Compound Analysis in FM Work Paper

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We will describe the compound algorithm of Functional Morphology and suggest a novel improvement.

The first step in the compound analysis of Functional Morphology is *deconstruct*, which deconstructs the input string into a set of sequences of forms, where the forms are word forms in our lexicon. The lexical lookup occurs in the function *lexical_prefix*, which divides the string into all prefixes occuring in the lexicon together with their suffixes. The suffixes are recursively deconstructed.

If we have sandhi-like phenomena in the word boundaries, e.g., the *three conso*nant rule¹ in Swedish, then *lexical_prefix* would be responsible of generating the candidates that the phenomena predict.

The function *deconstruct* is typically overgenerating, so in the next step we use the function *validate* to filter out impossible compounds. Note, if alphabetic characters are elements in the lexicon, we end up with a combinatorial explosion by using *deconstruct*. For this reason, we normally push the test *validate* into the generator *deconstruct*, or, as is the case in Functional Morphology, use a lazy language.

 $compound(s) = \{c \mid forms \in deconstruct(s) \land c \in validate(forms)\}$

It is the *validate* function we will focus on here, where we start with describing the current approach of Functional Morphology. Every morphosyntactic description in Functional Morphology are associated with a compound attribute integer value, encoding where a form with that morphosyntactic description may occur in a compound.

¹The rule concerns Swedish compound formation: if a compound boundary consists of three consonants that are the same, then these consonants are reduced into two consonants, e.g., glass + skål \rightarrow glasskål (Eng. 'ice cream bowl'). This reduction introduces ambiguity, since we have glass+skål and glas+skål (Eng. 'glass bowl'), and *lexical_prefix* is responsible of generating both candidates.

Naturally, a form may have many descriptions, and consequently, many compound attribute values, since forms are homographically ambiguous.

$$validate(c) = \{c \, | \, x \in attributes(c) \land valid_sequence(x)\}$$

The function *attributes* generates all possible compound parameter sequences, and *valid_sequence* is a boolean function that describes which sequences are considered possible.

The algorithm works efficiently, but the description of compounds is unsatisfactory: it is highly inflexible, we do not use all information that is actually available, and the use of integers to encode compounding behaviour is simply error-prone and unaesthetic.

Let us start by looking at what information we have available in an analysis in Functional Morphology, here for the Swedish word *ankans* (Eng. *the duck's*), which only has one analysis. The eight fields have the following meaning: *wf* is the current word form, *cf* its citation form, *pos* its word class, *msd* its morphosyntactic description, *inhs* its inherent feature, *lid* its lemma id, *pid* its paradigm identifier, and *attr* its compound attribute.

wf	ankans	cf	anka
pos	nn	msd	sg def gen
inhs	u	lid	ankann.1
pid	nn_1u_flicka	attr	0

We can now ask us the question — do we actually need the attr field, why not have compound rules based on all the other fields? This idea will be further pursued in the rest of the text.

For example, we may have a rule for Swedish noun compound looking like this, where words tagged *ci* are compound forms that may appear in initial positions and words tagged with *cm* are compound forms that may appear in medial positions.

$$\textbf{rule noun } [pos = nn] = \{msd = ci\}\{msd = cm\}^*\{msd \notin \{ci, cm\}\}$$

The name of the rule is noun, and the association pos=nn enclosed in square brackets is common for all patterns after the equal sign. The first pattern requires that the first word form has msd=ci, the second pattern requires zero or more word forms with msd=cm, and the third and last pattern requires a word form that has a msd which is not ci or cm.