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LITL at CLEF eHealth2016: recognizing entities in French biomedical documents

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Abstract. This paper describes the participation of master's students (LITL programme, university of Toulouse) and their teachers to the CLEF eHealth 2016 campaign. Two runs were submitted for task 2 (multilingual information extraction) which consisted in the recognition and categorization of medical entities in French biomedical documents. The system used consists of a CRF classifier based on a number of different features (POS tagging, generic word lists and syntactic parsing). In addition, several patterns were used on the CRF's output in order to extract more complex entities. The best run achieved high precision (0.64–0.78) but lower recall (0.32–0.40), with an overall F1-measure of 0.43–0.53.

1 Introduction

This article describes the participation of the students of the LITL master to the CLEF eHealth 2016 Lab [5].

LITL (stands for Linguistique, Informatique, Technologies du Langage, i.e. *Linguistics, IT, Language technologies*) is a new master's program at the University of Toulouse, France. Mainly aimed at linguistics and humanities students, it comprises, for a major part, courses in natural language processing (NLP), computational linguistics and practical aspects of corpus analysis through programming and using various computer tools. An important part of this curriculum is project-oriented, and the first year students have to build a fully operational processing system for a precise NLP task. This year's project was the participation to the CLEF eHealth challenge, more precisely task 2: multilingual Information Extraction [10].

The teachers in charge of this project (members of the CLLE-ERSS laboratory) deemed that this task was ideal for pedagogical purposes:

- information extraction (and more precisely named entity recognition – NER) is a well-known, well-defined and central task in modern NLP;
- state of the art information extraction systems are based on machine learning techniques but can also make use of symbolic handcrafted rule-based approaches;

- supervised learning systems such as CRF classifiers can take advantage of different kind of linguistic resources, many of these are available for the biomedical domain;
- a collaborative task is an excellent exercise for students, as it motivates them and gives them a clear feedback on their work;
- the target language of CLEF eHealth 2016 is French, the students' working language;
- the task's schedule was perfectly suited to the master's calendar.

Working as a team along the entire semester, the students were thus able (with help from their teachers) to submit two runs for the selected task, and got very satisfactory results for a first attempt.

This paper is organized as follows. Section 2 describes the tasks and get a closer look at the data. Section 3 gives a precise description of the different components of the system designed for the task, while the results are given and discussed in Section 4.

2 Task description

2.1 Overview

The LITL team participation only concerns the CLEF 2016 eHealth task 2 phase 1 addressing biomedical NER in French texts. The aim is to automatically detect and classify biomedical entities. Detection requires the system to provide start and end positions of each relevant entities. The classification step consists in associating each previously detected entity with one of the ten target categories corresponding to UMLS Semantic Group:

- Anatomy (ANAT),
- Chemical and Drugs (CHEM),
- Devices (DEVI),
- Disorders (DISO),
- Geographic Areas (GEOG),
- Living Beings (LIVB),
- Objects (OBJC),
- Phenomena (PHEN),
- Physiology (PHYS),
- Procedures (PROC).

Two text types are concerned with this task: drug inserts and biomedical research papers' titles and (sub)headings. Biomedical entities cover a wide range of linguistic expressions such as drug or city names, very common nouns (e.g. "*infirmière*" (*nurse*), "*études*" (*studies*)), technical specialized terms (e.g. "*thyroglobuline*", "*électroystagmographie*") or complex phrases (e.g. "*infectés par le virus de l'immunodéficience humaine*" (*infected with human immunodeficiency virus*), "*enfant âgé de plus de trois mois*" (*children over 3 months*)).

2.2 Data

The training data set corresponds to the QUAERO French Medical Corpus [11] previously used in CLEF 2015 eHealth task 1b [12] and made of two sub-corpora:

EMEA: 6 drug inserts written by the European Medicines Agency¹ for the general public ;

MEDLINE: 1665 titles and (sub)headings of biomedical academic papers indexed in the MEDLINE database².

Drug inserts are long texts (around 5,000 words/text on average) written in a less specialized language than MEDLINE's very short text segments (6 words/item on average), as illustrated in examples 1 from EMEA and 2 from MEDLINE, see below. MEDLINE texts are written with an uncommon syntax, considering that titles and (sub)headings usually correspond to noun phrases or non-finite sentences without final punctuation.

Example 1. Il est utilisé en association avec d ' autres médicaments antiviraux dans le traitement des adultes et des enfants infectés par le virus de l ' immunodéficience humaine (VIH), le virus qui provoque le syndrome d ' immunodéficience acquise (SIDA). [EMEA/118_1]

Example 2. Hypersensibilité retardée dans les affections thyroïdiennes étudiée par le test de migration des leucocytes en présence de thyroglobuline humaine . [MEDLINE/4573749]

Both sub-corpora have been manually annotated following similar guidelines [11]. Each annotation is encoded in the BRAT standoff annotation format³ and includes for each entity an id, the relevant UMLS category, the offset position (start and end) and the textual content of the annotation. Example 3 gives the manual annotations associated with example 2 and Figure 1 its visualization via the BRAT annotation tool.

Example 3.

T1	DISO	0 25	Hypersensibilité retardée
T2	DISO	0 16	Hypersensibilité
T3	DISO	35 59	affections thyroïdiennes
T4	DISO	35 45	affections
T5	ANAT	46 59	thyroïdiennes
T6	PROC	75 107	test de migration des leucocytes
T7	PHYS	83 107	migration des leucocytes
T8	PHYS	83 92	migration
T9	ANAT	97 107	leucocytes
T10	CHEM	123 137	thyroglobuline
T11	LIVB	138 145	humaine

¹ <http://opus.lingfil.uu.se/EMEA.php>

² <http://www.ncbi.nlm.nih.gov/pubmed/>

³ <http://brat.nlplab.org/standoff.html>

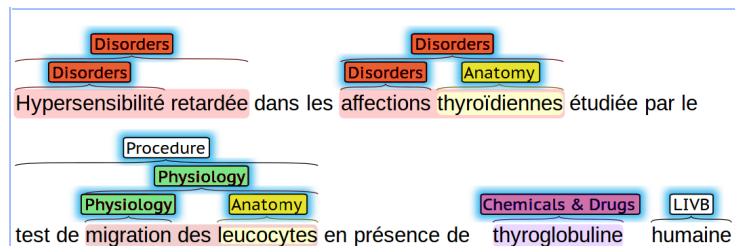


Fig. 1. Visualization of annotated entities through BRAT

As for the detection subtask, annotated entities can be single words (77%) or compounds (23%). Compound entities may be autonomous (e.g. "*prise en charge*"); nested such as in (3) where "*leucocytes*" is nested in "*migration des leucocytes*" which is in turn nested in "*test de migration des leucocytes*"; or discontinuous such as "*hépatites C*" and "*virus des hépatites C*" in (4).

Example 4. Prévalence des marqueurs des virus des hépatites A , B , C à La Réunion (Hôpital sud et prison de Saint Pierre).
[MEDLINE/10774493]

T2 LIVB 29 34 virus
T5 DISO 39 48;57 58 hépatites C
T7 LIVB 29 48;57 58 virus des hépatites C

Table 1 gives an overview of the amount of annotated data per subset.

Table 1. Amount of annotated data per subset

Subset	EMEA (%)	MEDLINE (%)	Total (%)
# of texts	6	1665	1671
# of words	28215	10503	38718
Annotated entities	4955	2977	7932
Compounds entities	995 20.1	846 28.5	1841 23.2
Discontinuous entities	42 0.8	21 0.7	63 0.8

Because discontinuous entities are very rare, we decided to not detect such entities. Concerning nested entities which are more frequent, we implemented post-processing as described in Section 3.

As for classification subtask, entities are heterogeneously distributed among ten types. Half of the annotated entities are categorized as DISO (26%) or CHEM (25%). The rest spread mainly among PROC (16%), ANAT (11%) and LIVB (11%) while types PHYS, OBJC, DEVI, GEOG and PHEN are fairly rare. When compound, entities seem to be usually categorized as the first (head) component (e.g. "*virus des hépatites C*" is labeled LIVB as for "*virus*").

Preliminary linguistic observations of data reveal three main characteristics that

will constitute features for our system. First, the length of single-word annotated entities (in characters) seems longer than non-annotated words with an average of 9.5 characters against 5.5. Secondly, single-word entities show some morphological complexity with a use of recurrent productive affixes such as *-cyte*, *-thérapie*, *endocrino-*, *trachéo-*. Finally, annotated entities may be mainly characterized as technical vocabulary in the biomedical domain especially for main types (DISO and CHEM).

3 System description

In this section we present in details the system we designed for this task. Its cornerstone is a Conditional Random Field (CRF) classifier [6] that is used to train a model based on the manually tagged datasets. Although CRFs are easily applied thanks to readily available toolkits such as *CRF++*⁴, they require a certain amount of preprocessing and are known to perform better when given additional information on the tokens to analyze. Also, they cannot by themselves provide all the solutions, especially when the target entities are nested and/or overlap, that's why several post-processing procedures were necessary as well.

3.1 Overview

As is mandatory with machine learning supervised techniques, we first had to build a model based on the training data. This was done according to the scheme presented in figure 2. As can be seen, this sequence starts with the raw text files from the training dataset, corrects their tokenization, performs POS tagging and syntactic parsing, then adds an additional set of features and finally provides, along with the annotated files, input for the CRF training phase. The result is a CRF model that can be used in the extraction phase.

The overall process used for extracting and categorizing entities from raw text files can be seen in figure 3. We can see that it applies roughly the same modules as for the training phase, but adds an additional post-processing step after the CRF classifier.

The stages are described in details in the following sections.

3.2 Preprocessing: correction, POS tagging and parsing

The first set of modules concerns the processing of text files. The main role of these modules is to provide a generic annotation layer for the tokens: POS tagging, lemmatization and dependency parsing, as these additional information are to be used by the CRF classifier.

For both phases, we used the Talismane toolkit [13] for POS tagging and dependency parsing, with the provided models for French and using the default

⁴ <https://taku910.github.io/crfpp/>

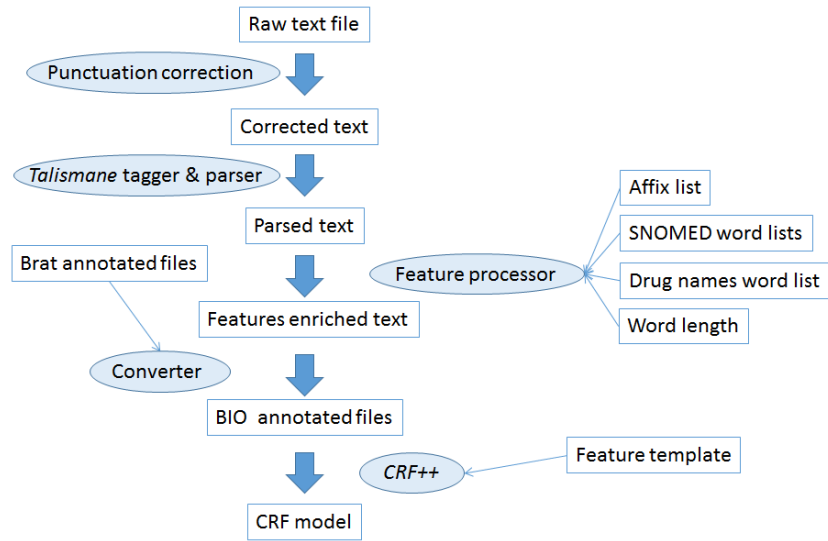


Fig. 2. System training phase

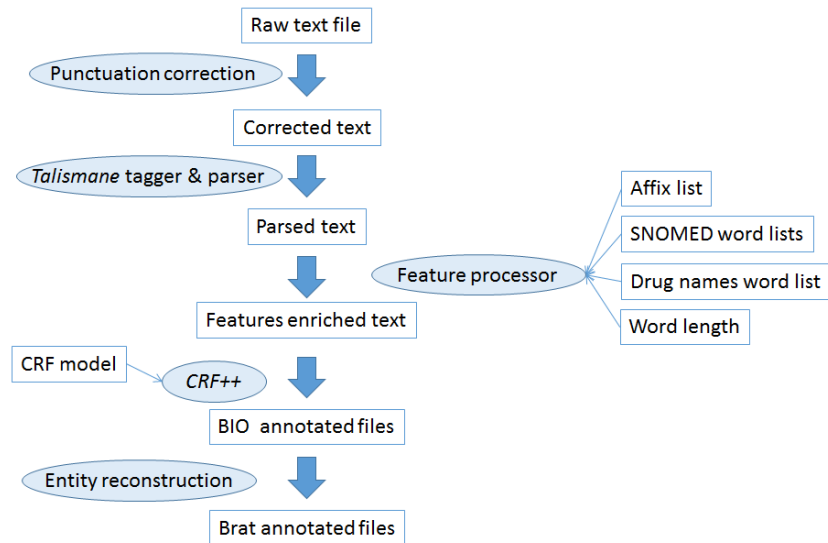


Fig. 3. Entities annotation phase

parameters. In addition to being a reliable tagger and dependency parser, Talismane provides the offset for each token, which is vital for dealing with the BRAT standoff annotation format.

The tokenization correction module has been developed in order to prevent many tagging errors due to the non-standard blank spaces that appear in both the training and test text files. The main problems were due to additional spaces before and/or after commas, hyphens, apostrophes, periods, digits, etc. For example, an extraneous space between "/" and the following apostrophe prevented the tagger and parser from identifying a determiner. This correction module is a simple Perl script using regular expressions to convert texts back to their supposedly original punctuation, while keeping the additional spaces in order to preserve the offsets for the annotated and extracted entities. For example, extract in (5) becomes (6) after correction:

Example 5. Par conséquent, lorsque vos serez traite par TYSABRI, vos ne constaterez peut-être pas d'amelioration mais le traitement par TYSABRI pourra empêcher l'aggravation de votre maladie. [EMEA/425_6]

Example 6. Par conséquent, lorsque vos serez traite par TYSABRI, vos ne constaterez peut-être pas d'amelioration mais le traitement par TYSABRI pourra empêcher l'aggravation de votre maladie.

The output of the parser follows a column-based format, in which each token is described on a separate line, as in the example (7) below (related to (5)), where columns indicate, in order: word form, POS tag, lemma, syntactic dependency, offset.

<i>Example 7.</i>	Par_conséquent	ADV	par_conséquent	mod	1398
	,	PONCT	,	ponct	1413
	lorsque	CS	lorsque	mod	1415
	vous	CLS	vous	subj	1423
	serez	V	être	aux_pass	1428
	traité	VPP	traiter	sub	1434
	par	P	par	p_obj	1441
	TYSABRI	NPP	-	prep	1445
	,	PONCT	,	ponct	1453
	vous	CLS	vous	subj	1455
	ne	ADV	ne	mod	1460
	constaterez	V	constater	root	1463
	peut-être	ADV	peut-être	mod	1475
	pas	ADV	pas	mod	1485
	d'	DET	de	det	1489
	amélioration	NC	amélioration	obj	1493
	mais	CC	mais	coord	1506
	le	DET	le	det	1511
	traitement	NC	traitement	subj	1514
	par	P	par	dep	1525
	TYSABRI	NPP	-	prep	1529
	pourra	V	pouvoir	dep_coord	1537
	empêcher	VINF	empêcher	obj	1544
	l'	DET	l'	det	1553
	aggravation	NC	aggravation	obj	1557
	de	P	de	dep	1569
	votre	DET	votre	det	1572
	maladie	NC	maladie	prep	1578
	.	PONCT	.	ponct	1586

As can be seen, unknown tokens (i.e. absent from the reference lexicon used by Talismane) have no corresponding lemma. We added correction procedure that reproduces the word form instead of the "_" placeholder. The POS tags indicate the token's nature (e.g. DETERMINER, Verb, ADVerb, etc.) while the syntactic tag indicate its function in the sentence, more precisely the relation it has with its syntactic governor, such as object, modifier, etc. Details on both tagsets can be found in the Talismane documentation.

3.3 Adding features from external resources

In addition to the lemma, POS and syntactic relations, we added several features we deemed relevant with the task (see 2). These features are the following:

- does the token appear in a specific word lists?
- what is the token's length in number of characters?
- does the token begin with a recognizable prefix?
- does the token end with a recognizable suffix?

These features and the way they were calculated are described in the following paragraphs

Word lists

We used several word lists in order to extend the lexical coverage beyond what is present in the training datasets. We used two main sources: SNOMED and a list of commercial drug names.

SNOMED [14] is a well-known and used resource for biomedical NLP, as it contains extensive word lists. We selected the 4 most relevant top categories, and extracted all the single-word terms in each one.

As noted above (Section 2), manual observation of the training data (especially the EMEA subset) revealed that a large number of commercial names of drug were present and systematically tagged as CHEM entities. Given that SNOMED only contains scientific names of chemicals, we wanted to use an additional resource to tag these specific tokens, as performed by several named entities recognition systems [8]

We used the Vidal website⁵, which is the reference compendium for pharmaceutical drugs in France. After downloading the list of raw drug names it provides, we developed an adhoc Perl script that identifies the main name through removal of extraneous information such as posology indications (i.e. transforming "ABSTRAL 100 μ g cp subling" into "*Abstral*").

Table 2 gives the number of terms used and a few examples for each of the selected 5 categories.

Table 2. Word lists extracted from SNOMED resource and VIDAL database

Category	Nb of terms	Examples
SNOMED Chimie (chem)	3505	<i>toxine, magnésium, métoxyphénamine</i>
SNOMED Morphologie (morph)	1033	<i>microfracture, antéflexion, hypomyélinisation</i>
SNOMED Procédure (proc)	62	<i>cystoméetrogramme, électronystagmographie, thérapie</i>
SNOMED Agents physiques (phys)	378	<i>garrot, oxymètre, hémocytomètre</i>
VIDAL drug names (chem)	3873	<i>aspirine, nicopatch, ventoline</i>

In the end, each token is then associated with a tag (column) containing the SNOMED/VIDAL category (**chem**, **morph**, **proc** or **phys**) if its lemma appears in the corresponding word list, or *none* in other cases.

Token length

As noted above from an observation of the training data, word length can be a good indicator for biomedical terms. Given that the CRF classifier cannot deal with numerical feature, we used a qualitative measure of the length using the following scale: *short* < 6 \leq *medium* < 10 \leq *long*.

Affixes

Two additional features based on affixes were designed in order to help technical specialized vocabulary detection. It is well known that biomedical technical

⁵ <http://www.vidal.fr>

terms are extensively coined through the use of standard suffixes and prefixes. Identifying these can be a useful addition to the necessarily limited reference word lists for entity recognition [8, 9]. We thus compiled lists of French prefixes and suffixes. We relied on existing lists (most of them seemingly compiled for the training of medicine students):

- *Lexique des racines, préfixes et suffixes des termes scientifiques et médicaux* by D. Pol, found at <http://www.didier-pol.net/>
- *Lexique des affixes (préfixes et suffixes)* by A. Abbara, found at <http://www.aly-abbara.com/litterature/medicale/affixes/a.html>
- *Terminologie médicale : préfixes et suffixes* by P. Cauwel, found at <https://sites.google.com/site/cauwelphilippe/Home/terminologie-medicale-prefixes-et-suffixes>

Once merged, these lists provided 394 prefixes and 126 suffixes.

For each token, the longest prefix (resp. suffix) in the list matching its lemma was used as an additional tag, and *none* when no match could be found.

3.4 From BRAT to BIO: selection of entities from the training set

Viewing the task of entity recognition and categorization as a tagging task requires the data (both training and testing) to be transformed into a compatible scheme. If the BRAT standoff annotation format is perfect for the visualization and declaration of these entities, it is not appropriate for an automated tagging process.

The BIO format is traditionally used for expressing token sequences such as chunks or named entities (cf. [3, 1, 2] for NER in biomedical texts). Its principle is the following: each token in a text can be at the Beginning, Inside or Outside an entity. Because entity categorization must be performed, the B (resp. I) letter is completed by the name of the entity's category. For example, to express the fact that "*Hypersensibilité retardée*" is a DISO we tag "*Hypersensibilité*" as DISO_B and "*retardée*" as DISO_I.

Thus defined, the task for the CRF classifier is to tag each token with one of the 21 possible value (there are 10 target entity categories, so 10 X_B and 10 X_I, but only one 0). This task is thus formally similar to other NLP tagging tasks such as POS tagging, where a target value has to be decided according to the descriptive features of the token (and, in the case of CRF, to the features and values of the neighboring tokens).

An alternative scheme is known as BILOU and adds the possibility for a token to be the Last token or to be the Unique one for this entity (cf. [4] for NER in biomedical domain). Although more precise, its main disadvantage is to increase the number of possible tags (41 in our case), making it harder for the classifier and generally requiring a larger amount of training data in order to be reliable (see [7] for a comparison between BIO and BILOU scores).

However, none of these schemes is able to faithfully represent nested, overlapping or discontinuous entities. As noted above, in section 2 (example 3), "*Hypersensibilité retardée*" contains two entities: "*Hypersensibilité*" and "*Hypersensibilité retardée*". Both are of the DISO category, and both begins with

the word "*Hypersensibilité*". However, only one of them can be represented using the BIO format. The same goes for more complex situations like the sequence "*test de migration des leucocytes*", still in example 3.

A decision had to be made when translating the annotated entities into the BIO format: do we keep the longest entities or the shortest? More precisely, do we consider "*leucocytes*" to be an ANAT entity by itself (thus receiving an ANAT_B tag) or part of the PHYS entity "*migration des leucocytes*" (with an PHYS_I tag)? This decision impacts the whole process, as what is decided for the training phase of the CRF will of course directly influence what is produced in the tagging phase.

This dilemma could be summarized as a choice between fewer but more complex entities versus more small ones. We decided to choose the latter, as we deemed it easier to "rebuild" complex entities from smaller ones than the other way around.

At this stage, each text is represented by a set of features available for each token, along with a BIO tag for the training data, as is the case in example (8) derived from (7):

Example 8.

Par conséquent	ADV	par conséquent	mod	1398	long	none	none	none	0
,	PONCT	,	ponct	1413	short	none	none	none	0
lorsque	CS	lorsque	mod	1415	medium	none	none	none	0
vous	CLS	vous	subj	1423	short	none	none	none	0
serez	V	être	aux_pass	1428	short	none	none	none	0
traité	VPP	traiter	sub	1434	medium	none	none	none	PROC_B
par	P	par	p_obj	1441	short	none	none	none	0
TYSABRI	NPP	TYSABRI	prep	1445	medium	none	none	chem	CHEM_B
,	PONCT	,	ponct	1453	short	none	none	none	0
vous	CLS	vous	subj	1455	short	none	none	none	0
ne	ADV	ne	mod	1460	short	none	none	none	0
constaterez	V	constater	root	1463	long	con	none	none	0
peut-être	ADV	peut-être	mod	1475	medium	none	none	none	0
pas	ADV	pas	mod	1485	short	none	none	none	0
d'	DET	de	det	1489	short	none	none	none	0
amélioration	NC	amélioration	obj	1493	long	none	tion	none	0
mais	CC	mais	coord	1506	short	none	none	none	0
le	DET	le	det	1511	short	none	none	none	0
traitement	NC	traitement	subj	1514	medium	none	ment	none	PROC_B
par	P	par	dep	1525	short	none	none	none	0
TYSABRI	NPP	TYSABRI	prep	1529	medium	none	none	chem	CHEM_B
pourra	V	pouvoir	dep_coord	1537	medium	none	none	none	0
empêcher	VINF	empêcher	obj	1544	medium	none	none	none	0
l'	DET	l'	det	1553	short	none	none	none	0
aggravation	NC	aggravation	obj	1557	long	none	tion	none	0
de	P	de	dep	1569	short	none	none	none	0
votre	DET	votre	det	1572	short	none	none	none	0
maladie	NC	maladie	prep	1578	medium	none	none	none	DISO_B
.	PONCT	.	ponct	1586	short	none	none	none	0

3.5 CRF templates and parameters

As noted above, we chose to use a CRF classifier (CRF++) in order to predict the BIO tag for each token given the features described in the previous sections. Training the CRF requires to define a template, i.e. a selection of which pieces of information are given as an input to the model. The specificity of CRF systems is that they can take into account both the features associated to the target token and the ones of its neighbors. Thus, a template is used to define which feature(s) of which neighbor(s) are used.

In summary, after a number of trial runs using the training data, we opted for the following:

- word form of target token and of the tokens appearing in a size-2 window around it;
- POS tag of target token and of the tokens appearing in a size-2 window around it;
- length, prefix, suffix, and presence in word lists of the target token;
- BIO tag attributed to the previous token.

Moreover, the second run submitted uses the syntactic dependency tag of the target token, in addition to the previous features. This decision followed a first experiment to evaluate the contribution of each different features. The system evaluation was conducted by using the original train/devel split provided for the training data. Table 3 gives some results of a lesion studies, i.e. indicating for each feature how their removal from the template affects the task system’s performances. F-scores were calculated by using the BRATEval.jar script provided by the organizers (exact matching option on true). As table 3 shows, syntac-

Table 3. Features contribution: F1 variation when feature is removed

F1-score	EMEA	MEDLINE
All features	0.5429	0.3821
- Syntactic relations	-0.0003	+0.0046
- Token length	+0.0109	-0.0038
- Affixes	-0.0085	-0.0227
- SNOMED and drugs lexicon	-0.0116	-0.0340

tic feature contribution depends on the syntactic characteristics of texts: when texts have uncommon syntax as for MEDLINE items (see 2), using the syntactic information may worsen results. All other features have a positive contribution to the model for both target subsets, and thus has been kept in the system.

We considered separating the training subsets (EMEA and MEDLINE) and creating different models, but experiments in this direction were inconclusive, so we decided to use all the training data as a whole and to use the same model for both test subsets.

3.6 From BIO to BRAT: identifying complex named entity – NE

The final stage of the tagging phase is the translation from the BIO format back to the target BRAT standoff annotation format. Beyond simple format conversion, the main problem here is the reconstruction of entities, assuming the choices made in the training phase and addressing the limitations of the BIO format.

This stage is performed in two steps. The first one is a simple identification of entities, blindly following the BIO format. It means that, for each token tagged as XXX_B we extract one (and only one) entity, comprising the initial tokens along with all following tokens tagged as YYY_I. For example, we extract "*hyperplasie focale modulaire*" as a single DISO entity from the following output:

Example 9. hyperplasie (NC) DISO_B
focale (ADJ) DISO_I
modulaire (ADJ) DISO_I

In case of inconsistency between the categories (i.e. if XXX is different from YYY), we attribute the initial (XXX) category to the NEs.

As explained above, the choices made initially imply that at this stage we only get non-nested entities, although most of the time they are parts of larger entities. For example, given the following sequence in the CRF output:

Example 10. tuberculose (NC) DISO_B
médiastinale (ADJ) ANAT_B

the first step extracts two separate entities: "*tuberculose*" as a DISO and "*médiastinale*" as a ANAT. In order to extract some of the more complex entities, we designed a few extraction patterns, based on the POS tags. The first pattern looks for a noun tagged as B, followed by an adjective tagged as B, i.e. the exact situation found in the example 10. Its output is the concatenation of both tokens, tagged with the category of the head noun. This means that this patterns produces "*tuberculose médiastinale*" as a DISO.

Similar patterns have been designed for longer sequences of adjectives: NC (B) ADJ (B) ADJ (B or I), and for nominal compounds such as NC (B) de/du/des/au/aux NC (B) and NC (B) P DET NC (B).

All extracted entities are collected in the BRAT standoff annotation format as noted above. The offsets are immediately available thanks to Talismane output format and the content of the entity is a simple concatenation of their tokens' word forms.

4 Results and discussion

In this last section we present and discuss the results obtained by our system on the task's test data.

4.1 Main results

As indicated in Table 4, our F1 scores are above the average (of submitted runs) for entity recognition in EMEA and slightly under it for MEDLINE with, for all subsets, a high precision and a low recall. The non-exact matching scoring procedure means that the offsets of the entities can partially overlap instead of being perfectly aligned. Run1 (without syntactic feature) and run2 (with

Table 4. LITL team scores on test data. For both target data and for each run, number of true positives (TP), false positives (FP) and false negatives (FN), along with recall, precision and F1 scores, with exact and non-exact matching. Average scores were computed on all submitted runs.

EMEA	exact matching						no exact matching					
	TP	FP	FN	Precision	Recall	F1	TP	FP	FN	Precision	Recall	F1
LITL-run1	879	242	1325	0.7841	0.3988	0.5287	990	131	1069	0.8831	0.4808	0.6226
LITL-run2	867	264	1337	0.7666	0.3934	0.5199	995	136	1052	0.8798	0.4861	0.6262
Average scores				0.5250	0.4114	0.4350				0.6377	0.5141	0.5423
MEDLINE	exact matching						no exact matching					
	TP	FP	FN	Precision	Recall	F1	TP	FP	FN	Precision	Recall	F1
LITL-run1	998	556	2105	0.6422	0.3216	0.4286	1247	307	1531	0.8024	0.4489	0.5757
LITL-run2	989	561	2114	0.6381	0.3187	0.4251	1237	313	1544	0.7981	0.4448	0.5712
Average scores				0.5030	0.4264	0.4455				0.6387	0.5707	0.5859

syntactic feature) scores show little differences as expected, although run 1 gets higher scores for both subsets with exact matching. The order is partly different without exact matching where run2 gets slightly higher results for EMEA only. It should be noted that matching option only concerns entity delimitation and not disagreement on entity classification.

A closer look at the scores per category shows that we get the highest performance on EMEA texts for LIVB entities recognition with a 0.86 F1 (0.93 P and 0.8 R, 268 entities), followed by PROC (0.7 F1, 269 entities) and CHEM (0.67 F1, 885 entities). The detection of DISO entities, which cover the largest part of biomedical entities (988 entities in MEDLINE and 342 in EMEA), is better in MEDLINE texts (0.66 F1) than in EMEA texts (0.57 F1).

4.2 Test data set overview and errors observation

To better understand our system weaknesses, we propose a quick observation of the test dataset, then an overview of the false negatives (FN) and false positives (FP). First of all, an overview of test data reveals a difference from the training data that may explain some of our FN. Indeed, as indicated in table 5, while the proportion of compounds is approximatively the same than in training data set,

Table 5. Quantitative overview of test data set

Subset	EMEA (%)	MEDLINE (%)	Total (%)
# of texts	4	833	1671
# of words	12042	10871	22913
Annotated entities	2070	3150	5220
Compound entities	499 <i>24.1</i>	886 <i>28.1</i>	1385 <i>26.5</i>
Discontinuous entities	42 <i>2.0</i>	23 <i>0.7</i>	65 <i>1.2</i>

the proportion of discontinuous entities – which were not taken into account by our system – is double.

If we take a closer look at FP and FN, we may distinguish several cases (all subsequent examples come from the EMEA subset). First, FPs may be due to a disagreement on entity category such as the CHEM *polydextrose* or *diacétate de glycérol* which our system both classified as DISO. A comparison between run1 and the gold standard shows 187 cases of such miscategorization (60 in EMEA and 127 in MEDLINE), with quite a lot of confusions about subtle distinctions such as between OBJC – physical objects and DEVI – devices or between PROC – procedures and CHEM – chemical and drugs. As for example, in (11), "*injection*" was automatically categorized PROC instead of CHEM and "*seringue*" (*syringe*) was automatically categorized OBJC instead of DEVI.

Example 11. L 'injection sous-cutanée est réalisée de la même façon qu ' avec une seringue classique . [EMEA/334_3]
The subcutaneous injection must be conducted in the same way as with a classical syringe

Classification errors may also be linked with polysemy as for example with the word "*bouton*" which means either a concrete object (*button*) or an anatomic/physiological entity (*pimple*).

A second group of FPs may be linked to the well-known problem of distinguishing between specialized vs. common usages. Such cases occur when a common word or compound was incorrectly recognized as biomedical entities (e.g. "*anomalies*" recognized as DISO or "*Mélange de couleur bleu*" as CHEM).

A last possible explanation for FPs is related to compounds boundaries as for example when a CHEM is syntactically linked to a LIVB but not manually annotated as a compound (e.g. "*olanzapine chez les enfants*" or "*olanzapine sur les protéines*"). Same mistakes may be observed due to prepositional phrase attachment ambiguity as for example in (12)

Example 12. Traitement de l' ankylostomiase par le tétrachloréthylène chez l' adulte et le grand enfant . [MEDLINE/13515790]

where our system recognized "*ankylostomiase par le tétrachloréthylène*" as a DISO because of the pattern NC (B) P DET NC (B) whereas the prepositional phrase "*par le tétrachloréthylène*" is syntactically attached to "*Traitement*" and not to "*ankylostomiase*".

Moreover, when exact matching, other FPs may be observed such as "*troubles hématologiques périphériques*" detected as a single entity instead of two entities "*troubles hématologiques*" and "*périphériques*".

This compound boundaries problem has very strong consequences on recall and may explain the large amount of FNs (more than 1,300 in EMEA and 2,100 in MEDLINE, see Table 4). Indeed, when "*troubles hématologiques périphériques*" is detected instead of two entities "*troubles hématologiques*" and "*périphériques*", it causes one FP and two FNs. A simple way for dealing with this problem will be to systematically split detected compounds into as many single entities as single words.

The converse is also observed i.e. when our system extracts only one term from a compound, as for example "*Olanzapine Teva*" manually annotated as CHEM while our system recognized only "*Olanzapine*" and not "*Teva*". Such FNs were essentially due to the limited coverage of our external resources.

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