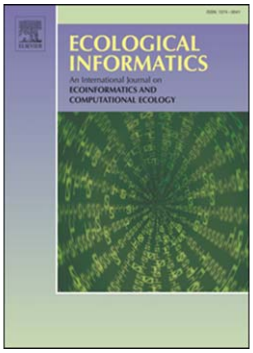
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ABSTRACT

Currently there are an overwhelming number of scientific publications in Life Sciences, especially in Genetics and Biotechnology. This huge amount of information is structured in corporate Data Warehouses (DW) or in Biological Databases (e.g. UniProt, RCSB Protein Data Bank, CEREALAB or GenBank), whose main drawback is its cost of updating that makes it obsolete easily. However, these Databases are the main tool for enterprises when they want to update their internal information, for example when a plant breeder enterprise needs to enrich its genetic information (internal structured Database) with recently discovered genes related to specific phenotypic traits (external unstructured data) in order to choose the desired parentals for breeding programs.

In this paper, we propose to complement the internal information with external data from the Web using Question Answering (QA) techniques. We go a step further by providing a complete framework for integrating unstructured and structured information by combining traditional Databases and DW architectures with QA systems. The great advantage of our framework is that decision makers can compare instantaneously internal data with external data from competitors, thereby allowing taking quick strategic decisions based on richer data.

Keywords

Business Intelligence, Data Warehouse, Question Answering, Information Extraction, Information Retrieval, Genetic Information.

1. INTRODUCTION AND MOTIVATION

According to the 2011 Gartner Group report (Gartner Group report, 2011), worldwide information volume is growing at a minimum rate of 59 percent annually. Thus, the available information for a company is progressively increasing. This information is accessible from any computer, and comes from both structured and unstructured sources of data. The structured data is predetermined, well defined, and usually managed by traditional Business Intelligence (BI) applications, based on a Data Warehouse (DW), which is a repository of historical data gathered from the heterogeneous operational databases of an organization (Inmon, 2005; Kimball & Ross, 2002).

The main benefit of a DW system is that it provides a common data model for all the company data of interest regardless of their source, in order to facilitate the report and analysis of the internal data of an organization. DW structures the data in terms of Facts and Dimensions. A fact is the center of the analysis, and typically represents a business activity. For example, gene effects on a trait could be considered a fact. In order to evaluate the performance of the activity, a fact includes fact attributes, also called measures, which are represented as cells in an OLAP cube. In our example, the influence degree of the gene could be a measure. Furthermore, a fact can be analyzed from different perspectives, which constitute dimensions that provide contextual information for the analysis, and are represented as axis in an OLAP cube. For example, we could analyze gene effects by looking at the trait associated or at the plant family whose traits are being studied. Moreover, each dimension may have its own structure, allowing us to analyze the fact at different levels of aggregation, and establishing relationships between levels. For example, the hierarchy for the species dimension could be species (lowest level), which can be aggregated into families, and families can be aggregated into classes.

However, there is a wide consensus in that the internal data of organizations to take right decisions is not enough, even more in current highly dynamic and changing markets where information from competitors and clients/users is extremely relevant for these decisions. Thus, the main disadvantage of traditional DW architectures is that they cannot deal with unstructured data (Rieger, Kleber, & von Maur, 2000). Currently, these unstructured data are of a high relevance in order to be able to make more accurate decisions, since the BI applications would empower their functionality by considering both data from inside the company (e.g. the reports or emails from the staff stored in the company intranet) and outside (e.g. the Webs of the company competitors) (Trujillo & Maté, 2012).

For example, let us consider a scenario where a plant breeder enterprise needs to enrich its genetic information (internal structured DW) with recently discovered genes related to specific phenotypic traits (external unstructured data obtained from the Web) in order to choose the desired parentals for breeding programs. The plant breeder enterprise will find that there are an overwhelming number of scientific publications in Life Sciences, specifically in Genetics and Biotechnology (Matos et al., 2010). According to the Medline database, about 2 scientific papers in Life Sciences are incorporated per minute, and there are more than 1.000 journals in Biology currently published worldwide[1]. Moreover, increasing bioinformatics work has resulted in a large amount of information stored in Biological Databases (e.g. UniProt, RCSB Protein Data Bank, GenBank, CEREALAB, etc.) that remains uninterpreted. For these reasons, current rate of scientific publications requires search strategies that allow us to extract biological information easily and efficiently (Jensen, Saric, & Bork, 2006; Altman et al., 2008).

So far, many attempts to integrate a corporate DW of structured data with unstructured data have been reported (Badia, 2006; Henrich & Morgenroth, 2003; McCabe et al., 2000; Pérez-Martínez, 2007; Pérez-Martínez et al., 2008a, 2008b; Pérez-Martínez, Berlanga, & Aramburu, 2009; Priebe & Pernul, 2003a, 2003b; Qu et al., 2007; Rieger, Kleber, & von Maur, 2000). They are mainly based on systems that use Natural Language Processing (NLP) techniques to access the unstructured data in order to extract the relevant information of them but they do not reach a full integration of structured and unstructured data as our proposal manages.

In this paper, we present a framework which combines traditional DW architectures with Question Answering (QA) systems. QA systems represent the potential future of Web search engines because QA returns specific answers as well as documents. It supposes the combination of Information Retrieval (IR) and Information Extraction (IE) techniques. IR is the activity of obtaining information resources relevant to an information need from a collection of information resources. This activity is currently quite popularized by the Web search engines as Google. On the other hand, IE is the task of automatically extracting specific structured information from unstructured and/or semi-structured machine-readable documents. A typical application of IE is to scan a set of documents written in a natural language and populate a database with the information extracted (e.g. the name of products and their prices).

We start with a question or query in Natural Language (NL) posed by the decision maker, who also identifies the sources where to search the required information. We distinguish between *queries* and *questions* in order to highlight that a query refers to a request of data to the DW system, whereas a question requests data to the QA system. The former are likely to be much more rich and complex than simple questions, which may force to divide the query into several questions. The questions are analyzed by the Distributor/Integrator service of the framework and are passed to the corresponding node (e.g. the QA node to access external data or the DW node to access internal data). Then, each node processes the question in an autonomous way on its corresponding sources. Once the system receives all the results from the nodes, like internal DW, Web services or API's, it is capable of integrating and showing a dashboard to the user that allows him/her to take the right decision. Finally, let us add that we also take advantage of our unique well-checked hybrid method for building data warehouses. Our method starts by analyzing user requirements by means of interviews. Then, each requirement is checked against the data sources to ensure that the necessary data exists. Afterwards, the data warehouse is built in order to support queries from the presented approach. Therefore, we can ensure that the query posed on the DW node will return the correct data required by the decision maker (Mazón & Trujillo, 2008; Mazón, Trujillo, & Lechtenbörger, 2007).

The paper is structured as follows. In Section 2, we summarize the most relevant related work regarding combining traditional DWs with unstructured data. In Section 3, we introduce our framework for analyzing and integrating different data sources into a common dashboard. In Section 4, and in order to clarify our proposal, we introduce the case study that will be evaluated in Section 5, where we provide detail on the evaluation of the application of our proposal. We conclude the paper with the summary of our main contributions and our directions for future works.

2. RELATED WORK

Several attempts to integrate search of structured and unstructured data have arisen, in which the structured data is handled by a DW or a DB system, and the unstructured data by an IR, IE or QA system. This integration should meet certain requirements in order to adequately provide integrated information for the users. These requirements include the detection of matching points between the structured and unstructured data, the integration of the results obtained by each system, and the preservation of high quality sources of information, i.e. the DW. In other words, the extraction of structured data from unstructured data is required in order to provide links with similar structured data. In this way, the user can represent and integrate the unstructured data in all the possible dimensions and hierarchies that a DW cube can contain. As a result the information returned by both systems could be perfectly integrated and analysed together. However, these data cannot be mixed, as that would result in potential decrease of the accuracy of the data stored.

Regarding the connection between a DW and an IR system, the work presented in (Rieger, Kleber, & von Maur, 2000) and (Henrich & Morgenroth, 2003) can be cited. However, as it is claimed in the work presented in (McCabe et al., 2000), those efforts do not take advantage of the hierarchical nature of structured data nor of classification hierarchies in the text, so they implement an IR system based on a multidimensional database. Specifically, they focus on the use of OLAP techniques as an approach to multidimensional IR, where the document collection is categorized by location and time. In this way, they can handle more complex queries, like retrieving the documents with the terms "financial crisis" published during the first quarter of 1998 in New York, and then drilling down to obtain those documents published in July 1998.

In (Priebe & Pernul, 2003a, 2003b), authors propose an architecture that introduces a communication bus where both systems publish their output. Each system picks up this output and uses it to show related information. For example, the query context of a DW access is used by an IR system in order to provide the user with related documents found in the organization's document management system. In order to solve the problem of the heterogeneity of both systems, they propose to use ontological concept mapping (e.g. the DW system uses "owner" for what is called "author" within the document metadata). They use an ontology for the integration, but it is only oriented to communicate both applications in enterprise knowledge portals. In this way, they handle queries like "sales of certain audio electronics products within the four quarters of 1998".

In (LaBrie & St. Louis, 2005), an alternative mechanism for IR ("dynamic hierarchies" based upon a recognition paradigm) that overcome many of the limitations inherent in traditional keyword searching is proposed. This IR approach was used in BI applications but no integration between both applications was made.

In (Pérez-Martínez, 2007; Pérez-Martínez et al., 2008a), authors provide a framework for the integration of a corporate warehouse of structured data with a warehouse of text-rich XML documents, resulting in what authors call a contextualized warehouse. These works are based on applying IR techniques to select the context of analysis from the document warehouses. In (Pérez-Martínez, Berlanga, & Aramburu, 2009), authors formalize a multidimensional model containing a new dimension for the returned documents. To the best of our knowledge, these papers are the most complete ones in combining and considering structured and unstructured data in a common DW architecture.

Regarding IE, (Losiewicz, Oard, & Kostoff, 2000) surveys applications of data mining techniques to large text collections, including IR from text collections, IE to obtain data from individual texts, DW for the extracted data. In (Badia, 2006), different IE-based (as well as IR) methods for integrating documents and databases are discussed. Specifically, the author proposes IE as the right technology to substitute IR, which fills the slots of a set of predefined templates that determines the information that is searched in the collection of documents. In (Bhide et al., 2008), authors claim that there exist BI products like QL2 (QL2, 2013) and IBM Business Insights Workbench (BIW) (IBM. Business insights workbench, 2013) that try to derive context from the unstructured data by using various IE and clustering techniques. However, no business intelligence product has tried to exploit context available in the structured data of the enterprise in order to allow us a seamless analysis of both structured and unstructured data fully integrated, in a consolidated manner. They propose the use of IE techniques to a specific task of linking common entities in a relational database and unstructured data.

With regard to work on the integration of DW and QA systems, in (Qu et al., 2007), a scheme about a DW design based on data mining techniques was put forward in order to overcome the defects of current Chinese QA systems. In (Roussinov & Robles-Flores, 2004), authors explored the feasibility of a completely trainable approach to automated QA on the Web for the purpose of business intelligence and other practical applications. They introduce an entirely self-learning approach based on patterns that do not involve any linguistic resources. In (Lim et al., 2009), the authors present a study of comparative and evaluative queries in the domain of Business Intelligence. These queries are conveniently processed by using a semantic interpretation of comparative expressions and converting them to quantifiable criteria, in order to obtain better results in a QA system for this domain. In our previous work of (Ferrández & Peral, 2010), we analyzed the main benefits of integrating QA systems with traditional DW systems in order to be able to complete internal data with precise returned answers from QA systems, instead of returning whole documents provided by IR systems.

Several work on NL questions to query the Semantic Web have been carried out, like Aqualog (Lopez, Pasin, & Motta, 2005), SQUALL (Ferré, 2012) or FREyA (Damljanovic, Agatonovic, & Cunningham, 2012), which use SPARQL for querying knowledge bases built in RDF. In PANTO (Wang et al., 2007) and Querix (Kaufmann, Bernstein, & Zumstein, 2006), they accept generic NL questions and outputs SPARQL queries.

Other works present the integration of structured and unstructured data but they do not use IR, IE or QA techniques. (Alqarni & Pardede, 2012) show the integration of DWs and unstructured business documents. They propose a multi-layer schema for mapping structured data stored in a data warehouse and unstructured data in business-related documents (invoices, contracts and catalogs). A linguistic matching mechanism using WordNet::Similarity (a free open software package) to find possible similarities between the elements has been used. However, this mapping is carried out at the schema level, and consequently, much information available in the document is not taken into account and cannot be incorporated into the DW. Furthermore, authors study a well-defined type of document and, therefore, a real enrichment of the DW with all the available information in any business document is not performed. In (Miller, Honavar, & Barta, 1997), authors propose the design of a DW system that allows the interaction of structured and unstructured data. The system makes use of Object Oriented views that define the construction, importation and exportation of resources and services. Once the materialized view is available in the DW, the user can apply any of the data mining tools to these views, and the obtained results can be stored in the knowledge base of the DW. However, a minor drawback is that authors do not fully explain the process and conclude that the data mining techniques are just at the beginning stages. Therefore, in these two proposals the real integration and enrichment of structured data together with unstructured data are not fully achieved.

Finally, in the field of Genetics and Biotechnology, as mentioned in Section 1, current rate of scientific publications requires search strategies that allow us to extract biological information easily and efficiently (Jensen, Saric, & Bork, 2006; Altman et al., 2008) to enrich and update the available information. A real application is the QTL (Quantitative Trait Locus) analysis, object of our case study. Quantitative traits refer to phenotypic characteristics that vary in degree and can be attributed to polygenic effects, i.e., product of two or more genes, and their environment.

QTL analysis is very useful in areas as diverse as agriculture, biomedicine and evolutionary biology (i.e. phylogeny) because allows us to relate a certain phenotypic trait to specific regions of chromosomes, which contains one or more genes involved in that characteristics.

The aim of QTL methodology is to identify the action, interaction, number, and precise location of the chromosomal regions responsible of specific phenotypic features (Falconer & Mackay, 1996; Kearsey, 1998; Lynch & Walsh, 1998; Miles & Wayne, 2008). However, the biological situation is more complex. For example, there are polygenic traits (such as eye and skin color in humans, wing morphology in fruit fly, or kernel color in wheat) which depends on several genes (sometimes located in different chromosomes). This so-called multifactorial inheritance makes very difficult to understand the basis of many phenotypic characteristics. Inversely, pleiotropy refers to the phenomenon in which a single gen controls two or more apparently unrelated phenotypic features (Stearns, 2011). It is associated to evolution and speciation processes (Latta & Gardner, 2009; Orr, 2000), human diseases (Wilkins, 2010) and aging phenomenon (Moorad & Promislow, 2009). The existence of polygenia and pleiotropy phenomena makes necessary to enrich genetical databases with recently discovered information (external data) in order to update our knowledge about biological traits: if they are controlled by several genes or if they are related to other biological characteristics, respectively.

For instance, a huge number of genetical disorders are polygenic, including cancer, type-II diabetes, Alzheimer disease, hypertension, Crohn disease, autism and many others (Pharoah et al., 2002; Pajović, 2007). For that reason, knowing the individual role of the genes involved in the diseases is essential to create new optimal therapies. Furthermore, in genetic engineering it is very important to take into account all the genes related to interesting traits, in order to design newer and easier working strategies, as there is not only one way of improving a biological trait (i.e. production of human insulin by recombinant DNA technology in *E. coli*, or yield of the rice plant). Considerations about pleiotropy could avoid undesired indirect effects in the previous examples or could provide specific benefits, depending on the proposed goal.

2.1.Contributions of our proposal to previous work

We overcome the data integration problems identified in previous work through the following four contributions. Contribution 1 is that we use QA in order to access to the unstructured data. We consider QA more suitable than only IR because the integration of whole documents returned by IR is weaker and less useful to the decision maker, since the information provided by QA is much more specific, and thus, can be integrated seamlessly into DW cubes. Moreover, we consider QA more suitable than IE because of the QA flexibility to afford any kind of question, and not only a set of predefined templates.

With regard to contribution 2, we deal with the weak point about the lack of full integration between systems that access the unstructured data (e.g. QA), whether it is external or internal, and the ones that access the structured data (DW). In this way, we allow the decision maker to compare both the internal data of a DW and the data gathered from the Web. This aim is managed by our proposed framework that completes the whole flow of data.

In contribution 3, we have improved the interaction with the user through: (i) the outputs of the nodes are fully integrated and presented to the user in a friendly dashboard (Eckerson, 2007), which allows the decision maker to immediately compare internal data of a company against external data; (ii) our NL interface (Llopis & Ferrández, 2012) outdoes previous work by its full portability to different DW systems; and by its query-authoring services. These services dramatically improve the system usability allowing the decision maker to early detect errors in the question by automatically distinguishing between linguistic (e.g. when the grammar in the interface cannot parse a question) and conceptual (e.g. entity-property mismatch, data type mismatch, etc.) failures.

Finally, in contribution 4, we have proved and evaluated the feasibility of our approach on the case scenario of a seed company that is interested in new advances in Genetics in order to improve its cereal breeding programs by obtaining new disease-resistant and high-yielding grain varieties. These new advances are obtained from the Web through the QA system. Therefore, from the initial request of data of "What QTLs are related to resistance to *Fusarium* in durum wheat?", our proposal can obtain the cube from the enterprise's DW, and the QA database with the QTLs extracted from the Web, where both results are integrated into a dashboard that immediately allows the user to analyze and compare them. Moreover, it can transform the initial DW query into the set of questions with information present in the DW scheme, such as "What QTLs are related to frost tolerance in durum wheat?", which facilitates to focus only on the traits stored in the DW.

3. OUR BUSINESS INTELLIGENCE FRAMEWORK

In our framework (Figure 1), we can distinguish two phases: (i) the system setup and (ii) the running phase, which are detailed in the next two subsections.

The setup phase prepares the source nodes, where the required information will be searched, by creating the corresponding ontologies. It is important to emphasize that several DW, Database, QA or Big Data source nodes can be connected, each one with its own implementation, model and domain (e.g. we can connect a QA node specialized in Genetics domain as well as a QA node specialized in legal domains), as long as an interpreter for the NL query is built for that type of node. In the case of different DBMS technologies, this task can be avoided since most OLAP servers already provide an interface to extract data from multiple DBMS. Thus, the OLAP server can be used as an intermediary for extracting the data. These ontologies are created just the first time that the source node is connected in our framework.

In the running phase, the user or decision maker (i) poses a NL question through the GUI (Graphical User Interface) element and (ii) selects the sources to be searched (e.g. in a specific database or DW, or in a specific QA domain). The GUI element passes the NL question to the Distributor/Integrator element that also sends it to the set of specialized nodes (e.g. the DW and QA nodes). Each specialized node disposes of the proper interface in order to process adequately the NL question and to produce the suitable output information. Then, the Distributor/Integrator coordinates the running of each specialized node, gathering the output of these nodes in order to send the fused information to the GUI element. Finally, the GUI is responsible for displaying the results as a dashboard, which integrates both external and internal data.

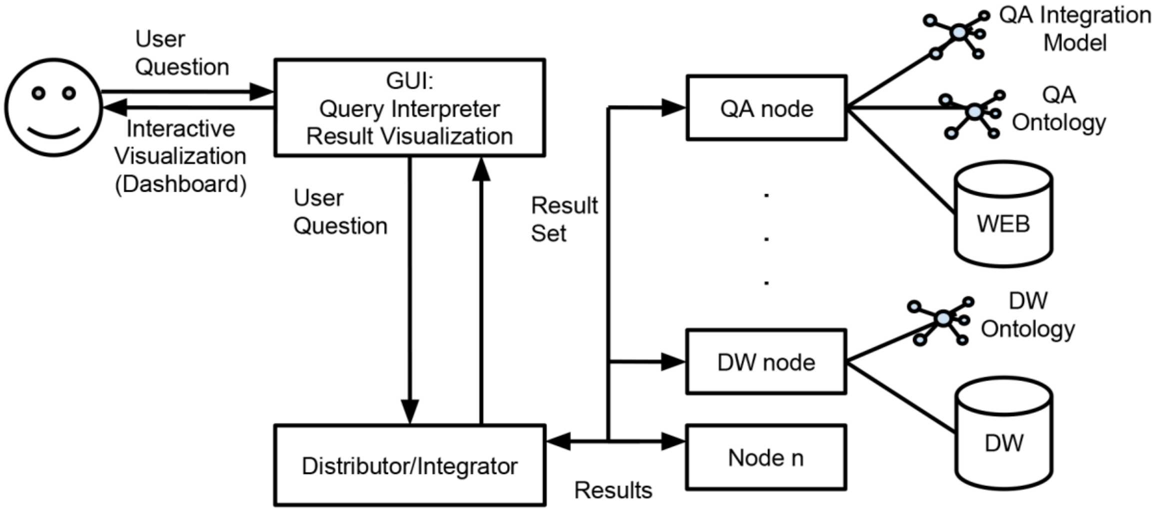


Figure 1. Framework to access/integrate structured/unstructured and internal/external data

This paper complements our approach to access different sources shown in (Maté, Llorens, & de Gregorio, 2012) (i) by reaching the full integration of unstructured and structured information through the ontologies and (ii) by displaying the data integration with a dashboard. In (Maté, Llorens, & de Gregorio, 2012) the authors describe an approach based on the MapReduce strategy (Dean & Ghemawat, 2008) where the query is divided and distributed to different nodes and then it integrates the results; this approach allows to maintain the internal structure of the different nodes, allowing to add or remove the nodes in a seamlessly way. A similar proposal is (Abelló, Ferrarons, & Romero, 2011) where the authors present a framework for create cubes using MapReduce; this proposal differs from ours, where we consider the cube with the OLAP server a single node. For more information on theoretical foundation see (Gray et al., 1997).

3.1.Setup phase

In this phase, the specialized source nodes, both DW and QA, are prepared just the first time that they are connected to our framework, in order to integrate them in the global system. In each QA node, we create (i) its QA integration model and (ii) its QA ontology; whereas in each DW node we create its DW ontology that describes the DW scheme, which will allow its integration with the QA nodes through a semi-automatic mapping process that detects connections between the QA and DW ontologies.

Thus, a repository of ontologies is constructed just the first time the corresponding node is connected to our framework. Therefore, the following connection to the node, our approach consults the catalog and schema in order to check if it has been modified, in which case the ontology is reconstructed, since the computational cost is not significant and this phase is run off-line.

QA node. (i) The QA integration model contains information about the answer that is returned to the Distributor/Integrator element in order to be integrated with the data returned by the DW node. For example, Figure 2 depicts a QA integration model that specifies the database schema in which the set of answers extracted by the QA system will be stored. It contains the answer (as a noun phrase and as a string of fixed size), the expected answer type (e.g. the “QTL” type for the question “What QTLs are related to resistance to *Fusarium* in durum wheat?”), the entities detected in the question (e.g. ”durum wheat” as plant type), the URL or document that contains the answer and the passage or answer context (i.e. the surrounding text around the answer, with which the user can decide whether the answer is correct for its purposes without reading the whole document). The QA integration model can vary in different QA systems. For example, a QA system can return an answer context of three sentences (such as the one depicted in Figure 2), whereas other QA systems can return only a fixed number of words around the answer.

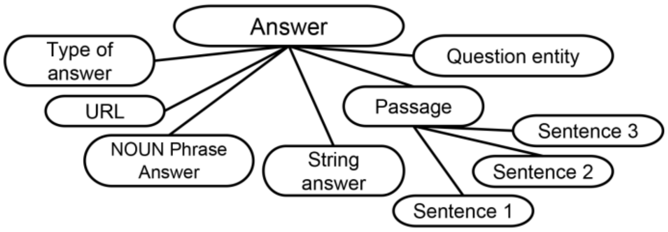


Figure 2. QA Integration Model

QA node. (ii) The QA ontology contains information about the set of answer types considered in the QA system. For example, Figure 3 depicts an excerpt of an answer ontology, where a set of WordNet top concepts (e.g. group or person) are used with some extensions (e.g. phenotypic characteristic –used to classify the entities that do not belong to any defined type– or plant type in the object type).

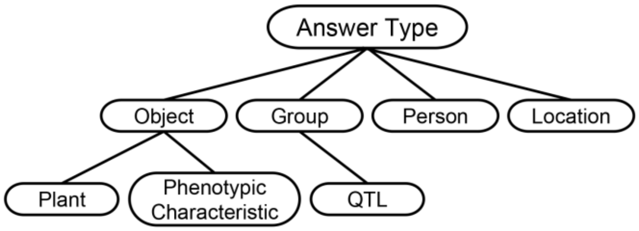


Figure 3. QA Ontology

DW node. The DW ontology (Santoso, Haw, & Abdul-Mehdi, 2010) is created, which will allow us to analyze an integrated view of data. The ontology relates the tables and attributes considered as the internal data. In Figure 4, an excerpt of a DW ontology is shown.

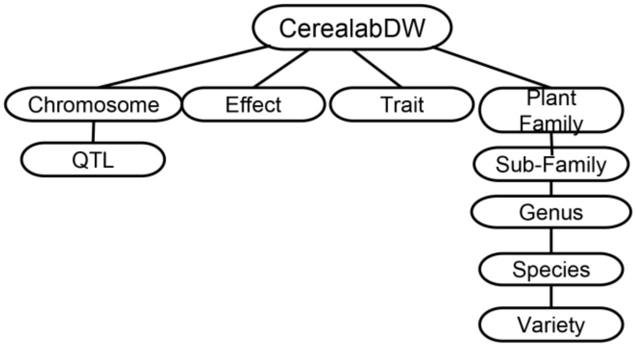


Figure 4. DW Ontology

QA and DW ontology mapping. Finally, a semi-automatic mapping process is carried out in order to detect connections between the QA and DW ontologies (Wang et al., 2007) (see Figure 5):

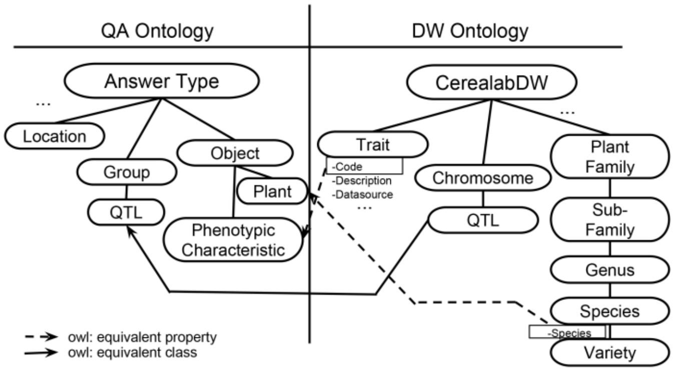


Figure 5. Mapping between subsets of QA ontology and DW ontology

(a) We detect equivalent classes/properties in both ontologies. Firstly, the exact matches between the two ontologies are retrieved (e.g. in Figure 5 the equivalent class "QTL" is detected since they appear in Figure 3 and 4). After that, the remaining concepts are matched using the information of the lexical-semantic resources used in QA (WordNet, lexicons, dictionaries, glossaries, etc.) and prompting the user to confirm the match. For example, in Figure 5, the equivalent property "Species" in DW vs. "Plant" in QA is established due to the hyperonym relation between "Plant Family" and "Species";

(b) We add new subclasses –extracted from the DW ontology– in the QA ontology (e.g. "Sub-Family" which is added to the "Plant" type thanks to the hyperonym relation between "Plant Family" and "Sub-Family");

(c) We enrich the lexical-semantic resources used in QA with instances from the DW ontology (see Figure 6). In the Figure, the enrichment of WordNet can be seen, where the instances of QTLs stored in the DW (QFhs.pur.2D, QFhs.inra-3A, etc.) are added to the lexical resource. In this way, questions about these new instances can be treated by the system.

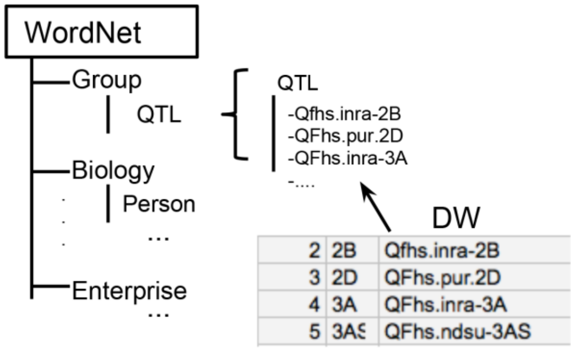


Figure 6. Enriching QA lexical-semantic resources with knowledge from the DW

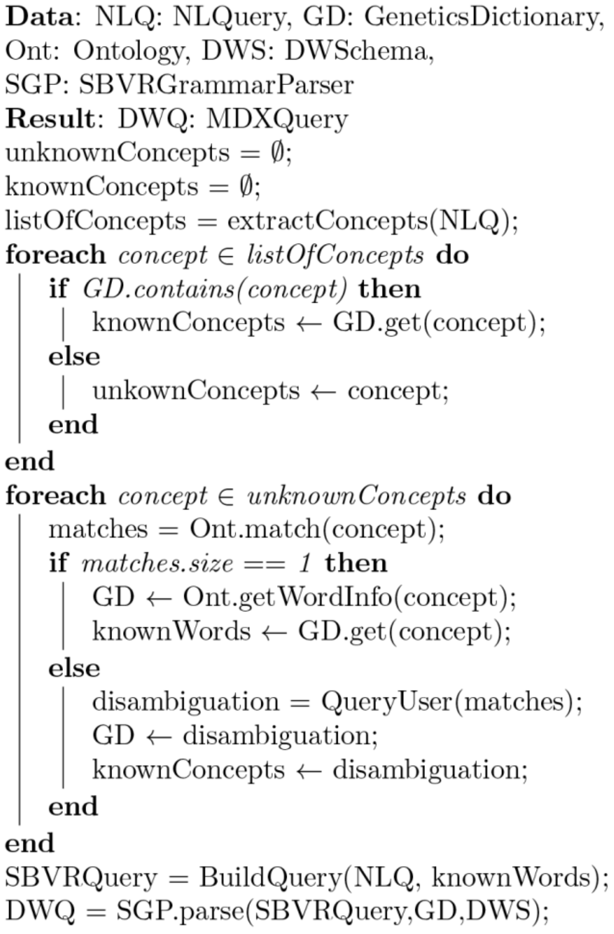
3.2. Running phase

The GUI element. Firstly, the GUI element receives the NL request of data through our NL interface (Llopis & Ferrández, 2012), which thanks to its query-authoring services improves the system usability allowing the decision maker to early detect errors in questions by automatically distinguishing between linguistic (e.g. errors due to lexical or syntactic mistakes) and conceptual failures (e.g. errors due to the lack of an specific relation between tables in the DW). Secondly, the decision maker selects the sources to be searched for the required information.

Then the ***Distributor/Integrator*** performs a coordinator role by distributing the NL request of data to each DW and QA node; and by receiving and creating an integrated view of the data returned from all nodes.

The DW node. The NL query is transformed into a MultiDimensional eXpression (MDX), which can be interpreted by the OLAP engine. This transformation is performed by combining NL processing tasks with schema matching techniques (Maté, Trujillo, & Mylopoulos, 2012; Rahm & Bernstein, 2001).

First, the system analyzes the NL query and extracts the main concepts involved in the query. For example, consider the query "What QTLs are related to resistance to *Fusarium* in durum wheat?" The main concepts extracted are "QTLs", "resistance to *Fusarium*" and "durum wheat". Note that concepts may not only refer to structures in the model, but also to instances or conditions. For each concept, first we retrieve the exact matches from a Genetics Dictionary (Maté, Trujillo, & Mylopoulos, 2012). The Genetics Dictionary returns a formalized version of the concept, which includes mappings to the data warehouse schema if the concept has been used before. The remaining unknown concepts are matched by means of the DW Ontology (Figure 4) and WordNet (Figure 6). For example, "QTL" matches with the level "QTL", thus it is added along with the mapping information to the dictionary. Next, "durum wheat" is not matched against any element in the Ontology, thus it is expanded by means of WordNet. As a result of the expansion, "durum wheat" is matched as an instance of the level "Species" of plants. As in the previous case, the concept and its mapping information are stored in the dictionary. If any concept can be matched against multiple candidates in the Ontology or it cannot be found, then the user is prompted to disambiguate the concept. In the case of concepts that are not found in the Ontology, the user can directly specify the mapping by means of a formal mapping. For example, "resistance to *Fusarium*" cannot be matched to any element in the schema, thus it is expanded by means of WordNet. As no element matches are found, the user is prompted for a match. Therefore, the user introduces a formal translation for this concept as "with Trait code equal to resistance to *Fusarium*", which is stored in the Genetics Dictionary for future queries. Once all the concepts have been identified, the query is reformulated as a valid controlled language expression (Maté, Trujillo, & Mylopoulos, 2012). In our example, the posed query is transformed into "Evidence of QTL and Trait with Trait code equal to resistance to *Fusarium* and Species with species equal to durum wheat", where Evidence is added to the query because most DW systems require at least one measure to be queried to the system in order to correctly retrieve the data. Finally, the controlled language query is sent to the parser module that processes the query and outputs a MDX query understandable by OLAP engines.



```
Data: NLQ: NLQuery, GD: GeneticsDictionary,
Ont: Ontology, DWS: DWSchema,
SGP: SBVRGrammarParser
Result: DWQ: MDXQuery
unknownConcepts = $\emptyset$;
knownConcepts = $\emptyset$;
listOfConcepts = extractConcepts(NLQ);
foreach $concept \in listOfConcepts$ do
    if $GD.contains(concept)$ then
        knownConcepts $\leftarrow$ GD.get(concept);
    else
        unkownConcepts $\leftarrow$ concept;
    end
end
foreach $concept \in unknownConcepts$ do
    matches = Ont.match(concept);
    if $matches.size == 1$ then
        GD $\leftarrow$ Ont.getWordInfo(concept);
        knownWords $\leftarrow$ GD.get(concept);
    else
        disambiguation = QueryUser(matches);
        GD $\leftarrow$ disambiguation;
        knownConcepts $\leftarrow$ disambiguation;
    end
end
SBVRQuery = BuildQuery(NLQ, knownWords);
DWQ = SGP.parse(SBVRQuery,GD,DWS);
```

Algorithm 1. Natural language query parsing algorithm

In the event that the parser module can obtain multiple MDX queries, i.e. the formal concepts have multiple mappings to the DW schema and allow for several valid queries, then the user is notified to select the desired query to be posed to the DW system.

As a result, the DW node returns a cube which contains the information specified by the NL query, which can be navigated using the traditional OLAP operations, such as roll-up or drill-down.

The QA node. The NL question is internally processed through a set of NLP tools (e.g. POS-taggers or partial parsing) in order to detect the type of the answer to be searched (e.g. for the previously mentioned question "What QTLs are related to resistance to *Fusarium* in durum wheat?", given the "QTL" answer type, it supposes that the searched information consists of a string followed or preceded by the word QTL, or associated to –gene, allele, etc–), as well as the most salience entities in the question (e.g. “durum wheat” as an entity of plant-object type). After that, the processed answer is posed to an Information Retrieval tool in order to obtain the set of documents that is more likely to contain the answer. These documents are analyzed in order to extract a set of answers sorted by the probability of correction certainty. The extraction process is specialized for each answer type. For example, in the case of the “QTL” type, for the previously mentioned question, several patterns are used to extract the answer from the NOUN Phrase answer. In the sentences a) “…the QTL Qfhs.ndsu-3AS in order to develop durum wheat plasm and cultivars with higher level of *Fusarium* resistance.” and b) “…*Fusarium* resistance, especially that mediated by Fhb1 gene.”, the syntactic patterns allow flexibility in order to detect the solution noun phrase “QTL Qfhs.ndsu-3AS” extracting the specific QTL solution (“Qfhs.ndsu-3AS”); similarly with the second solution (“Fhb1 gene”) that is extracted thanks to the hyperonym relation between QTL and Gene.

Finally, the set of answers extracted by the QA system is stored in a relational database (Stanojevic & Vraneš, 2012; Kerui et al., 2011) with the structure defined in the QA integration model (see Figure 2). Subsequently, this database and the flattened DW cube will be joined (through the union points) in a resulting table as it is explained in detail in the following step.

The integration of the results. Once the running of each DW and QA node is finished, the Distributor/Integrator element creates an integrated view of the data returned from both nodes. In order to integrate the results from both the QA and the DW without storing the information directly into the DW, a transformation must be made. DWs represent information in a multidimensional manner, whereas QA retrieves information in a table format. Therefore, we apply the following process. First, we lower the dimensionality of the DW information retrieved by transforming the DW cube into a table (i.e. flattening process). This process is formalized as follows:

Let $C = \{M, D\}$ be a cube where M is a set of measures represented by the cube and D is a set of dimensions that determine the coordinates of the cube. A Relation R containing the equivalent information can be obtained by the following process. For each level selected L_j in dimension $d_i \in D$, a column is created in R. Afterwards, the columns corresponding to the measures $m_n \in M$ are created. Finally, R is populated by a set of tuples $n_1...n_n$ where the domain of each column $c_j = \{L_j\}$ for the columns corresponding to the dimensions and $c_n = \{m_n\}$ for the columns corresponding to the measures. A similar result can be obtained in current BI tools by pivoting all dimensions to one side of the pivot table.

The information in the QA node is represented by an ontology as the one shown in Figure 5. Let $QAont,DWont = \{C,R\}$ be the ontologies for the QA system and the DW respectively, containing a set of concepts C and a set of relationships R, and M is a set of mappings from attributes in *DWont* concepts to $C_n \in QAont$, A minimal relation T from the QA system containing only the minimum information can be obtained by obtaining a set of tuples $n_1,…n_n$, by extracting all $C_n \in M$ from each result n_i obtained by the QA system. The domain of each column $c_{j<n-1} \in T$ is $c_j = \{C_j\}$, and the domain of the last two columns is $c_{n-1} = \{0..1\}$ and $c_n=\{urls\}$ respectively, where c_{n-1} represents the confidence in the result obtained and c_n contains the url where the result was obtained from. As can be seen, T can be joined with R, as long as both recover at least one concept $C_n \in M$.

After that, we have obtained a compatible representation of the DW data and a set of union points (that we have called connections and are identified by means of the ontological mappings as it is depicted in Figure 5). In the next step, the user filters the QA results and selects those elements that the decision maker considers relevant to be joined to the flattened DW cube through the union points in a resulting table created on the fly: DW⋈QA (where the symbol ⋈ indicates the natural join between the two tables). Therefore, the DW system is not altered in any way, keeping the data clean and avoiding being affected by inaccuracies in the information retrieved by the QA system.

Finally, the dashboard (feeding on the mentioned joined table) shows both data from inside the company and outside. Moreover, these connections points would allow the automatic generation of new questions, such as the questions about the specific traits stored in the DW (e.g. “What QTLs are related to frost tolerance in durum wheat?”), which facilitates to focus only on the new advances about the traits present in the DW.

Repository of questions. Our approach stores the QA results in a persistent way through a new DW repository. This repository is created from the QA integration model (Figure 2) and a generic set of dimensions. The logical design has four dimensions: *Date*, contains the information about when the question was made; *Query*, with the NL question; *Fields*, with the QA integration model fields and the union points; and one degenerated dimension with *ID*, that links with the specific NL question and the QA rows obtained in a concrete date. The fact table of this repository has the elements retrieved after the matching phase. The purpose of this repository is double: on the one hand, the external data obtained through the QA system are stored in a permanent way in order to have a historical file with relevant data to the different questions, overcoming the intrinsic dynamic character of the external information –e.g. the biomedical papers present in the MEDLINE database returned by the search engine PubMed (PubMed, 2013)–; on the other hand, a comparison of the obtained results with different questions or even the same question with different dates can be made.

Advantages of our proposal. The main advantages of this integration of results are: (1) the decision maker can browse all the information (passage, context, precise answer, etc.) about every tuple of the QA database so the user does not need to explore the whole document; (2) the user can delete the incorrect tuples returned by the QA node; (3) new questions can be automatically generated from the instances stored in the DW taking into account the ontology integration and the detected question entities; and (4) the connections between the QA and DW ontologies have been detected in order to facilitate the data integration.

Finally, it is important to emphasize the modularity and scalability of our framework. It is independent of the DW and the QA systems specifically used, because the integration of these systems is carried out by the detected connection points between the respective ontologies, thereby having a more integrated and scalable view of internal and external data. Furthermore, several QA nodes can be used and, subsequently, several QA databases are shown to the user in the dashboard. Moreover, the user can easily store different questions and results (DW cube and QA database), allowing the user to save time in the access and analysis of external information.

4. A CASE SCENARIO

4.1.The case scenario description

After introducing the system architecture, we illustrate the application of our framework, and later we will evaluate it through the following case scenario: a plant breeder enterprise wants to carry out new breeding programs experimenting with the new advances in Genetics. An optimal breeding program must consider all the current scientific knowledge to obtain the maximum efficiency. As explained in Section 1, the present rate of scientific publications on ecological and biomedical sciences justifies the need of developing efficient data mining approaches. The data mining purpose is not only to facilitate the work by gathering all the updated information about an area of expertise, but also to create new biological knowledge (Krallinger & Valencia, 2005). Therefore, the decision maker of the breeding program can easily access to external data about relevant agronomic traits and draw up new molecular protocols to design genetically modified crops in order to increase the productivity of the seed industry. Further applications of these enrichment techniques could include scenarios of metabolic pathways (i.e. protein networks).

The corresponding model for the mentioned scenario, shown in Figure 7, is based on a UML profile for modeling DWs presented in (Luján-Mora, Trujillo, & Song, 2006). DW models structure data according to a multidimensional space, where events of interest for an analyst (e.g., *sales*, *treatments of patients*, *molecular markers…*) are represented as facts which are associated with cells or points in the multidimensional space, and which are described in terms of a set of measures. These measures can be analyzed by means of dimensions which specify different ways the data can be viewed, aggregated or sorted (e.g. according to *time, store, customer, plant variety,* etc.). Importantly, dimensions are organized as hierarchies of levels, which are of paramount importance in BI systems in order to empower data analysis by aggregating data at different levels of detail.

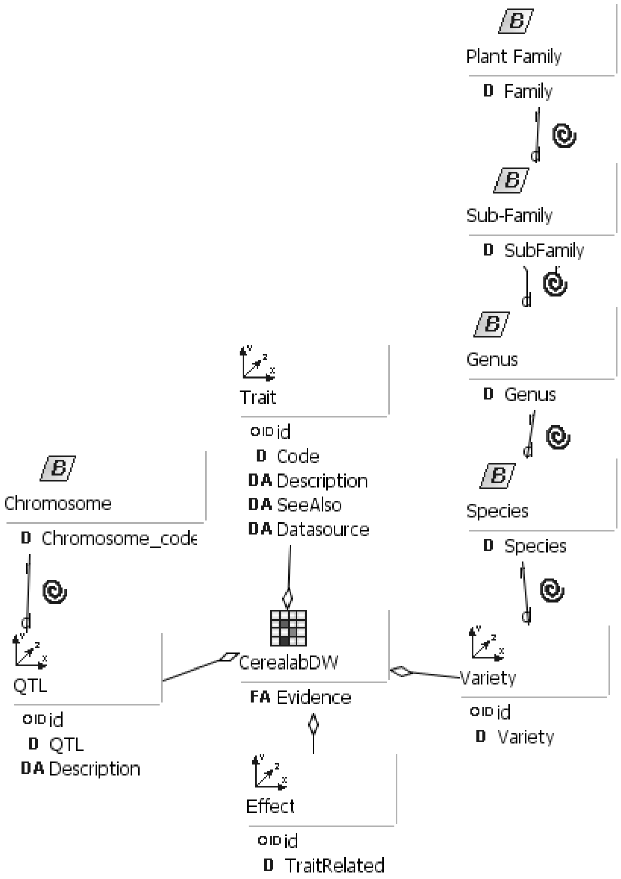


Figure 7. Excerpt of the multidimensional model for our case scenario on QTLs related to key Traits

The model shown in Figure 7 captures the structure of the initial information to be analyzed. We can see four different dimensions in our model: QTL, Trait, Variety and Effect.

First, the QTL dimension captures the information regarding the QTLs involved in the different traits shown by the various species of plants. The QTL dimension is composed by two hierarchy levels, each of them identified by the corresponding scientific code or name given to the element. QTLs are grouped into their corresponding Chromosomes that represent the highest level of aggregation.

Second, the Trait dimension captures the traits affected by the presence of the QTLs. Traits are identified by the code name assigned to them. Some examples can be "Frost resistance" or "Ash content". Traits also can have a description and can be related to other traits, captured by means of the SeeAlso attribute. Finally, if the trait has been extracted from a datasource, it is stored within the DataSource attribute.

Third, the Variety dimension captures the information about the varieties of plants which has the QTLs. This dimension contains all the information about each variety, including the Species, Genus, Sub-Family and Family. Each of these levels includes the corresponding identifier of the group that the variety pertains to. In our case, we will only store information about Wheat, Barley and Rice at the highest level of the hierarchy, although additional information could be added regarding other groups.

Fourth, the Effect dimension captures the effect that a certain QTL has on a Trait of a Variety. The reason to include this separate dimension is because most data warehouse technologies are designed to contain numerical values within the fact. As the effect of the QTLs on the traits presents a wide variety, from changing colors shown to changing the percentage of certain chemical elements present in the plant, we add this dimension to store this information.

Finally, our fact includes a measure that provides an idea of how much evidence there is in terms of the number of studies that support the effect of a QTL on the trait of a plant variety. This information is retrieved from the enterprise internal data. The measure is aggregated with the addition of evidence encountered that a trait is affected by a QTL.

It is important to mention that in our case scenario the enterprise internal data consist of the CEREALAB database (Milc et al., 2011). The CEREALAB database aims to store genotypic and phenotypic data obtained by the CEREALAB project and to integrate them with already existing data sources in order to create a tool for plant breeders and geneticists. The database can help them in unravelling the genetics of economically important phenotypic traits; in identifying and choosing molecular markers associated to key traits; and in choosing the desired parentals for breeding programs. The database is divided into three sub-schemas corresponding to the species of interest: wheat, barley and rice; each sub-schema is then divided into two sub-ontologies, regarding genotypic and phenotypic data, respectively.

Although some databases designed to store and manage both phenotypic and genotyping data have been reported, such as AppleBreed (Antofite et al.,

2007) or PlantDB (Exner et al., 2008) among others, we have decided to use CEREALAB because those databases are often designed to store the experimental data and the data available are generally restricted to those implemented by the developers/users with no possibility to take advantage of already available information that resides in other data sources. Moreover, CEREALAB is the first database specific for breeding of wheat, barley and rice, fundamental crops for the world agriculture (Milc et al., 2011).

In order to use the CEREALAB database, a multidimensional repository (data mart) of the information to be analyzed was created. There are two main reasons for this approach: (i) multidimensional databases are structured to optimize reading operations, which is the main focus of our database, and (ii) it is usually easier for the users to use dimensions in order to filter the data and pose broad questions than using tables directly.

With the UML model of Figure 7, users (the decision makers) can request a set of queries to retrieve useful information from the system. For instance, they are probably interested in obtaining all the phenotypic characteristics related to a specific QTL. Many other queries can be similarly defined to support the decision making process. However, the allowed queries are constrained by the information contained in the schema in such a way that other important information may be missed. For example, the following scenario is likely to happen: the company wants to offer interesting new breeding programs based on the last advances in Genetics. Normally, the company has not any internal report about this information; however, it is likely to obtain this information from the Web.

4.2. The application of our proposal on the case scenario

Let us apply our framework detailed in section 3 to this case scenario supposing that the following user's NL request of data is formulated: "What QTLs are related to resistance to *Fusarium* in durum wheat?"

Setup phase. QA and DW node. With regard to the system setup phase, on the one hand, in the QA node, the QA integration model and the QA ontology of answer types are generated in Figure 2 and 3 respectively. As it can be seen in these Figures, the QA integration model specifies: the answer type, the entities detected in the question, the URL or document identifier, the noun phrase and the passage (formed by three sentences) that contains the answer. On the other hand, in the DW node the DW ontology is created (Figure 4).

Setup phase. QA and DW ontology mapping. Next, the connections between the DW and QA ontologies are detected. In Figure 5 and 6 can be seen: (a) one equivalent class in both ontologies (QTL) and two equivalent properties (Species.species vs. Plant and Trait.code vs. Phenotypic characteristic); (b) four new subclasses are added in the QA ontology: Sub-Family, Genus, Species and Variety; (c) the lexical-semantic resource used in QA is enriched with the set of specific QTLs stored in the DW.

Running phase. The GUI and Distributor/Integrator element. In the running phase, the GUI element receives the NL request of data, which is distributed to each specialized node by the Distributor/Integrator element.

Running phase. The DW node. In the DW node, the NL query is transformed into MDX as presented in section 3.2., and the cube shown in Figure 8 is returned. In this scenario the following MDX query is obtained:

```
with
set Trait_Filter as '{Filter([Trait].Children,
([Trait].CurrentMember.Name = "Resistance to
Fusarium"))}'
 set Variety_Filter as
'{Filter([Variety].[Species].Members,
([Variety].[Species].CurrentMember.Name = "
durum wheat"))}'

select NON EMPTY {[Measures].[Evidence]} ON
COLUMNS,
  NON EMPTY
Hierarchize(Union(Crossjoin([Trait_Filter],
Crossjoin([Variety_Filter],
[Chromosome].[Chromosome].Members)),
Crossjoin([Trait_Filter], Crossjoin([Variety_Filter],
[Chromosome].[QTL].Members)))) ON ROWS
from [CerealabDW]
```

Running phase. The QA node. In the QA node, the NL question is processed, and its output is structured as the QA integration model specifies. It returns "QTL" type as the answer type according to the QA ontology; the Question Entities "resistance to *Fusarium*" as an entity of Phenotypic Characteristic type; and “durum wheat” as an entity of Plant type. Both entities are used to trace and restrict possible right entity solutions of QTL type (e.g. when the document contains the noun phrase “durum wheat”). Then, the set of answers extracted by the QA system is stored in the database shown in Figure 9, in which the first column (“w”) means the confidence of the QA system in this answer (this value ranges between 0 and 1); the second one means the string answer that is extracted from the fourth column that means the noun phrase that contains the answer (e.g. the “AtNPR1” QTL entity is extracted from the noun phrase solution in “the Arabidopsis thaliana NPR1 gene (AtNPR1)” thanks to the pattern “QTL/gene/allele + QTL/gene/allele_Name” that specifies the word “QTL” or synonym/hyponym/hyperonym followed by a string which denotes the QTL name); the third one means the QA system internal code of the Web page; the following three columns represent the passage in which the solution appears. The passage is formed by three sentences, where the sentence 2 contains the answer. In this way, the user has a context to decide whether the answer is right: the text around the solution, as well as the link to the corresponding URL to access the whole document. Therefore the user can filter this QA database by deleting the wrong extracted information. The last two columns mean the question entities extracted in the document by means of a name entity tagger, which can be used as connection points in the integration phase. For example, from the document with URL code “www.ncbi.nlm.nih.gov/pubmed/18943578” the following Question Entities are detected “*Fusarium* Head Blight Resistance” as Phenotypic Characteristic type and “Tetraploid Wheat” as Plant type; it is important to mention the need of using lexical resources and specialized dictionaries to identify synonym/hyponym /hyperonym relations (for instance “tetraploid wheat”, “durum wheat” and “*triticum durum*” are synonyms). Moreover, the Noun Phrase Answer is extracted from the three sentences that contain the solution “a single QTL designated Qfhs.fcu-7AL” and, consequently, the new QTL Qfhs.fcu-7AL is obtained. This example is very important in order to justify our approach due to the QTL extracted from the mentioned PubMed paper –dated May 2007– is not present in the CEREALAB DW as QTL related to resistance to *Fusarium* in durum wheat. Similarly, from the document with URL code “www.ncbi.nlm.nih.gov/pubmed/16529374” the Question Entities “resistance to *Fusarium* head blight” and “wheat”, and the Noun Phrase Answer “the Arabidopsis thaliana NPR1 gene (AtNPR1)” are detected; consequently, the new Gene AtNPR1 –not present in CEREALAB as gen related to *Fusarium* resistance in wheat– is obtained. In this way, these obtained data could be used in Genetic Engineering approaches in order to improve the resistance of the wheat.

Running phase. The integration of the results. The DW cube and the QA database are sent to the Distributor/Integrator element, which merges the different results and sends them to the GUI element. The merge is performed in our scenario as follows. The results obtained from the DW node are obtained in a cube (Figure 8) that is flattened, obtaining a set of tuples that contain the relevant columns to the query posed, including “Species”, “Trait”, “Chromosome”, “QTL” and “Evidence”. Then, these results are joined with the information recovered from the QA system (Figure 9). Both results are joined by means of the candidate union points identified in the ontology (see Figure 5) and selected by the user –in this scenario the union point “QTL” is only selected–. The result is a table created on the fly (Figure 10) that contains the natural join (⋈) between the flattened DW cube and the QA result. By default, the natural join is only carried out with the top twenty answers of the QA database and this information is initially shown at the dashboard.

For example, in Figure 10, using the connection “QTL”, each DW row is joined with the QA result whose QTL query entity matches. In the Figure, the QTLs “QFhs.ndsu.2A” or “Qfhs.inra-2B” matches so they are shown both the DW and the QA result. In case of no matching between the union point, as occurs in the QA results “AtNPR1”, ”Qfhs.fcu-7AL” and “Fhb1”, our proposal shows these results to emphasize that they are new data not present in the DW. In the same way it should happen with the DW results that do not match with the QA results.

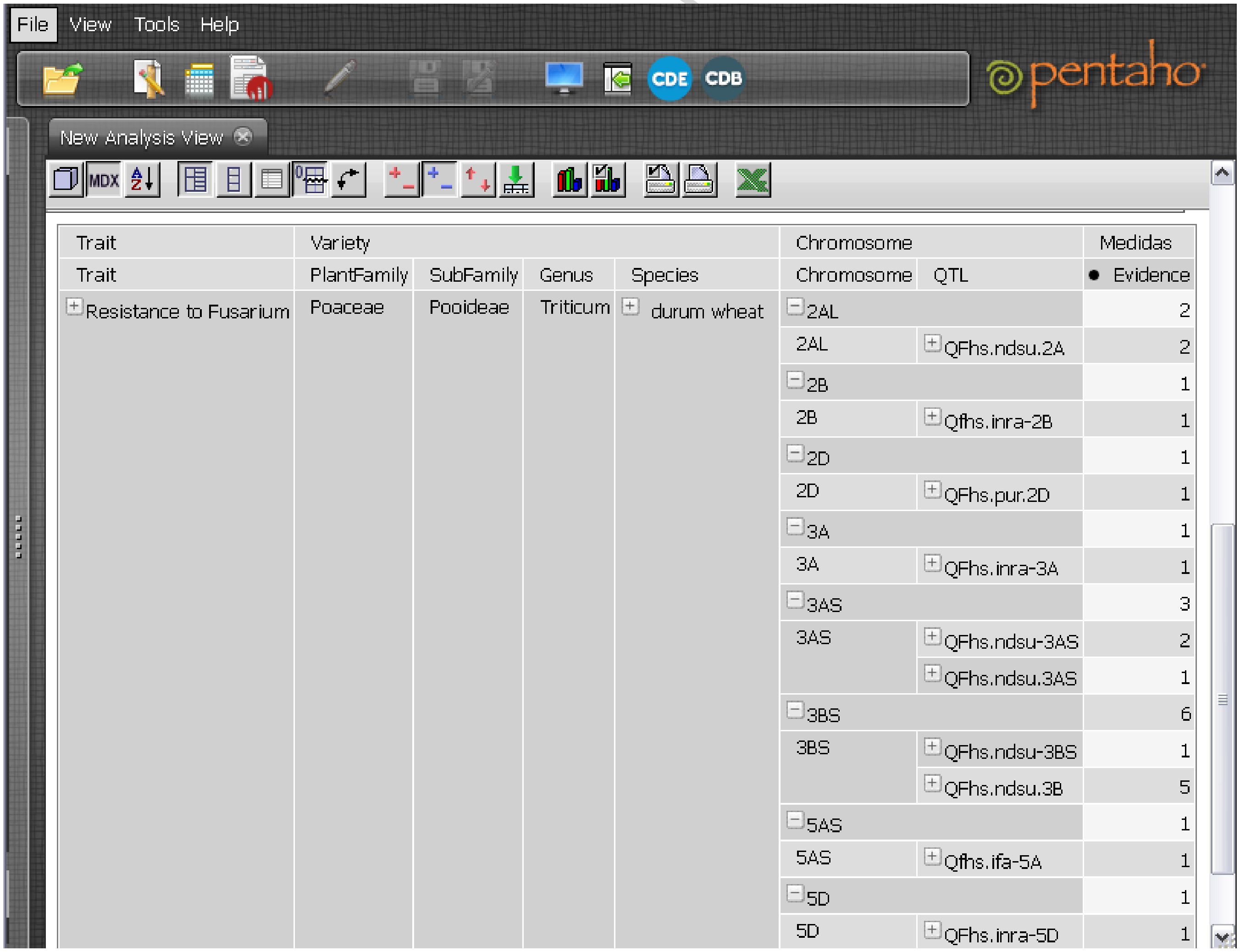
If other connections were established, like “Trait”, every “QTL” and “Trait” in the DW will be joined with their equivalent QA results.

After creating the joined table, the integrated results can be viewed in the dashboard (see Figure 11). At the top of figure, two charts are shown: (1) “Final results” that indicates the percentage of results extracted from the web not present in the DW (in the figure, 9.1% represent the new QTLs not considered in the DW); (2) "QA Performance" that denotes the QA total results (correct answers) vs. QA filtered results (incorrect answers).

After the charts, the previous mentioned join table is presented. In this table, the user can select the rows to analyze. Additionally, the dashboard allows the user configure how many QA results will be joined (by default, the top twenty answers).

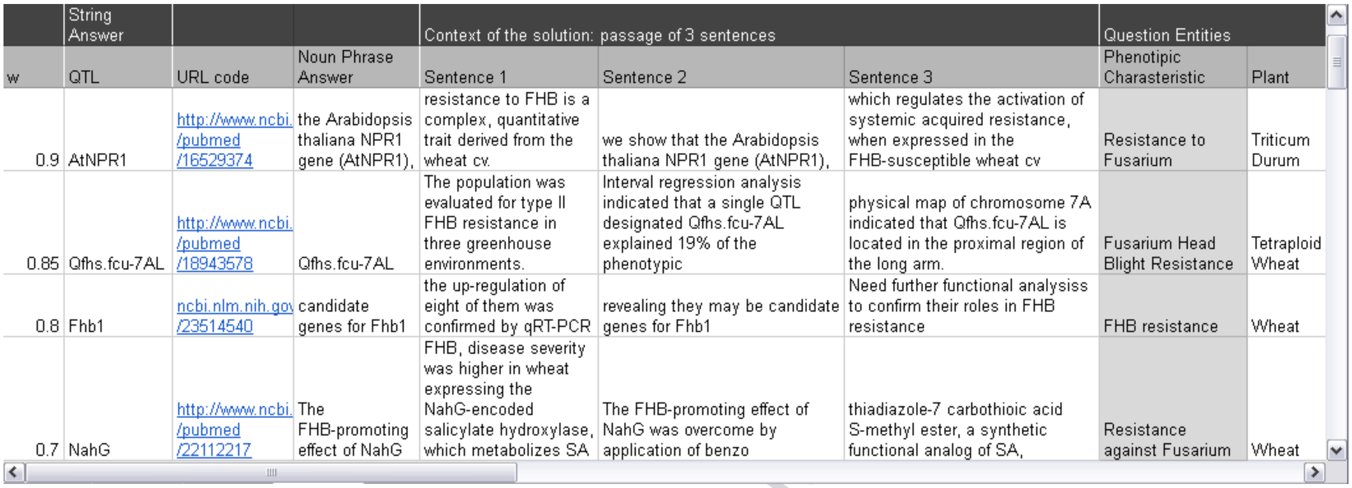
At last, a chart shows the answer evidence in both the DW and the QA results. This evidence denotes the number of the papers/passages that contains the answer (obtained from the information stored in the DW and the QA results). In the example, it is important to note the new QTLs extracted from the web ("AtNPR1", "Qfhs.fcu-7AL" and "Fhb1") that can be seen in the chart.

Repository of questions. The QA database is stored in a persistent way through the new DW repository as well as the date when the question was made, and the NL question. In order to avoid information redundancy, the DW extracted cube is not stored because this information would be easily extracted again whenever the decision maker runs the same query. That is to say, we only stores in the repository of questions, the dynamic external information.



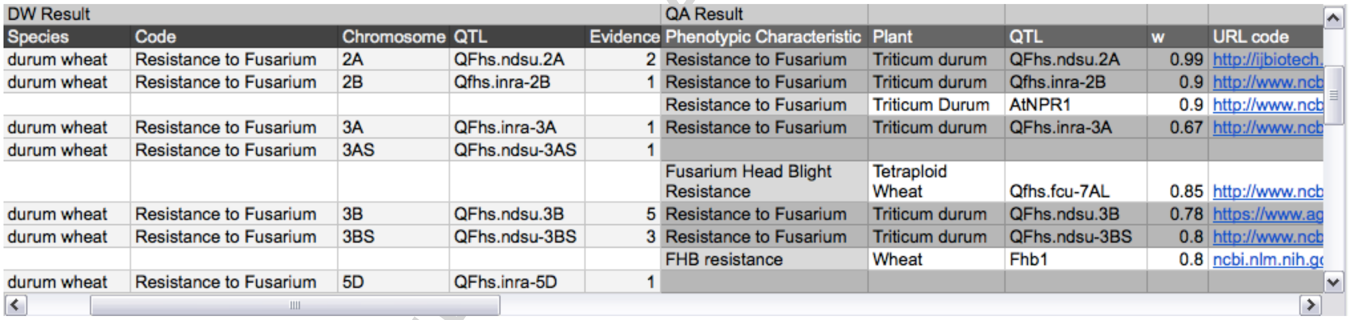
Trait	Variety				Chromosome		Medidas
Trait	PlantFamily	SubFamily	Genus	Species	Chromosome	QTL	● Evidence
Resistance to Fusarium	Poaceae	Pooideae	Triticum	durum wheat	2AL		2
					2AL	QFhs.ndsu.2A	2
					2B		1
					2B	Qfhs.inra-2B	1
					2D		1
					2D	QFhs.pur.2D	1
					3A		1
					3A	QFhs.inra-3A	1
					3AS		3
					3AS	QFhs.ndsu-3AS	2
						QFhs.ndsu.3AS	1
					3BS		6
					3BS	QFhs.ndsu-3BS	1
						QFhs.ndsu.3B	5
					5AS		1
					5AS	Qfhs.ifa-5A	1
					5D		1
					5D	QFhs.inra-5D	1

Figure 8. Cube retrieved from the DW



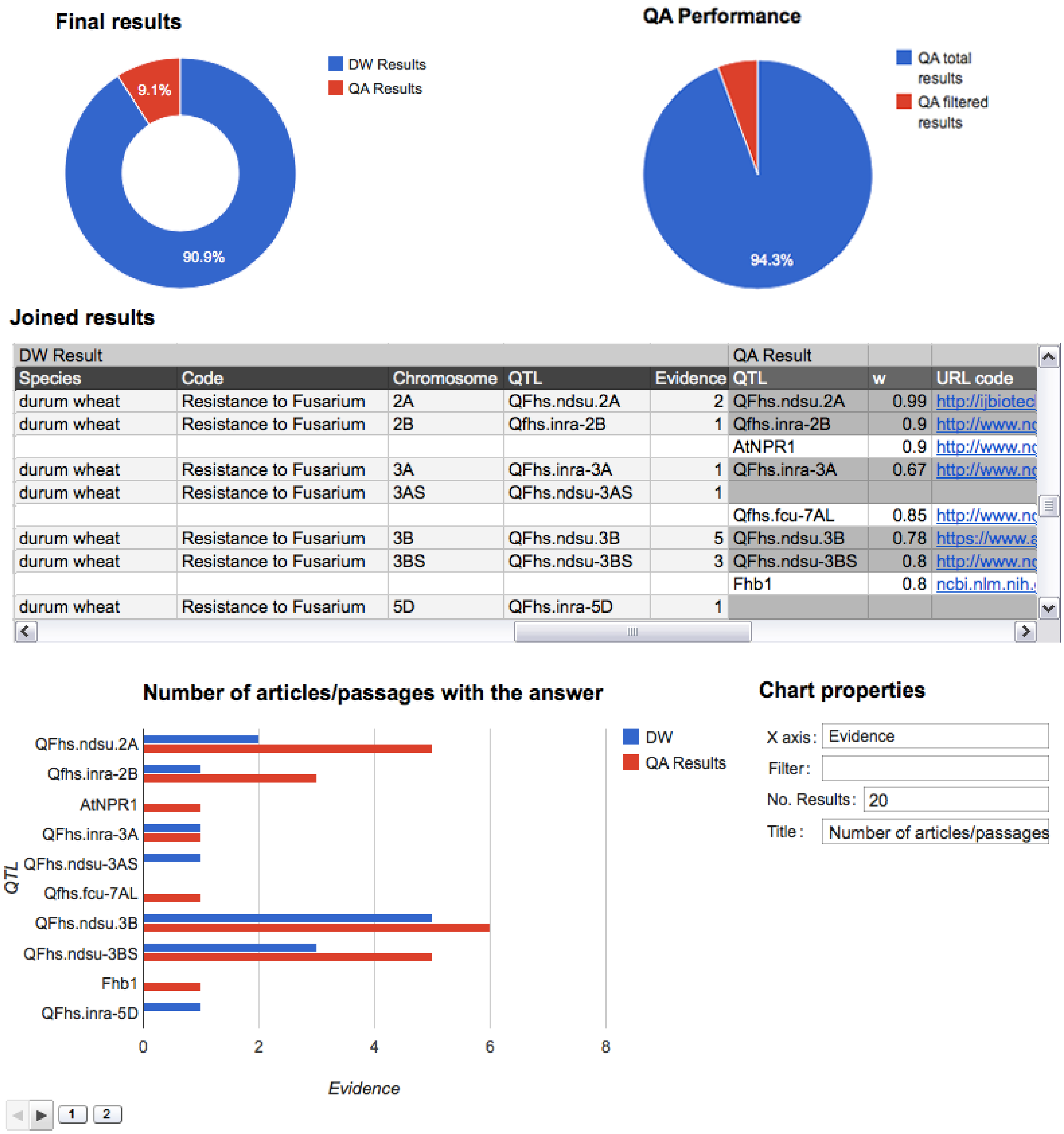
	String Answer			Context of the solution: passage of 3 sentences			Question Entities	
w	QTL	URL code	Noun Phrase Answer	Sentence 1	Sentence 2	Sentence 3	Phenotipic Charasteristic	Plant
0.9	AtNPR1	http://www.ncbi. /pubmed /16529374	the Arabidopsis thaliana NPR1 gene (AtNPR1),	resistance to FHB is a complex, quantitative trait derived from the wheat cv.	we show that the Arabidopsis thaliana NPR1 gene (AtNPR1),	which regulates the activation of systemic acquired resistance, when expressed in the FHB-susceptible wheat cv	Resistance to Fusarium	Triticum Durum
0.85	Qfhs.fcu-7AL	http://www.ncbi. /pubmed /18943578	Qfhs.fcu-7AL	The population was evaluated for type II FHB resistance in three greenhouse environments.	Interval regression analysis indicated that a single QTL designated Qfhs.fcu-7AL explained 19% of the phenotypic	physical map of chromosome 7A indicated that Qfhs.fcu-7AL is located in the proximal region of the long arm.	Fusarium Head Blight Resistance	Tetraploid Wheat
0.8	Fhb1	ncbi.nlm.nih.gov /23514540	candidate genes for Fhb1	the up-regulation of eight of them was confirmed by qRT-PCR	revealing they may be candidate genes for Fhb1	Need further functional analysiss to confirm their roles in FHB resistance	FHB resistance	Wheat
0.7	NahG	http://www.ncbi. /pubmed /22112217	The FHB-promoting effect of NahG	FHB, disease severity was higher in wheat expressing the NahG-encoded salicylate hydroxylase, which metabolizes SA	The FHB-promoting effect of NahG was overcome by application of benzo	thiadiazole-7 carbothioic acid S-methyl ester, a synthetic functional analog of SA,	Resistance against Fusarium	Wheat

Figure 9. QA database for the question "What QTLs are related to resistance to *Fusarium* in durum wheat?"



DW Result					QA Result				
Species	Code	Chromosome	QTL	Evidence	Phenotypic Characteristic	Plant	QTL	w	URL code
durum wheat	Resistance to Fusarium	2A	QFhs.ndsu.2A	2	Resistance to Fusarium	Triticum durum	QFhs.ndsu.2A	0.99	http://ijbiotech.
durum wheat	Resistance to Fusarium	2B	Qfhs.inra-2B	1	Resistance to Fusarium	Triticum durum	Qfhs.inra-2B	0.9	http://www.ncb
					Resistance to Fusarium	Triticum Durum	AtNPR1	0.9	http://www.ncb
durum wheat	Resistance to Fusarium	3A	QFhs.inra-3A	1	Resistance to Fusarium	Triticum durum	QFhs.inra-3A	0.67	http://www.ncb
durum wheat	Resistance to Fusarium	3AS	QFhs.ndsu-3AS	1					
					Fusarium Head Blight Resistance	Tetraploid Wheat	Qfhs.fcu-7AL	0.85	http://www.ncb
durum wheat	Resistance to Fusarium	3B	QFhs.ndsu.3B	5	Resistance to Fusarium	Triticum durum	QFhs.ndsu.3B	0.78	https://www.ag
durum wheat	Resistance to Fusarium	3BS	QFhs.ndsu-3BS	3	Resistance to Fusarium	Triticum durum	QFhs.ndsu-3BS	0.8	http://www.ncb
					FHB resistance	Wheat	Fhb1	0.8	ncbi.nlm.nih.gc
durum wheat	Resistance to Fusarium	5D	QFhs.inra-5D	1					

Figure 10. Result of the join operation between the DW and the QA results



Joined results

DW Result					QA Result		
Species	Code	Chromosome	QTL	Evidence	QTL	w	URL code
durum wheat	Resistance to Fusarium	2A	QFhs.ndsu.2A	2	QFhs.ndsu.2A	0.99	http://ijbiotec
durum wheat	Resistance to Fusarium	2B	Qfhs.inra-2B	1	Qfhs.inra-2B	0.9	http://www.nc
					AtNPR1	0.9	http://www.nc
durum wheat	Resistance to Fusarium	3A	QFhs.inra-3A	1	QFhs.inra-3A	0.67	http://www.nc
durum wheat	Resistance to Fusarium	3AS	QFhs.ndsu-3AS	1			
					Qfhs.fcu-7AL	0.85	http://www.nc
durum wheat	Resistance to Fusarium	3B	QFhs.ndsu.3B	5	QFhs.ndsu.3B	0.78	https://www.g
durum wheat	Resistance to Fusarium	3BS	QFhs.ndsu-3BS	3	QFhs.ndsu-3BS	0.8	http://www.nc
					Fhb1	0.8	ncbi.nlm.nih.
durum wheat	Resistance to Fusarium	5D	QFhs.inra-5D	1			

Chart properties

X axis: Evidence

Filter:

No. Results: 20

Title: Number of articles/passages

Figure 11. Dashboard presented to the user

5. EVALUATION

5.1. Description of the QA system

The QA system used for this experiment is called AliQAn, with which we have participated in several CLEF[2] competitions in both monolingual (Roger et al., 2009) and cross-lingual tasks (Ferrández et al., 2009). AliQAn consists of two phases: the indexation and the search phase. The first one is carried out in an off-line mode previous to the search phase, where its main aim is to prepare all the information required for the subsequent phase, in order to speed up as much as possible the searching process. There are two independent indexations, one for the QA process, and another for the IR process. The first indexation involves Natural Language Processing tools in order to reach a better understanding of the documents (e.g. a morphological analyzer such as Maco+[3] or TreeTagger[4], a shallow parser such as SUPAR (Ferrández, Palomar, & Moreno, 1999) and a Word Sense Disambiguation, WSD, algorithm (Ferrández et al., 2006) that is applied on WordNet/EuroWordNet[5], EWN). The second indexation is used for the IR tool that filters the quantity of text on which the QA process is applied (AliQAn uses the IR-n system (Llopis, Vicedo, & Ferrández, 2003)).

With regard to the search phase, it is accomplished in three sequential modules: (1) Question Analysis (2) Selection of relevant passages (3) Extraction of the answer. Module 1 uses the same NLP tools as in the indexation phase (Maco+, SUPAR, WSD and EWN) with the aim of reaching a syntactic analysis of the question, and eliciting its Syntactic Blocks (SBs). These SBs are matched with a set of syntactic-semantic question patterns designed for the detection of the expected answer type and the identification of the main SBs of the question. The answer type is classified into a taxonomy based on WordNet Based-Types and EuroWordNet Top-Concepts. AliQAn's taxonomy consists of the following categories: person, profession, group, object, place city, place country, place capital, place, abbreviation, event, numerical economic, numerical age, numerical measure, numerical period, numerical percentage, numerical quantity, temporal year, temporal month, temporal date and definition. Each taxonomy class stands for the type of information that the answer needs to contain in order to become a candidate answer (e.g. for the "person" type, a proper noun will be required, or for the "temporal" type, a date will be required). The main SBs of the question are used in Module 2 in order to extract the passages[6] of text on which Module 3 will search for the answer. For example, the CLEF 2006 question "Which country did Iraq invade in 1990?" is matched by the pattern "[WHICH] [synonym of COUNTRY] [...]", where the "place" answer-type is assigned, so a proper noun is required in the answer, with a semantic preference to the hyponyms of "country" in WordNet. Finally, the following SBs are used in Module 2: "[Iraq] [to invade] [in 1990]", in order to select the most relevant passages between all the documents. You can notice that the SB "country" is not used in Module 2 because it is not usual to find a country description in the form of "the country of Kuwait". Module 3 also uses a set of syntactic-semantic answer patterns to search for the correct answer. For example, for the question "What is the brightest star visible in the universe?", AliQAn extracts "Sirius" from the following sentence: "All stars shine but none do it like Sirius, the brightest star in the night sky", although a complete matching is not reached between the SBs of the question and those of the sentence.

5.2.Experiment Results on the Case Scenario

This experiment is run on the case scenario previously detailed. The DW server in our experiment is configured to use the open-source BI platform called Pentaho. Pentaho provides the necessary OLAP capabilities by means of the Mondrian OLAP server. The OLAP server is connected to a MySQL Server 5.6 DBMS that stores the data for the analysis. Since our approach transforms the input into a MDX query, it can be sent directly to the OLAP server, without performing modifications in the platform.

In respect of the ontologies, they have been formalized using the Web Ontology Language (OWL) following W3C Recommendations (Dean & Schreiber, 2004; Patel-Schneider, Hayes, & Horrocks, 2004). We have used Protégé 4 (ontology editing environment) to create the ontologies (http://protege.stanford.edu/).

With regard to the information extracted from the Web, the following URLs corpus is crawled:

PubMed (www.ncbi.nlm.nih.gov/pubmed)

PLoS ONE (www.plosone.org)

The Cuban Journal of Agricultural Science or RCCA (http://www.ciencia-animal.org/cuban-journal-of-agricultural-science/)

The initial NL request of data is "What QTLs are related to resistance to *Fusarium* in durum wheat?", which is classified by AliQAn as "QTL" type.

With regard to the results obtained on the previously mentioned corpus, our framework obtained a Mean Reciprocal Rank (MRR[7]) of 0.23. In the previous participations of AliQAn in CLEF between 2003 and 2008, there were 76 questions of group type (the hyperonym of QTL), where AliQAn obtained a MRR of 0.32. This lower MRR obtained on this corpus is due to a number of reasons. Firstly, the conversion of the Web pages into text should be improved, mainly in the process of tables in order to link each dimension of the table. Secondly, the AliQAn system has been designed for the CLEF competitions, but it requires a deeper adaptation to the case scenario, through the inclusion of new domain resources (e.g. an ontology of QTLs/genes/alleles), and the adaptation of the patterns to extract an answer in this domain.

An excerpt of the results extracted is shown in Figure 9, in which it is observed a high confidence in each answer (see column 1).

In respect of time and space performances for all the phases of our approach, the system setup phase is run off-line so the time efficiency is not so critical. The QA integration model and the QA ontology construction does not involve a great computational cost (both in time and space) because the range of QA systems and question types are not so broad. Moreover, most QA systems already use ontologies, which facilitate the construction of the QA ontology. Regarding the construction of the DW ontology, it is run by analysing the DW catalog and schema in order to build the ontology that captures the domain entities, properties, relationships and constraints. In order to build the DW ontology, and keep the system within a manageable range of data volume, only the minimal information needed from the DW is stored into the ontology. Concretely, entity names, properties and value types are mapped from the DW into the ontology, while the actual data is not. Therefore, the DW ontology mapping is not computationally costly, for example as the one performed by the OWLminer's approach (Santoso, Haw, & Abdul-Mehdi, 2010), which consists on implementing the algorithm known as Feature and Relation Selection, FARS (Hu et al., 2008).

Finally, in order to reduce the computational cost of this phase, a repository of these ontologies is constructed in order to perform this phase just the first time the corresponding node is connected to our framework.

Regarding the running phase, the computational cost is well known through the costs of standard DW and QA systems. With reference to the integration of the results, the relations returned by each of node are sorted by the union points selected before performing the join operation in order to optimize its performance.

In the future, we wish to provide an in-depth analysis adequately comparing the results of integrating an increasing number of nodes, tuples per node, and number of QA answers among other factors, although due to its size and focus it is out of the scope of this paper.

6. CONCLUSIONS AND FUTURE RESEARCH

Nowadays, DWs play a decisive role in BI applications due to the fact that they can provide many years of historical information in an accurate way for the decision making process. It is widely accepted that current BI solutions should incorporate both structured and unstructured data for better decisions. Unfortunately, research in this direction has two main weak points: (i) the use of IR and IE techniques instead of QA; (ii) the lack of full integration between systems that access the unstructured and structured data. Our proposal overcomes these two points (see section 2.1.) by using QA techniques, which allows a seamlessly integration with structured information, and a high flexibility to afford any kind of question, and not only a set of predefined templates; and by using ontologies to achieve the full integration between DW and QA. The results are presented to the user by a dashboard, which allows the decision maker to: (i) compare immediately internal data of a company against competitors; (ii) select the set of QA tuples without exploring the whole document; (iii) store the results of each question as QA DW; (iv) automatically generate new questions from the instances stored in the DW according to the ontology integration and the detected question entities.

Regarding to the full integration between unstructured and structured data, just enumerate the main contributions of our proposal to previous work: (i) the use of ontologies for data integration; (ii) the presentation of results by means of dashboards, which allows a more integrated view of data; (iii) the authoring services for the NL interface in order to improve the system usability; (iv) the scalability of the proposal since it is independent of the number or types of QA/DW systems to integrate.

Our framework is based on well-checked steps that are accomplished in a semi-automatic way, whose application is illustrated through the case scenario of a plant breeder enterprise. This is integrated and evaluated by using the QA system called AliQAn, with which we have participated in several CLEF competitions both in monolingual and cross-lingual tasks. AliQAn has successfully generated a structured database with the information that can be automatically processed by a BI system.

As future work, we will study how the different steps of our framework can be better automated, for example, the mapping process between QA and DW ontologies. Another issue to improve in the future is the question analysis in the Distributor/Integrator element, in order to (i) automatically detect the sources to be searched for the required information; and (ii) automatically split the question to be passed to each specific node (e.g. when a more complex query is posed such as “What QTLs and alleles are related to frost tolerance in barley?”, it must be split into two QA questions such as “What QTLs are related to frost tolerance in barley?” and “What alleles are related to frost tolerance in barley?”). A medium-term future work is to adapt this framework to a NOSQL server (e.g. Hadoop) and take advantage from the MapReduce algorithm to process more complex data sources.

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9. FOOTNOTES

[1] http://www.e-journals.org/botany/ (visited on 24th of March, 2013).

[2] (http://www.clef-initiative.eu// (visited on 24th of March, 2013).

[3] http://nlp.lsi.upc.edu/freeling/ (visited on 24th of March, 2013).

[4] http://www.ims.uni-stuttgart.de/projekte/corplex/TreeTagger/ (visited on 24th of March, 2013).

[5] We have used the WordNet-Online version of WordNet. http://www.wordnet-online.com (visited on 24th of March, 2013).

[6] Each passage is formed by a number of consecutive sentences in the document. In this case, the IR-n system (our passage retrieval tool) returns the most relevant passage formed by eight consecutive sentences.

[7] MRR means the inverse of the rank of the first correct answer. For example, MRR = 1 if the first returned document contains the answer for the query, MRR=1/2 if the first returned document that contains a correct answer is in the second position, and so on.

“Enrichment of the Phenotypic and Genotypic Data Warehouse analysis using Question Answering systems to facilitate the decision making process in cereal breeding programs.” (Submission ECOINF-D-13-00131)

Bullet points

- Enterprise information is integrated with external data from the web using Question Answering.

- Unstructured and structured data is combined through Data Warehouse and Question Answering.

- Ontologies have been used to achieve the full integration.

- The case scenario: a plant breeder enterprise develops new programs with the advances in Genetics.

- A dashboard is shown to the user: it integrates both external and internal data.