

# Biomedical Question Types Classification using Syntactic and Rule based Approach

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**Abstract:** Biomedical Question Types (QTs) Classification is an important component of Biomedical Question Answering Systems and it attracted a notable amount of research since the past decade. Biomedical QTs Classification is the task for determining the QTs to a given Biomedical Question. It classifies Biomedical Questions into several Questions Types. Moreover, the Question Types aim to determine the appropriate Answer Extraction Algorithms. In this paper, we have proposed an effective and efficient method for Biomedical QTs Classification. We have classified the Biomedical Questions into three broad categories. We have also defined the Syntactic Patterns for particular category of Biomedical Questions. Therefore, using these Biomedical Question Patterns, we have proposed an algorithm for classifying the question into particular category. The proposed method was evaluated on the Benchmark datasets of Biomedical Questions. The experimental results show that the proposed method can be used to effectively classify Biomedical Questions with higher accuracy.

## 1 INTRODUCTION

Unlike Information Retrieval (IR) System that retrieve a large number of documents that are potentially relevant for the questions posed by the inquirers, Question Answering (QA) System aims to provide inquirers with direct, precise answers to their questions, by employing Information Extraction (IE) and Natural Language Processing (NLP) methods (Athenikos and Han, 2009).

Typically an automated QA System consists of three main phases (Athenikos and Han, 2009; Gupta and Gupta, 2012): Questions Processing, Documents Processing and Answers Processing phases. Figure 1 illustrates the generic architecture of Biomedical QA System.

Biomedical QTs Classification is a crucial task of any Biomedical QA System. It classifies Biomedical Questions into several Biomedical QTs. In addition, the main goal of Biomedical QTs Classification is to determine the Excepted Answer Type to a given Biomedical Question, such as whether the answer should be a Biomedical Entity Names, short text summarization, paragraph or just “Yes” or “No”.

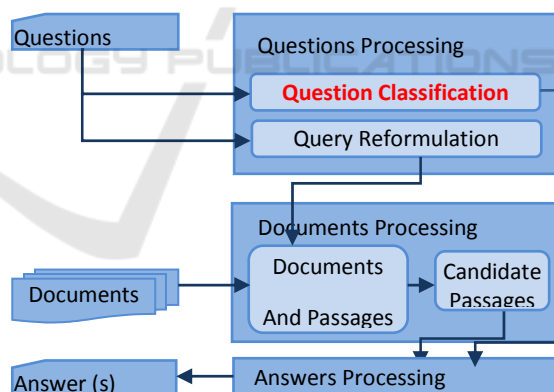


Figure 1: Generic Architecture of Question Answering System.

Indeed, in order to extract the answer for a given Biomedical Question, the system should know in advance the Excepted Answer Type that allows a Biomedical QA System to use type-specific answer retrieval algorithms and to reject possible answers of the wrong type. Therefore, Biomedical QTs Classification task plays a vital role in Biomedical QA System that can strongly affect positively or negatively the Answers Processing phase and hence

determines the quality and overall performance of the Biomedical QA System.

In recent years, several works have been done in this field for open domain QA System (Zhang et al., 2007; Tomuro, 2004), as well as for Biomedical QA System. Ely et al. (1999,2000,2002) have proposed a generic taxonomy of common Medical QTs and another taxonomy which classifies questions into Clinical vs Non-Clinical, General vs Specific, Evidence vs No Evidence, and Intervention vs No Intervention. For instance, question taxonomies have some expressiveness limits. For example, Ely et al., (2000)'s question taxonomy provides only some forms of expression for each question category, when in the real world we may often retrieve several other expressions for the same categories.

In fact, there are important factors that distinguish Biomedical QA System from open-domain QA System. Those factors include: (1) size of data, (2) domain context, and (3) resources. Indeed, in biomedical domain QA, the domain of application provides a context for the QA process. This involves domain-specific terminologies and domain-specific types of questions, which also differ between domain experts and non-expert users. Athenikos and Han (2009) report the following characteristics for restricted-domain QA in the biomedical domain: (1) large-sized textual corpora, (e.g., MEDLINE), (2) highly complex domain specific terminology, that is covered by domain-specific lexical, terminological, and ontological resources, (e.g., Unified Medical Language System (UMLS)), (3) tools and methods for exploiting the semantic information (e.g., MetaMap), and (4) Domain-specific format and typology of questions.

Therefore from the above remarks, the Biomedical QTs Classification block needs its own methods that are different from others used for open domain QA System that have been proposed for the following Question Types: Location, Date, Person, Organization, etc (Khoury, 2011).

In light of this, there are two main approaches of Questions Classification: Syntactic Patterns-based approach and Machine Learning. Due to the limited number of Question Types and due to the lack of quantity of labeled data, the Syntactic Patterns-based methods have become the most popular methods in QTs Classification System (Sung et al., 2008).

As far as we know, there are no studies that have discussed QTs Classification problem in the biomedical domain and that is why several Biomedical QA System that have been presented deal only with one Question Type (Weissenborn et al., 2013; Yang et al., 2015). In this paper, we have proposed an efficient and

effective method for Biomedical QTs Classification. Indeed, we have taken into account all Biomedical QTs. We have defined the Syntactic Patterns of each Biomedical QTs. In particular, we have classified the Biomedical Questions into three broad categories: *Yes/No*, *Factoid* and *Summary Questions*. We denote that all the Excepted Answer Types are summarized by these categories (Tsatsaronis et al., 2012).

- **Yes/No Questions:** These are questions that require "Yes" or "No" as an answer. For example, "*Is COL5A2 gene associated to ischemic heart disease?*" is a Yes/No Question.

- **Factoid Questions:** These are questions that require a particular one or more of Biomedical Entity Names (e.g., of a disease, drug, gene, a list of gene names, etc.), a number(s), or a similar short expression as an answer. For example, "*Which genes have been found mutated in Gray platelet syndrome patients?*" is a Factoid Question.

- **Summary Questions:** These are questions that can only be answered by phrase extracted from relevant document or by producing a short text summarizing the most prominent relevant information. For example, "*What is the role of anhedonia in coronary disease patients?*" is a Summary Question (Tsatsaronis et al., 2012).

The rest of this paper is organized as follows: In Section 2, we review a representative sample of work done on the task of QTs Classification. Our proposed method for Biomedical QTs Classification is presented in Section 3. The experimental results are presented and discussed in Section 4. Finally, we conclude the paper and describe future work in Section 5.

## 2 RELATED WORK

Although research on QA System has boomed in recent years, Question Classification has been a large part in the research community of text mining after the introduction of QA Track in the Text REtrieval Conference (TREC) in 1999 as well as the presentation of Biomedical QA in the BioASK (Tsatsaronis et al., 2012). Several works that have been presented for open domain QTs Classification are usually based on Syntactic Patterns or rule-based approach such as (Prager et al., 1999; Khoury, 2011; Haris and Omar, 2012; Biswas et al., 2014).

However, laborious researcher's effort is required to create these rules. Some researchers have used machine-learning approach. Li and Roth (2002) have presented a hierarchical classifier for open

domain QTs Classification based on the Sparse Network of Windows. Two classifiers were involved in this work: the first one classified questions into the coarse categories; and the other classified questions into fine categories. Several syntactic and semantic features were extracted and compared in their experiments. Their result showed that the hierarchical classifier achieved an accuracy of 90%.

Yu et al., (2005) have improved the Bayesian model by applying the tf-idf measure to deal with the weight of words for Chinese Question Classification. They have achieved an accuracy of 72.4%. Xu et al., (2006) have employed affiliated ingredients as the features of the model and used the results obtained by the syntactic analysis for extracting the question word. They have also achieved an accuracy of 86.62% for the coarse grained categories. Sun et al., (2007) have got features for classification using HowNet as the Semantic resource, whereas Yu et al., (2005) have used Support Vector Machine model, and choose word, part of speech, chunk, Named Entity, word meaning, synonyms and Categories coherence word.

Li et al., (2008) have classified open domain what-type questions into proper semantic categories using Conditional Random Fields (CRFs). They have used several syntactic and semantic features were extracted and compared in their experiments. They have used the CRFs model to label all the words in a question, and then choose the label of head noun as the question category and achieved an accuracy of 85.60%.

Yu et al., (2007) have presented their implemented medical QA system, MedQA, which generates paragraph-level answers from both the MEDLINE collection and the Web. The system in its current implementation deals with just definitional questions (e.g., “What is X?”).

Jacquemart and Zweigenbaum (2003) have described semantic based approach toward the development of a French Language Medical QA System. They have proposed a semantic model of Medical Questions Classification. In fact, they have modeled the forms of the 100 Medical Questions as Syntactic-Semantic Patterns and with one hundred questions that have been used in their study cannot cover all QTs. For example, the authors don't take into account the *What type* of questions that considered one of the most complicate questions to classify (Li et al., 2008).

Weissenborn et al. (2013) have presented a QA System for factoid questions in the biomedical domain. Their system is able to answer only factoid questions (e.g. “Where in the cell do we find the

*protein Cep135?*”). The authors have not taken into account other QTs and have not addressed the Biomedical QTs Classification problem.

Yang et al. (2015) have described a Biomedical QA System deals with just factoid questions. However, the authors have not addressed the Biomedical QTs Classification challenge. They have clearly noted that the Biomedical QTs Classification is a big challenge for building an extensible Biomedical QA System.

To our knowledge, the literature has not discussed the QTs Classification problem in the biomedical domain, whereas our study addresses this problem of Biomedical QTs Classification and takes into account all Biomedical QTs in order to build an extensible Biomedical QA System.

### 3 PROPOSED METHOD

Our main goal is to classify the Biomedical Questions into three broad categories: Yes/No, Factoid and Summary Questions. To achieve this goal, we propose several Syntactic Patterns of each Biomedical QTs. We first run a POS Tagger on each question of Benchmark dataset using the Stanford's POS Tagger (Toutanova and Manning, 2000) and manually analyze these questions and constructing Syntactic Patterns for QTs. On the basis of that we have classified each QTs into three categories.

Table 1 show that *Which, How* and *What Types* of questions could belongs to Factoid and Summary Questions, while *Why Type* of questions belongs to only Summary Questions, etc.

Table 1: Question Categories and their Excepted Answer Types.

Question	Category	Answer(s)
How	Factoid	Biomedical Entity Names, Number(s), short expression
	Summary	Phrase, Paragraph, short text summarization
Why	Summary	Phrase, Paragraph, short text summarization
Where	Factoid	Biomedical Entity Names, Number(s), short expression
Which	Factoid	Biomedical Entity Names, Number(s), short expression
	Summary	Phrase, Paragraph, short text summarization
What	Factoid	Biomedical Entity Names, Number(s), short expression
	Summary	Phrase, Paragraph, short text summarization
Yes/No	Yes/No	Yes or No

To detect Yes/No Questions we used the regular expression (see pattern (1)), where the questions should start with three types of words. We found that this method is significantly efficient.

$$[\text{Be verbs} | \text{Modal verbs} | \text{Auxiliary verbs}] + [.*] + ? \quad (1)$$

Where:

- Be verbs = «am, is, are, been, being, was, were»
- Modal verbs = «can, could, shall, should, will, would, may, might»
- Auxiliary verbs = «do, did, does, have, had, has»

Examples:

*Is intense physical activity associated with longevity?*

*Does Serca2a bind PLN in the heart?*

As it is difficult to distinguish Factoid Type of Question Wh-word, from Summary Type of Question Wh-word (Biswas et al., 2014). In this paper, we have used WordNet in order to improve the performance of classification. Indeed, The WordNet (Fellbaum, 1998) is a large English lexicon in which meaningfully related words are connected via cognitive synonyms (synsets). The WordNet is a useful tool for word semantics analysis and has been widely used in Question Classification as semantic feature for machine learning approach such as (Schlaefter et al., 2007).

Additionally, we have used MetaMap (Aronson, 2001) for mapping terms in questions to UMLS in order to extract the Biomedical Entity Names (BENs). The UMLS (Bodenreider, 2004) is a repository of biomedical vocabularies developed by the US National Library of Medicine.

To overcome this issue, we list all regular expression patterns of each QTs that are used in our experiments as follow (NOUN is a noun, JJ is an Adjective):

**What** — Question category: Summary or Factoid  
Question Pattern:

$$\text{What} + [\text{is|are}] + \left\{ \begin{array}{l} \text{definition} \\ \text{role} \\ \text{treatment} \\ \text{aim} + [\text{of}] + [\text{NOUN}| \text{JJ} + \text{NOUN}] + ? \\ \text{effect} \\ \text{mechanism} \\ \text{Synonyms of those words} \\ \text{Where NOUN is BEN} \end{array} \right. \quad \langle \text{Summary} \rangle \quad (2)$$

Examples:

*What is the definition of autophagy?*

*What is the function of the yeast protein Aft1?*

$$\text{What} + [\text{is|are}] + \left\{ \begin{array}{l} [\text{NOUN}] + ? \\ \text{Where NOUN is BEN} \end{array} \right. \quad \langle \text{Summary} \rangle \quad (3)$$

Examples:

*What is clathrin?*

*What is the ubiquitin proteome?*

$$\text{What} + [\text{Modal: does}] + \left\{ \begin{array}{l} [\text{NOUN}] + [.*] + [\text{do}] + ? \\ \text{Where NOUN is BEN} \end{array} \right. \quad \langle \text{Summary} \rangle \quad (4)$$

$$\text{What} + \left\{ \begin{array}{l} [\text{NOUN}] + [.*] + ? \\ \text{Or} \\ [\text{Modal (does| do)}] + [.*] + [\text{stand for} \\ | \text{bind to}] + ? \end{array} \right. \quad \langle \text{Factoid} \rangle \quad (5)$$

Example:

*What types of cancers and inherited diseases have been associated to mutations in the Notch pathway?*

$$\text{What} + [\text{is|are}] + \left\{ \begin{array}{l} \text{number} \\ \text{name} \\ \text{indication} \\ \text{value} + [\text{of}] + [\text{NOUN}| \text{JJ} + \text{NOUN}] + ? \\ \text{frequency} \\ \text{prevalence} \\ \text{frequency} \\ \text{Synonyms of those words} \\ \text{Where NOUN is BEN} \end{array} \right. \quad \langle \text{Factoid} \rangle \quad (6)$$

Examples:

*What is the indication of Daonil (Glibenclamide)?*

*What is the prevalence of short QT syndrome?*

**Which** — Question category: Summary or Factoid  
Question Pattern:

$$\text{Which} + \left\{ \begin{array}{l} [\text{NOUN}] \text{ where NOUN is BEN} \\ \text{Or} \\ [\text{Verb}] + [.*] + [\text{NOUN}] + [.*] + [\text{NOUN}] + ? \\ \text{Or} \\ [\text{JJ} + \text{NOUN}] \end{array} \right. \quad \langle \text{Factoid} \rangle \quad (7)$$

Example:

*Which is the phosphorylated residue in the promoter paused form of RNA polymerase II?*

$$\text{Which} + [\text{is|are}] + \left\{ \begin{array}{l} \text{number} \\ \text{name} \\ \text{indication} \\ \text{value} + [\text{of}] + [\text{NOUN}| \text{JJ} + \text{NOUN}] + ? \\ \text{frequency} \\ \text{prevalence} \\ \text{frequency} \\ \text{Synonyms of those words} \\ \text{Where NOUN is BEN} \end{array} \right. \quad \langle \text{Factoid} \rangle \quad (8)$$

Example:

*Which is the prevalence of cystic fibrosis in the human population?*



**Which**+ [is|are]+  $\left\{ \begin{array}{l} \text{definition} \\ \text{role} \\ \text{treatment} \\ \text{aim}+[\text{of}]+[\text{NOUN}|JJ+\text{NOUN}]? \\ \text{effect} \\ \text{mechanism} \\ \text{Synonyms of those words} \\ \text{Where NOUN is BEN} \end{array} \right. \llcorner \text{Summary} \gg \text{ (9)}$

Example:

*Which is the definition of pyknons in DNA?*

**Where** — Question category: Always Factoid

Question Pattern:

**Where** + [.\*] +?  $\llcorner \text{Always Factoid} \gg \text{ (10)}$

Example:

*Where in the cell do we find the protein Cep135?*

**Why** — Question category: Always Factoid

Question Pattern:

**Why** + [.\*] +?  $\llcorner \text{Always Summary} \gg \text{ (11)}$

Examples:

*Why does the prodrug amifostine (ethyol) create hypoxia?*

**How** — Question category: Factoid or Summary

Question Pattern:

**How** +  $\left\{ \begin{array}{l} [\text{Adverb}] \\ \text{Or} \\ [\text{Adjective}] \end{array} \right. + [.*] +? \llcorner \text{Factoid} \gg \text{ (12)}$

Example:

*How many recombination hotspots have been found in the yeast genome?*

**How** +  $\left\{ \begin{array}{l} [\text{Modal}] \\ \text{Or} \\ [\text{Verb}] + [.*] +? \\ \text{Or} \\ [\text{NOUN}] \text{ where NOUN is BEN} \end{array} \right. \llcorner \text{Summary} \gg \text{ (13)}$

Example:

*How does adrenergic signaling affect thyroid hormone receptors?*

*How are thyroid hormones involved in the development of diabetic cardiomyopathy?* (14)

**Define| Synonyms**+  $\left\{ \begin{array}{l} [\text{NOUN}] +? \\ \text{Where NOUN is BEN} \end{array} \right. \llcorner \text{Summary} \gg$

Example:

*Define marine metaproteomics.*

In addition, we have proposed an algorithm (see algorithm (1)) to classify the given Biomedical Question into any one of the predefined categories using the questions patterns presented above. Then,

the appropriate Answer Extraction Algorithms can be applied for extracting the precise and most appropriate answer for that Biomedical Question.

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**Algorithm 1:** Biomedical QTs Classification.

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**Input:** Biomedical Questions

**Output:** Biomedical QTs /\*Yes/No, Factoid or Summary\*/

**1: If** Biomedical Question **matched** to [Be verbs | Modal verbs | Auxiliary verbs] + [.\*] +? **then**

**2: Return** “Yes/No Question”

**3: Else**

**4: Case 1:** Wh-word = “How”

**If** wh-word+ [Adjective| Adverb] **then**

**Return** “Factoid”

**6: Else if** wh-word+ [Modal| Verb] **then**

**Return** “Summary”

**7: Else if** wh-word+[Noun] && Noun =

BEN **then Return** “Summary”

**8: End if**

**9: Case 2:** Wh-word = “Why” **Return** “Summary”

**10: Case 3:** Wh-word = “Where” **Return** “Factoid”

**11: Case 4:** Wh-word = “Which”

**12: If** wh-word+ [Noun| Verb|JJ+Noun]&& Noun = BEN **then Return** “Factoid”

**13: Else if** wh-word+ [is| are]+ [[indication of] [number of]]... [synonym of those words] + [NOUN|JJ+NOUN] && Noun= BEN **then Return** “Factoid”

**14: Else if** wh-word+ [is| are] + [[definition of] [role of]]... [synonym of those words] + [NOUN|JJ+NOUN] && Noun= BEN **then Return** “Summary”

**15: End if**

**16: Case 5:** Wh-word = “What”

**17: If** wh-word+ [is| are] + [Noun] && Noun = BEN | wh-word+ [Modal: does] + [NOUN] + [.\*] + [do] +? **Then Return** “Summary”

**18: Else if** wh-word+ [Noun] | wh-word+[Modal]+[.\*]+[ stand for| bind to]+? **Then Return** “Factoid”

**19: Else if** wh-word+ [is| are]+ [[indication of] [number of]]... [synonym of those words] + [NOUN|JJ+NOUN] && Noun= BEN **then Return** “Factoid”

**20: Else if** wh-word+ [is| are] + [[definition of] [role of]]... [synonym of those words] + [NOUN|JJ+NOUN] && Noun= BEN **then Return** “Summary”

**21: End if**

**22: Case 6:** Biomedical Question **matched** to [Define| Synonyms] + [NOUN] +? && NOUN=BEN

**23: Return** “Summary”

**24: End if**

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## 4 EXPERIMENTS AND RESULTS

In this section, we evaluate our proposed method for

Biomedical QTs Classification through the study of the performance of Biomedical Syntactic Patterns for each type of questions.

### 4.1 Datasets

The 1433 Biomedical Questions of the Benchmark datasets are the evaluation text collection of our study. Those over one thousand Biomedical Questions were obtained from BioAsk challenges (Tsatsaronis et al., 2012). Each type of question was assigned to one category. For example, the question “What is the role of the Tsix gene during X chromosome inactivation?” was assigned to Summary Questions.

Table 2 shows the 3 categories and the number of Questions Types assigned to each one. For example, 198 *What Type* of questions were assigned to Factoid Questions, 234 *What Type* of questions were assigned to Summary Questions, etc.

Table 2: Question Types and their Question Categories.

Question Types	Question Categories			Total
	Yes/No	Factoid	Summary	
How	0	29	37	66
Why	0	2	12	14
Where	0	15	0	15
Which	0	394	55	439
What	0	198	234	432
Yes/No	467	0	0	467
Total	467	638	328	1433

### 4.2 Results and Discussion

To conduct the experiments, we have used the Benchmark datasets (Tsatsaronis et al., 2012) that have been presented above. We have applied Stanford’s POS Tagger (Toutanova and Manning, 2000) for finding the syntactic structure of questions. We proceeded by passing the questions one by one to Stanford’s POS Tagger in order to capture their syntactic structure. Additionally, We have applied MetaMap (Aronson, 2001) to extract the Biomedical Entity Names of each Biomedical Questions. Moreover, we have used WordNet in order to generate synonyms of words (e.g. treatment, effect, etc.) that have been presented in patterns [2,6,8,9]. We have exploited the Syntactic patterns that have been presented in section 3.

For evaluation, accuracy performance have been widely used to evaluate Question Types Classification methods (Li and Roth, 2002; Zhang et al., 2003; Metzler et al., 2004; Biswas et al., 2014).

Table 3: Accuracy Performance of Biomedical QTs Questions.

Question Types	Total	Matched	Mismatched	Accuracy
How	66	63	3	95.45%
Why	14	13	1	92.85%
Where	15	14	1	93.33%
Which	439	434	5	98.86%
What	432	299	133	69.21%
Yes/No	467	467	0	100%

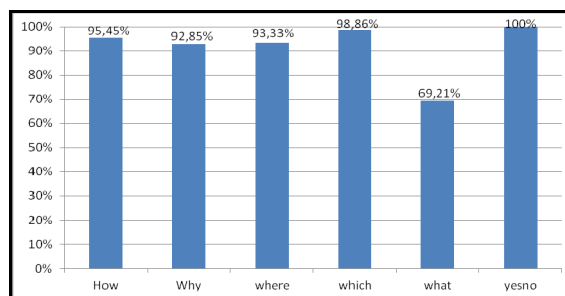


Figure 2: Performance Measurement.

Table 4: Increase performance of *what* and *which* types of questions with/without synonyms.

Question Types	What	Which
Without Synonyms	59.30%	94.75%
With Synonyms	69.21%	98.86%
Increase Performance	+10%	+4%

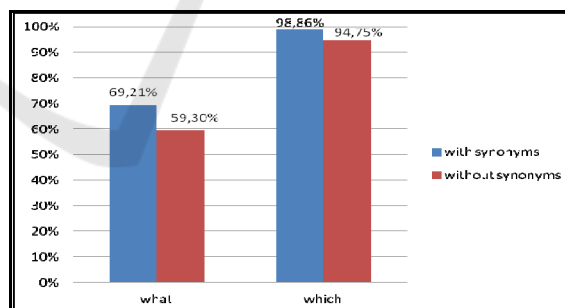


Figure 3: Accuracy performance of *what* and *which* types of questions with/without synonyms.

Overall, from the results presented in Table 3 and Figure 2, it can clearly be seen that the overall accuracy of our proposed method for Biomedical QTs Classification is very interesting. The average performance for automatically assigning a category to a question was accuracy of 91.62%.

In fact, the proposed method led to the highest accuracy of 100% and 98.68% for classifying the Yes/No Biomedical Questions and *Which Type* of

questions. As it is difficult to distinguish Factoid Type from Summary Type of *What Type* of questions, nevertheless, our proposed have achieved an accuracy of 69.21%. Indeed, we can see from Table 4 and Figure 3 that synonyms extracted from WordNet of words (e.g. definition, indication, etc.) that have been presented in section 3 (see pattern (2) and pattern (6)) enhanced the performance (+10%) for classifying *What Type* of questions. In addition, using synonyms in pattern (8) and pattern (9) enhanced the performance (+4%) for classifying *Which Type* of questions.

We have shown that the proposed method can classify the Biomedical Questions into three broad categories: Yes/No, Factoid and Summary Questions. Indeed those three categories can summarize all Question Type that can be posed by user (Tsatsaronis et al., 2012). In other words, these categories can summarize all possible cases of the Expected Answer Types. For example: “*Which diseases are caused by mutations in Calsequestrin 2 (CASQ2) gene?*” is a Factoid Questions and the answer is a Biomedical Named Entity (BNE) “CPVT”, “*catecholaminergic polymorphic ventricular tachycardia*”. In addition, one of the most advantages of our proposed method is that it does not require a learning phase and therefore it can be easily integrated in a Biomedical QA System in order to build an extensible Biomedical QA System.

As mentioned in the Introduction, so far no one appears to have discussed QTs Classification in the biomedical domain. Therefore, the importance of our results using our proposed method thus lies both in their generality and their relative ease of application to Biomedical QA System.

In addition, maybe one limitation of our research was the patterns used for classifying *What Type* of question if we take into account its difficulty to distinguish Factoid Type from Summary Type of *What Type* of question. Clearly these patterns that have been used for classifying *What Type* question are not enough to make generalizations about this one. However, The 69.21% for the *What Type* of question is quite low compared to the rest of the results. The 69.21% stay satisfactory and it could be improved with more patterns. Indeed the presence of large numbers of such rules does not introduce any problems because the rules are represented by a set of patterns, and Question Types Classification is conducted by pattern matching.

Remarkably, the comparative studies that have been done have focused on QA Systems and due to the lack of baseline of Biomedical QTs Classification methods we could not have comparative study.

The main goal of our project is to develop an extensible Biomedical QA System capable to answer all Biomedical QTs that is Yes/No, Factoid and Summary Questions which is composed by three main components: Questions Processing, Documents Processing and Answers Processing. Significantly, we believe that QT Classification may impact positively or negatively on the reset of the QA process. Indeed, the output of QTs Classification will be used to determine the appropriate Answer Extraction Algorithm.

## 5 CONCLUSION

In this paper we have presented a novel method for classifying the Biomedical Questions into three broad categories that summarize all possible cases of the Expected Answer Types: Yes/No, Factoid and Summary Questions. We first defined the syntactic structure of the Biomedical Questions using Stanford’s POS Tagger (Toutanova and Manning, 2000) as well as MetaMap for Biomedical Named Entities Recognition (BNER). We presented the rules that are represented by a set of patterns for each Biomedical QTs. Our experimental results using our proposed algorithm prove that the Biomedical QTs classification problem can be solved quite accurately using our proposed method. The proposed method will allow selecting the appropriate Answer Extraction Algorithm and therefore the Biomedical QA System will be able to treat all types of questions.

In future work we plan to improve the performance for classifying *What Type* of questions by presenting more patterns. We will pay more attention to integrate our Biomedical QTs classification system in a Biomedical QA System.

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