Generating and using probabilistic morphological resources for the biomedical domain

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Abstract
In most Indo-European languages, many biomedical terms are rich morphological structures composed of several constituents mainly originating from Greek or Latin. The interpretation of these compounds are keystones to access information. In this paper, we present morphological resources aiming at coping with these biomedical morphological compounds. Following previous work (Claveau and Kijak, 2011; Claveau, 2012), these resources are automatically built using Japanese terms in Kanjis as a pivot language and alignment techniques. We show how these alignment information can be used for segmenting compounds, attaching semantic interpretation to each part, proposing definitions (gloses) of the compounds... When possible, these tasks are compared with state-of-the-art tools, and the results show the interest of our automatically built probabilistic resources.

Keywords: Morpho-semantic analysis, biomedical terminology, probabilistic morphological resources

1. Introduction

In the biomedical field, specialized terms are keystones to access information. However, in most Indo-European languages, these terms are rich morphological structures composed of several constituents mainly originating from Greek or Latin. Such morphological complexity is important to take into account for basic processes (translation, establish semantic relations...) as well as higher-level HLT, like machine translation or Information Retrieval (IR).

In this paper, we present morphological resources aiming at coping with these biomedical morphological compounds. Following previous work (Claveau and Kijak, 2011; Claveau, 2012), these resources are built automatically from the UMLS MetaThesaurus (Tuttle et al., 1990) (a multilingual database grouping several biomedical terminologies), and are now available in several languages (including, English, French, Spanish...). Our approach relies on the use of Japanese as the pivot language, and more specifically on terms written in kanjis to help the decomposition of words in other languages. In a fully automatic way, they are cut into morphemes and each morpheme is associated with the corresponding kanji.

For example, the term photochemotherapy can be translated into Japanese by 光化学法; indeed, by decomposing and aligning these two terms, we have:

- photo ↔ 光 (‘light’);
- chemo ↔ 化 (‘chemistry’, ‘drug’);
- therapy ↔ 法 (‘therapy’).

As we see here, each morpheme is associated with kanji that can be seen as semantic descriptors, more suitable for NLP problems than the initial full term. Thus, our morphological analysis is chiefly based on the alignment between morphemes and kanjis which is performed with a forward-backward algorithm adapted to the manipulated data. As a side effect, this process generates a probabilistic correspondence table (for each language) between kanjis and morphemes. These tables are the main component of the morphological resources presented in this paper, as they can be used in many applications as we will see. In addition, this paper also describes how the UMLS can be used again to attach a biomedically suited translation to the morpheme/kanji pair (eg. the morpheme hemo, aligned to 血液, is translated by ‘bloody’).

The remaining of the paper is structured as follows. We first review related work and resources (Sect. 2.). In Sect. 3., we describe the processes that make it possible to generate the morphological resources for most European languages. In Sect. 4., several evaluations are reported on different aspects of the generated resources.

2. Related work

Different studies rely on morphology to perform some terminological analysis. It is especially the case in the biomedical domain. Indeed, on the one hand, terminologies are a keystone for many applications, and on the other hand, those terms are usually built by a morphological operation said neoclassical composition. For example, terms like magnetoencephalography can be decomposed into three morphs: magneto/encephalo/raphy. The nature of the implied morphological units (Iacobini, 1999; Dal and Amiot, 2008) as well as the rules governing the way these units are composed (Dal and Amiot, 2008; Fradin, 2005) make these morphologically-complex terms particular linguistic objects. Besides that, the many terms that are built this way and the productive property of the neoclassical composition (it serves to produce many neologisms) make this phenomenon also important from an applicative point of view.

There exists some databases containing morphological information for the biomedical domain, like Biotop1 in

1georges.dolisi.free.fr/
French or Dorland’s² in English. Yet, these resources are far from being complete, and their use for automatic analysis is difficult (each morpheme is solely described with an informal definition) and no information is given on how to combine them.

Apart from that, morphological analysis systems have been proposed. Some of them adopt a lexematic approach, in which the term forms are used to exhibit relations between terms, but without decomposing explicitly into morphemes (Grabar and Zweigenbaum, 2002; Claveau and L’Homme, 2005; Hathout, 2009, for example). Other studies adopt a morphemic approach in which terms are decomposed into morphemes. These studies can be grouped according to the amount of expert knowledge or resources on which they are based. Some fully automatic techniques only necessitate a list of terms in which recurrent letter sequences will be considered as morphemes (Creutz and Lagus, 2005; Kurimo et al., 2010, *inter alia*). Yet, such approaches cannot associate any knowledge with the morphemes. Other morphemic work relies on expert knowledge: morphemes, their semantic information, and the morphological composition rules are mostly manually given as facts or heuristics (Baud et al., 1999). Among this family of approach, one can further distinguish the techniques according to their applicative goal and the more or less detailed analysis that they provide. For instance, some provide a segmentation of the morphological compounds and assign interlingua identifiers to the morphological units found (Markó et al., 2005).

Other techniques provide a hierarchical decomposition and an interpretation of the compound (Namer, 2007; Deléger et al., 2008). The work presented in this paper adopts the same morphemic approach, but our resources are automatically built, which makes them more complete and easily available in many languages. From a technical point of view, the approaches used to generate and exploit our probabilistic morphological resources can be compared with existing work on transliteration, in particular of Arab or of terms written in Katakana, for both direct translation (Knight and Graehl, 1998, for example), or for the search of translation (Chiao and Zweigenbaum, 2002; Tsuji et al., 2002). From this point of view, a close work is proposed by (Morin and Daille, 2010); they propose to find equivalence between French terms and Japanese terms written in Kanjis based on morphological considerations. Yet, here again, the few rules at the heart of their approach have to be built by an expert, and only a simple morphological phenomenon (derivation) is considered. Their approach cannot be used for neo-classic compounds as we are aiming to do.

### 3. Generating biomedical morphological resources from the UMLS

#### 3.1. On the use of kanjis as pivot

As explained before, the generation of our morphological resources relies on an alignment step of terms from the studied language with their translations in kanjis. It is worth noting that the choice of kanjis as pivot language is not fortuitous. Kanjis, one of the three Japanese writing systems, are very used in specialized domain; inherited from the Chinese sinograms, they are mostly pictograms or ideograms. They are suited to our problem, since they are invariable whatever their position in the term and neighboring kanjis. Obviously, they are also independent from Latin and Greek, which prevent our approach to find fortuitous regularities based on common etymology.

Our approach makes a strong hypothesis of parallelism: the kanji terms have to be built in a similar way than the morphological composition of the terms in the other language. This hypothesis is verified in most cases since the Japanese word order and the morphological composition rules at stake are identical. Indeed, Japanese is sometimes qualified as a free-order language, but one of its basic principles is to indicate the characteristic of an object before the object, arguments before the predicate, and more generally the governed before the governing (Nakamura-Delloye, 2007). This order is also the one used in Roman languages for neo-classical composition (on the contrary of ordinary composition) in which the semantically governed morphological unit is before the governing one (Dal and Amiot, 2008).

#### 3.2. Previous work: alignment

In previous studies (Claveau and Kijak, 2011; Claveau, 2012), we have proposed an original approach to align morphologically-complex compounds with their Kanjis translations. The only requirement is a list of terms in the studied language with their Kanjis translations, without any pre-processing. The result of our alignment approach produces at the same time the decomposition of the terms into morphs and aligns the morphs to the corresponding kanjis.

This alignment is performed with an Expectation-Maximization (EM) algorithm that we briefly present hereafter (Jiampojamarn et al., 2007, for more details and use examples). It is based on a *Baum-Welch* algorithm (Rabiner, 1989), more precisely a forward-backward algorithm, extended to allow the alignment of sub-sequences of symbols instead of 1-1 alignments only. The principle of the algorithm is to alternate two operations: the first one computes a table of counts recording which possible alignment is seen with a weight based on the probability of this alignment in each training pair. The second step estimates the alignment probabilities based in turn on the table of counts. These two steps are detailed more formally in Algorithm 1. The first one (Expectation, in Algorithm 2) processes each pair \((x^T, y^V)\) of term with its Kanji translation to be aligned \((T \text{ and } V \text{ are respectively the number of letters in the term } x \text{ and number of Kanjis in the Japanese translation } y)\) with a Forward-backward approach (Algorithm 4), and outputs an updated table of counts named \(\gamma\). The second step, the Maximization (Algorithm 3), uses this table of counts to produce an alignment probability table named \(\delta\). This table is used in the remaining of the paper to propose morphological analyses; an excerpt of this table in given in Figure 1. For the interested reader, more details are available in (Claveau and Kijak, 2011; Claveau, 2012).

²www.dorlands.com/wsearch.jsp
3.3. Probabilistic morphological information

The probabilistic correspondence tables between mor-
phemes and kanjis are generated by an alignment process
based on the forward-backward algorithm presented in
the previous section. Beside the alignment results, it pro-
tuces the δ table (see the excerpt given in Figure 1), con-
taining the alignment probability iteratively computed from
the pairs of terms associated with their Kanji translations.
Thus, in practice, the algorithm only needs a list of pairs of
terms (of the studied language) with their Kanji trans-
nlations: morphs sharing the same (first-order) neighbors.
In this paper, we are also interested in second-order re-
lations: morphs sharing the same (first-order) neighbors.
We have shown in previous work how this graph could be
mined to discover semantic relations between the morphs
(Claveau, 2012). In particular, first order relations are
morphs that are close to each other in this weighted
graph. In this paper, we are also interested in second-order re-
lations: morphs sharing the same (first-order) neighbors.
An example of these second-order neighbors for the French
morph gastro (stomach) is given in the form of word cloud
in Figure 3.

3.4. Attaching relevant translations to kanjis

One limit of the probability tables, as produced by the
algorithm explained above, is that the kanjis are not un-
derstandable by non Japanese speakers. This does not
prevent their use in applications like information retrieval
(Claveau, 2012), but they cannot be used for providing
human-readable interpretation of the morphological com-
ounds. It is of course possible to use bilingual dictionaries,
but they may not provide the most relevant translation given
our biomedical domain (for instance, 胃, commonly trans-

Figure 1: Abstract of the probability table δ for English produced by the alignment algorithm.

We have shown in previous work how this graph could be
mined to discover semantic relations between the morphs
(Claveau, 2012). In particular, first order relations are
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lations: morphs sharing the same (first-order) neighbors.
An example of these second-order neighbors for the French
morph gastro (stomach) is given in the form of word cloud
in Figure 3.

Figure 2: Morphosemantic graph of morphs-kanjis
Figure 3: Cloud of the second-order neighbors of the French morph gastro

| inflammation | a | b |
| any other kanjis | c | d |

Table 1: Cooccurrence values to compute the strength of the association 炎/inflammation

Table 4.1: Linear segmentation of the morphological compounds

Figure 4: Abstract of the multi-word English terms/kanjis list extracted from the UMLS.

To associate these simpler words with the kanjis, one could use again an alignment process, but it is made more difficult since the hypothesis of parallelism does not hold here. Instead, we use a simple method based on the cooccurrences of words and (any substring of) kanjis in any pair of the list. As it is done for collocation extraction, many statistical indices based on these cooccurrence counts (Pearce, 2002) can be used to measure the strength of the relation between each word and each kanji combination. In this work, we use the point-wise Mutual Information (MI) score which has proved useful for many applications. Consider the example given in Tab. 1, the MI score for 炎/inflammation is

\[ MI = \log \frac{a \cdot (a + c)}{a \cdot (a + b)} \]

The retained translation for a given kanji or combination of kanjis is the word that maximizes its MI score.

4. Experimental validation

As the resources are automatically built, it is important to evaluate their relevance in real tasks. In this paper, we present evaluation through three tasks (linear segmentation of terms, hierarchical structuration of terms, morphological analysis).

4.1. Linear segmentation of the morphological compounds

Segmenting a morphological compound into morphemes can be useful for many applications. Our probabilistic resources can be used for such a task with a simple Viterbi algorithm which will propose the most probable decomposition of the term, based on the probabilities of each element found in the table. In order to evaluate the precision of this approach, a ground-truth has been developed for French terms; it is composed of 1 000 terms that have been manually segmented into morphemes. The Viterbi algorithm is thus given the probability table generated by the alignment algorithm applied to French/Kanji pairs extracted from the UMLS. As baselines, we also compare this approach with two well known tools of the domain: Morfessor\(^3\) (Creutz and Lagus, 2005) and DeriFi\(^4\) (Namer, 2007). Morfessor being based on a learning approach, it is given the list of (non multi-word) French terms extracted from the UMLS (about 13 000 terms). As illustrated in Fig. 5, our approach, based on automatically generated resources, rivals the expert-based system DeriF, and outperforms MorphoSaurus.

Figure 5: Precision (%) of term segmentation on French.

It is also interesting to examine how the precision of the systems evolves with respect to the amount of training data used, that is, the number of words for Morfessor, and number of pairs for our system. These results are presented in Figure 6. The results of Morfessor are almost constant whatever the amount of training data processed. This somewhat surprising result is explained when examining the errors: Morfessor tends to over-segment on the basis of fortuitous similarity between words. When given the same amount of training data, our approach yields better results, but it should be noticed that it also exploits more information than the kanji translations. DeriF’s results are close

\(^3\)www.cis.hut.fi/projects/morpho
\(^4\)www.cnrtl.fr/outils/DeriF/requete.php
rule 2. DeriF

[52x53]adenocystoma

or

meningo

[52x65]...ture should be:

meningoencephalitis

the structure of terms like

cholangite

argyrose

mented), or by certain configurations of morphs (argyrose,
cholanigite, angiocholite). In rarer cases, the proposed seg-
mentation is wrong; this is due to incorrectly recognized
morphs (e.g. rétinoblastoma). The absence of segmentation,
or under-segmentation are also the major causes of
errors of our approach. In our case, they are due to the pre-
ence of rare morphs or kanjis that are seldom represented
in the training data. Obviously, these errors tend to dimin-
ish when the training dataset is larger. On the whole, DeriF
and our approach agree on 70.5% of the segmentation, and
more than 80% of the correct segmentations found by one
are also found by the other.

4.2. Structural (hierarchical) analysis

The segmentation analyses examined in the previous sub-
section are linear: the morphological units are put on a
same level. Yet, the morphological compounds have an
inner hierarchical structure which brings important infor-
mation to understand the term. As it was mentioned in
Section 3.1., the order used to build the biomedical mor-
phological compounds, as other scientific compounds, is
particular in Roman languages. In general, the governed
morphological units appear before (i.e. at the left of) their
governing units (Dal and Amiot, 2008). It seems reason-
able to use this general rule as a default structuring rule;
it is noted rule 1 hereafter. Each morph is thus considered
as a modifier of the compounds it precedes, which may be
written as follows:

\[ m_1m_2...m_n = [ m_1 [ m_2 [ ... [ m_n ] ] ] ] \]

Of course, there are exceptions. One of the most common is
the structure of terms like meningoencephalitis whose struc-
ture should be:

\[ [ [ [ mening ] [ encephal ] ] ] ]

or adenocystoma that is structured as:

\[ [ [ adeno ] [ cysto ] ] oma ] \]

To decide whether this structuring rule should be used in-
stead of rule 1, we simply look at the morph appearing in
the term. If two consecutive morphs are found to be second-
order neighbors (i.e. at least one of them is in the 10 closest
neighbors of the other; see Sec. 3.3.), they are considered
in parallel, that is like mening and encephal, and not in the
governing-governed relation of rule 1. This modification to
rule 1 is noted rule 2.

Even with this second structuring rule, there are other ex-
ceptions such as angiocardiography, whose structure should
be:

\[ [ angio [ cardio ] ] graphy ] \]

Such terms would thus require additional rules, but in the
experiment reported hereafter, only the two previous rules
were implemented.

To evaluate the relevance of this structuring approach, we
have conducted a small experiment on about 200 French
terms that were manually structured by the authors. In or-
der to evaluate the quality of the structuring rules only, our
approach was given the correct segmentation of the terms.
The performance is evaluated in term of precision, that is
the amount of terms completely and correctly structured by
this approach. As a comparison, we also indicate the re-
sults obtained by DeriF; for a fair comparison, only terms
that were correctly segmented by DeriF are considered in
these structuration results.

| Method         | rule 1 only | rule 1 + rule 2 | DeniF  |
|----------------|-------------|-----------------|--------|
| Precision      | 63.1        | 76.2            | 78.4   |

Table 2: Precision (%) of different methods to hierarchi-
cally structure biomedical morphological compounds.

These results highlight the preponderance of the governed-
governing scheme (denoted rule 1) in the construction of
the neo-classical morphological compounds. With the addi-
tion of the rule 2, that relies on the second-order affini-
ties, we rival the performance of expert systems like DeriF
which heavily rely on expert knowledge.

4.3. Morphological analysis

Beside the segmentation performance, it is also interesting
to investigate the semantic interpretation given by the kanjis
and their translations (generated as explained in Sect. 3.4.).
Building a direct evaluation is difficult but comparing the
analysis with DeriF is insightful. We show in Tab. 3 some
analyses provided by DeriF that may benefit from our more
complete resources (the DeriF gloses, initially in French,
are translated by us, words in italics are errors or invention
by DeriF).

5. Conclusion

The alignment and translation techniques described in this
paper make it possible to generate automatically morpho-
 logical resources of the biomedical domain for many lan-
guages, by exploiting existing multilingual terminologies
like the UMLS. Indeed, our approach relies on the use of
Kanjis as a pivot language and on alignment algorithm as
well as cooccurrence mining. In previous work, we have
shown that the alignment process makes it possible to segment morphologically complex terms and to align the segments to their corresponding Kanjis (Claveau and Kijak, 2011). We have also proved that this way of decomposing the morphological compounds into smaller meaningful units, with Kanjis serving as labeled, could be beneficial to biomedical information retrieval tasks (Claveau, 2012). In this paper, we propose new evaluations of these resources and show that they are also useful for other tasks. In particular, we first come back on the task of linear segmentation of morphological compounds; we show that our automatically built resources, used with simple algorithms, rival the best existing system, without requiring any expert knowledge. We also show that, when combined with two simple analysis rules, the resources make it possible to easily develop very competitive systems to find the hierarchical structure of terms. Last, with simple techniques based on cooccurrence mining in multi-word terms of the UMLS, we build correspondences between morphs and terms (such as 'osis'/'disease') which allow to build tools for easily interpret the morphologically complex term for a human reader.

So far, we have generated these resources (probability tables and translation tables) for English, French, Spanish and Portuguese. Their distribution is foreseen but may require the agreement of the copyright holders of the terminologies included in the UMLS MetaThesaurus.

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