach to this problem would be to create a separate system for distinguishing the "right" name from a small(er) selection of possible candidates. The aforementioned Jaccard index (or similar distance metric) might be used to narrow down the problem space to something managable, then a much more sophisticated (yet slower) system could choose the right name from the smaller set.

Since there are a number of string comparison algorithms, one could (if time permitted) implement several of them and use a combined metric to evaluate the names for fitness. For example, a feed-forward neural net could be trained to recognize the 'right' name based on a number of factors:

- String comparison functions (Jaccard, Levenshtein, etc.)
- The self-information [19] of the input and potential match names

- The closeness of other potential match names
- The prevalence of the potential match entity in the RDF data
- The frequency of queries involving the potential match entity
- Etc.

5 Top-Down Parsing

Historically, top-down parsers were been coded manually or else generated from a context free grammar specification. [14, 15] Coding a RDP manually is tedious, error prone, and difficult to maintain. Programatically generating a top-down parser from a grammar still isn't ideal - converting a context free grammar into a top-down parsable form may not preserve the *strong equivalence* of the grammar. And as a result, parse trees generated by that RDP will not be in the same form as they might appear in the initial (non-RD-parsable) grammar, which is often a more natural representation of the desired language [21].

In this work, we hope to describe a useful adaptation to top-down parsing which addresses these problems. Our system compiles a context free grammar specification into a top-down parseable grammar. A parser is generated from the top-down parseable grammar, and used to parse a input streams. The resulting parse trees are then transformed back into equivalent parse trees under the original grammar. (Figure 1)

5.1 Introduction to Top-Down Parsing without Syntax Diagrams

Introductory material by Dr. Lewis [14] describes a recursive-descent parser as a piece of software which takes a sentence and turns it into a parse tree by performing a 'depth-first' search. But a search of what? One might try to call it a search of the parse tree, but that's not exactly right. The 'recursive descent' name comes from the way that a RDP traverses through a syntax diagram of a context free grammar [21].

Recursive decent is just one form of top down parsing. The top-down parsing in this thesis does not use syntax diagrams (in hindsight, this was a questionable design choice, but such is life). This section will describe how top-down parsing works without using syntax diagrams.

Consider a context-free grammar with the following production rules:

$$S \rightarrow aS \quad (1)$$

$$S \rightarrow bS \quad (2)$$

$$S \rightarrow \epsilon \quad (3)$$

And the following string which we will attempt to parse: "ab"

We know, right off the bat, that the start symbol S will be the root of any parse tree created under this grammar, by virtue of it being the start symbol. (Figure 9)

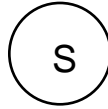


Figure 9: Parse Tree 0

The next parse tree we should consider is the parse tree that is generated when we follow the first production rule. (Figure 10) Notice that, in this instance, the parse tree does not conflict with the string we are trying to parse - i.e. regardless of the production rules we follow the string that is produced from any further production rules we follow will start with "a".

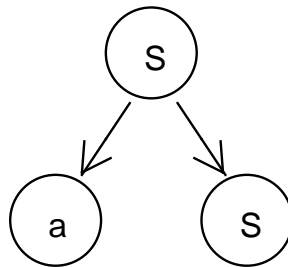


Figure 10: Parse Tree 1 - Valid

For the next parse tree, we will try to repeat our last action (following the first possible production rule). (Figure 11) This parse tree conflicts with

the string we are trying to produce since any string produced by further production rule applications will produce a string starting with "aa". In this case, we go back to the previous parse tree and try a different production rule.

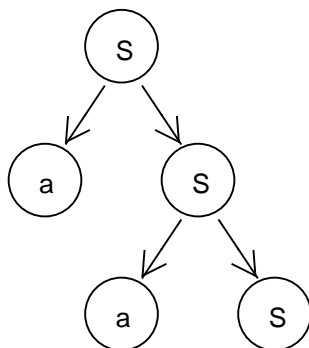


Figure 11: Parse Tree 2 - Invalid

In figure 12, we've followed the second production rule and our new parse tree fits with the input string, so we can continue our descent.

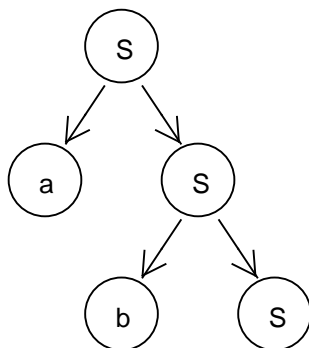


Figure 12: Parse Tree 3 - Valid

The next two parse trees (Figure 13), created by applying the first and second production rules to Parse Tree 3, are both invalid because they extend past the length of our input string.

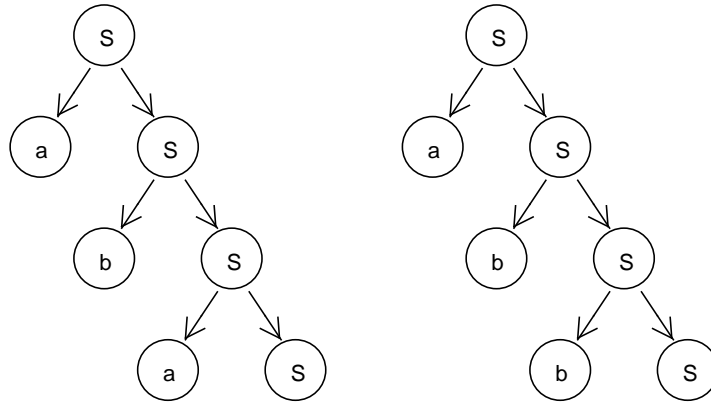


Figure 13: Parse Trees 4 and 5 - Both Invalid

In the last step, by applying the third production rule to Parse Tree 3, we have a parse tree which terminates and produces the desired input string, "ab". (Figure 14)

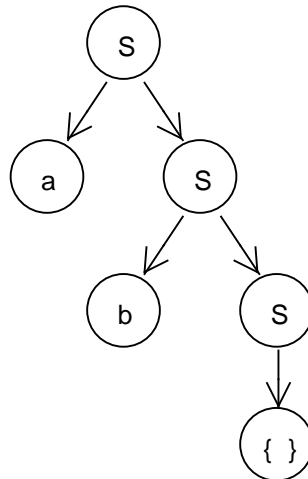


Figure 14: Parse Tree 6 - Complete

Finally, let's diagram our traversal through the possible parse trees (Figure 15). Shown this way, one can notice a pattern in our attempt to build

the tree. The top-down parser performs a depth first search of the graph of possible parse trees, looking for a parse tree which fits the input string. The child nodes from each PT (Parse Tree) node in the graph are PT nodes generated by applying each of the production rules to the first (left, deepest) nonterminal symbol in that PT node. The depth of each node in the PT tree corresponds with the number of production rules that have been applied.

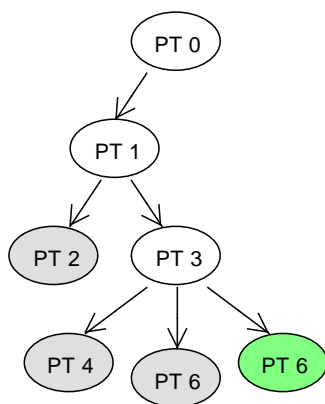


Figure 15: Parse Tree Search Progression

5.2 Effect of Grammar Transformations on Parse Trees

Left recursion is a problem for top-down parsers because it may cause them to go into an infinite loop. Using the model described in section 5.1: when a PT node is reach where the first non-terminal symbol has a production rule with left recursion, it's child node will have the same non-terminal symbol so it will produce a child node with the same non-terminal symbol ad infinitum - and none of those children will consume any terminals from the input stream so the parser will not proceed.

So, removing left recursion from context free grammars is a necessary evil for top-down parsing. It just takes two transformations to turn any context free grammar with left recursion into a *weakly equivalent* grammar with only right recursion. These two transformations are direct left recursion elimination, $DLRE(G; R_\alpha, R_\beta) \rightarrow G'$ and substitution, $Sub(G; r_\alpha, R_\beta) \rightarrow G'$, which is used to remove indirect left recursion. [3, 14] These sections will describe how these transformations work on the grammar and on their parse trees.

5.2.1 Direct Left Recursion Elimination

A left recursive grammar, G , has rules for some non-terminal A of the form $A \rightarrow A\alpha_i$ and $A \rightarrow \beta_j$, $i \in [1, m]$, $j \in [1, n]$. Let R_α and R_β represent the sets of those rules respectively where the notation $R_\alpha(1)$ represents $A \rightarrow A\alpha_1$. Such a grammar represents a language which contains strings of the form $\beta_y \alpha_{x_1} \alpha_{x_2} \dots \alpha_{x_p} \dots \alpha_{x_{k-1}} \alpha_{x_k}$ where $y \in [1, m]$ and each $x_p \in [1, n]$. However, to produce such a string, the alpha rules need to be followed in reverse order:

$$R_\alpha(x_k), R_\alpha(x_{k-1}), \dots R_\alpha(x_p), \dots R_\alpha(x_2), R_\alpha(x_1), R_\beta(y)$$

The transformation [3] $DLRE(G; R_\alpha, R_\beta) \rightarrow G'$ changes each rule in R_α to the form $A' \rightarrow \alpha_i A'$, each rule in R_β to the form $A \rightarrow \beta_j A'$, and adds an additional rule $R_\epsilon = A' \rightarrow \epsilon$. Consequently, the order of the followed production rules in G' results in alpha rules being followed in forward order:

$$R_\beta(y), R_\alpha(x_1), R_\alpha(x_2), \dots R_\alpha(x_p), \dots R_\alpha(x_{k-1}), R_\alpha(x_k), R_\epsilon$$

The transformation effects the parse trees by flipping and reversing A chains, replacing lower A nodes with A' nodes, moving the β up, and adding an A' node and ϵ node to the end of the chain. (Figure 16) The inverse transformation removes last A' and ϵ nodes, moves the β back down to the end of the chain, and changes the A' nodes back into A nodes, then flips and reverses the A chain. Note that the α and β nodes are arbitrary strings,

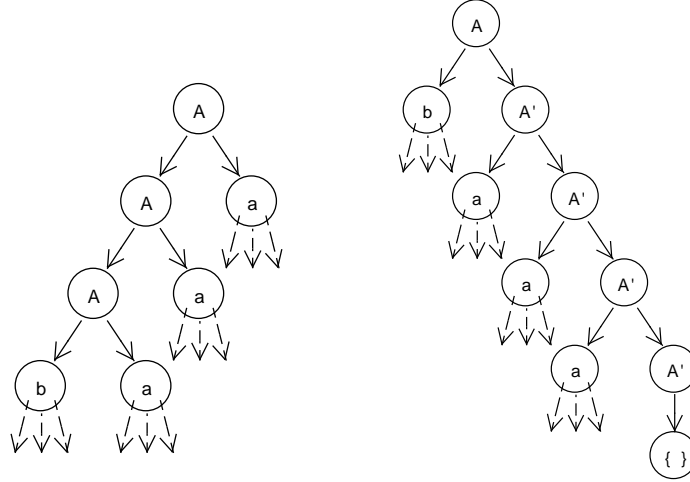


Figure 16: Original and Transformed Parse Trees

so in reality they might be multiple nodes which might have any number of children.

More formally, for each A node in the RD-parsable grammar, the inverse transformation $DLRE^{-1}(T'; A, A') \rightarrow T$ modifies chains of A/A' nodes where the children of the A node are C_A , of all but the last A'_{x_p} node are $C_{A'_{x_p}}$, and the last A'_ϵ node has only the child ϵ . From the $DLRE$ transformation rules we know that the C_A will be of the form $\beta_y A'_{x_1}$. We can also conclude from the $DLRE$ transformation that each $C_{A'_{x_p}}$ will be of the form $\alpha_p A'_{x_{p+1}}$ when $p < k$ and A'_ϵ when $p = k$.

The inverse transformation first removes the A'_ϵ node. Then it changes each remaining A'_{x_p} node into an A_{x_p} node with the same children. Next the A_{x_p} are restructured such that each $C_{A_{x_p}}$ is equal to $A_{x_{p-1}}\alpha_p$ where $1 < p$ and $\beta_y\alpha_k$ where $p = 1$. The top node of the chain, A , is replaced with A_{x_k} . And this process is repeated for each chain.

5.2.2 Substitution

TODO

5.3 Compiling a Context Free Grammar for RD Parsing

It is important to notice that not all context free grammars can be directly parsed by a top-down parser. Some context free grammars require a bit of manipulation to remove left recursion (direct or otherwise) [21]. This process of converting a context free grammar into a *weakly equivalent* top-down parsable grammar shall be referred to as *compiling* the grammar.

In this section, a grammar will be defined from an ordered collection of production rules. My parser uses context-free grammar rules, which are comprised of a 'head' (the single-symbol left hand side of the production rule), and a 'tail' (one or more symbols comprising the right hand side of the production rule).

These grammars may be 'compiled' using the four procedures: factoring, substitution, removing left recursion, and removing useless rules. Let 'decision list' define an ordered list of production rule choices which produces a parse tree. As each of these four procedures produces a weakly equivalent grammar, there exists a mapping for any decision list in a compiled grammar back into a same-terminal-producing decision list in the pre-compiled (parent) grammar. My parser keeps track of these inverse transformation rules as it performs its compilation procedure so that a compiled grammar's decision list can be easily converted to the initial grammar's equivalent decision list.

Take this simple grammar for example:

$$S \rightarrow AB \tag{1}$$

$$A \rightarrow a \tag{2}$$

$$A \rightarrow SA \tag{3}$$

$$B \rightarrow b \tag{4}$$

$$B \rightarrow SB \tag{5}$$

It compiles into the weakly equivalent grammar:

$$Z \rightarrow \epsilon \quad (1)$$

$$B \rightarrow b \quad (2)$$

$$S \rightarrow aBS' \quad (3)$$

$$S' \rightarrow \epsilon \quad (4)$$

$$A \rightarrow aZ \quad (5)$$

$$B \rightarrow aBS'B \quad (6)$$

$$S' \rightarrow aZBS' \quad (7)$$

$$Z \rightarrow bS'A \quad (8)$$

$$Z \rightarrow aBS'BS'A \quad (9)$$

So when the terminal stream "aabb" is parsed in the compiled grammar to the decision list [3,6,2,4,2,4] it can be transformed into the parent-grammar-equivalent decision list: [1,2,5,1,2,4,4].

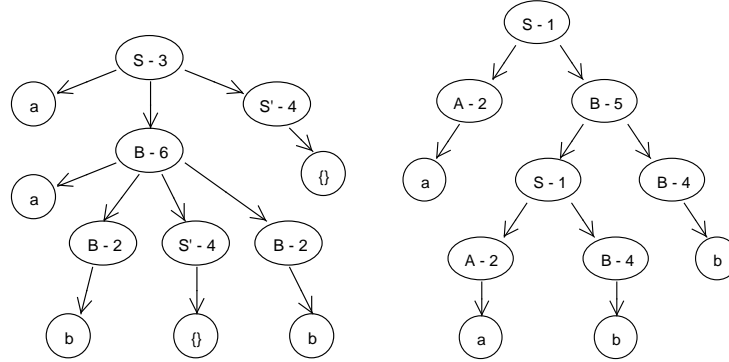


Figure 17: Compiled Grammar Parse Tree (left) Parent Grammar Parse Tree (right)

Terms

- **Grammar:** a phrase-structure grammar is defined by a finite vocabulary (alphabet), a finite set of initial strings, and a finite set of rules... [6] (see Production Rule)
- **Context-Free Grammar:** a context free grammar is one which only has production rules whose head is a single non-terminal symbol. [10, 15, 21]
- **Production, Production Rule, Rewrite Rule:** rules of the form $X \rightarrow Y$ where X and Y are strings in [a grammar] [6]; define the nonterminal symbols by sequences of terminals and nonterminal symbols [21]; rules which specify how nonterminal symbols may be expanded into new sequences of symbols (terminal or otherwise).
- **Head (Production Rule):** the left hand side of a production rule
- **Tail (Production Rule):** the right hand side of a production rule
- **Parse Tree:** an ordered, rooted tree whose nodes are symbols in a context-free grammar where the children of each brach node correspond to the tail of some production rule in said grammar; a tree-representation of the grammatical structure of [an input stream] [10]
- **Weakly Equivalent (Grammar):** two grammars are [weakly] equivalent if they define the same language. [18]
- **Strongly/Structurally Equivalent (Grammar):** two grammars are strongly or structurally equivalent if they are weakly equivalent and can assign any sentence the same parse tree. [18]

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