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Integrating Data and Knowledge to Support the Selection of Service Plant Species in Agroecology

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Abstract

There is a crucial need for tools to help designing sustainable agroecosystems based on agroecology. Indeed, such agroecosystems are inherently complex and their design requires to integrate various data and unstabilized scientific knowledge. In this paper, we consider the issue of selecting service plant species according to their potential to provide ecosystem services. The architecture of our system is inspired by the ontology-based data access paradigm, which allows to combine data and knowledge in a principled way. We provide a methodology to acquire scientific knowledge in the form of diagrams linked to data sources, as well as a formalization in a logical rule-based language. Importantly, our rules are independent from specific diagrams and data, to ensure genericity and facilitate the evolution of the system. We detail the construction of a knowledge base devoted to vine grassing, i.e., installing herbaceous service plants in vineyards, and present an evaluation of the system's results on this use case. We finally discuss the lessons learned and further challenges to be met.

Keywords:
Functional trait, Ecosystem service, Service crop, Ontology-based data access, Rules, Reasoning

Contents

1 Introduction

During the second half of the 20th century, the increased use of chemical inputs (e.g. pesticides, fertilizers) in agriculture allowed a rapid increase in the productivity of land and labour. However, this caused serious threats for the environment and human health such as soil, water and air pollution, loss of biodiversity, contribution to climate change, etc. It is now established that the restoration of sustainable farming systems requires the adoption of agroecological practices supporting the reintroduction of biodiversity in agroecosystems [Duru et al., 2015]. These practices lead to more complex agroecosystems including a higher number of plant species, whether cash crops (providing food, energy, fiber, or raw materials) and service crops (providing various ecosystem services) [Garcia et al., 2018b].

There is a crucial need for tools that would assist users in the design of such complex agroecosystems, from researchers in agronomy to agricultural advisors and farmers. A major difficulty to develop such tools is that agroecological engineering requires to integrate knowledge from various domains : agronomy, which provides knowledge on functions, design and management of agroecosystems, and ecology, which studies the relationships between living organisms and their natural environment, as well as other expertise domains like management sciences, and agricultural know-how [Lescourret et al., 2015]; moreover, such knowledge is heterogeneous, scattered and not stabilised.

In this paper, we more specifically consider the issue of selecting service plant species according to targeted ecosystem services. To tackle that issue, we adopt an approach based both on a formalized representation of domain knowledge, which enables reasoning, and on the exploitation of data, which has been collected independently of the targeted application.

On the one hand, recent scholarly work identified relationships between plants *functional traits* and the ecosystem *functions* they provide, which support ecosystem *services* [Garcia et al., 2019, 2020, Damour et al., 2015]. Functional traits are measurable characteristics of individual organisms (namely, morphological, physiological, or phenological) that are relevant to study the response of these organisms to environmental disturbances and/or their effects on ecosystem properties [Violle et al., 2007]. Ecosystem functions are often rendered by combinations of traits, which can each contribute positively or negatively to the function. For example, several functional traits of the root system of a plant can be positively associated with the function of soil structural stability, which supports the service of maintenance of soil quality [Garcia et al., 2019].

On the other hand, the ecology community has compiled functional trait values collected from a large number of plants under a wide range of environmental conditions into the TRY database[1] [Kattge et al., 2011, 2020]. TRY currently integrates experimental observations coming from more than 400 datasets, and concerning 4 millions individual plants, 2100 traits and about 280k plant taxa (mostly species). This constitutes a very rich source of information that has not yet been exploited to select service species in agriculture. Hence, we made the hypothesis that, as soon as we were able to associate the expected services and functions with functional trait values, this database, and possibly others, would make it possible to identify species that are favourable to these functions and services.

More generally, our leading question was the following: can we exploit currently available data on plant functional traits and combine it with a suitable representation of scientific knowledge on the trait-function-service relationships, to assess the potential contribution of any plant species to targeted ecosystem services?

While there are numerous decision support tools in agriculture, still few of them integrate the notion of ecosystem service, and to the best of our knowledge, none of them exploits preexisting data sources on functional traits, like TRY in ecology. In particular, available tools for selecting service species rely on local field experiments, farmers' know-how and workshops between experts in agronomy. As collecting the relevant information is time and budget demanding, these tools are typically restricted to a small set of service species. To illustrate, let us cite a tool in agroforestry to select shade tree species in coffee and cocoa agrosystems [Van der Wolf et al., 2019], based on an inventory of local practices; a tool devoted to banana and yam crops with a list of a hundred service plant species and five targeted services [Ozier-Lafontaine et al., 2010]; and a tool devoted to rapeseed crops with eleven service plant species and three targeted services[2]. Interestingly, the two latter tools consider functional traits among other criteria, however they do not do it in a principled manner nor exploit preexisting datasets. Moreover, most existing tools are designed for farmers (or agricultural consultants) and give a recommendation adapted to a particular cultivation context, which has to be precisely known. Their objective is to deliver an accurate recommendation, whose computation remains a black-box. In contrast, our objective is to support the design activity of researchers and technicians in agroecology. We aim at "widening the space of possibilities", by suggesting new associations of species to be tried, while being able to give the reasons behind the suggestions. In other words, innovation and explanability prevail over contextualized accuracy.

To integrate data and knowledge in a principled manner, we built an architecture inspired by the paradigm of *ontology-based data access* (OBDA)[Poggi et al., 2008, Xiao et al., 2018, Lenzerini, 2018], which makes a fundamental distinction between the data and the conceptual levels. An OBDA system is composed of a data layer, made of one or several data sources that may have been built for independent purposes, and a conceptual layer, which describes knowledge (typically under the form of an ontology) using a vocabulary adapted to the intended application and users; declarative mappings between both levels allow to select and aggregate relevant data and to translate it at the conceptual level. The conceptual layer is formalized in a knowledge representation (KR) language provided with reasoning capabilities. Queries to the OBDA system are expressed at the conceptual level and answers to queries take into account inferences made by the system. This paradigm has several advantages. First, it allows a user to formulate queries using a familiar vocabulary,

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[1] `www.try-db.org`.

[2] `https://www6.versailles-grignon.inrae.fr/agronomie/Recherche/Axe-2-Les-biodiversites-et-les-services-ecosystemiques-rendus/Projets-de-recherche/Projet-CASDAR-Alliance/Caps-Colza-associe`.

Figure 1: Different examples of service crops sown in inter-rows in vineyards. From left to right, *Hordeum vulgare*, *Phacelia tanacetifolia*, and *Vicia villosa*. Pictures by Alexis Thoumazeau, Léo Garcia and Yvan Bouisson.

without knowing how the data is actually encoded and stored. Second, it provides richer answers, since not only facts directly coming from the data are considered, but also those that are inferred from both the data and the ontology. Finally, the conceptual vocabulary can act as a mediating layer to integrate several data sources.

The OBDA paradigm has attracted a lot of interest from the 2010s. Several implementations are now available, from mature systems [Calvanese et al., 2011, 2017] to research prototypes [Sequeda et al., 2014, Buron et al., 2020], all based on semantic web languages, namely the lightweight OWL 2 QL profile, or RDF Schema and slight extensions of it. While OBDA has been deployed in various companies and public organizations [Calvanese et al., 2011, Civili et al., 2013, Kharlamov et al., 2017, 2018, Kalayci et al., 2020], it has seemingly not been applied in agriculture / agroecology yet.

Our approach requires first to acquire and formalize knowledge on the relationships between plant traits, functions and services, based on the scientific (and grey) literature. Such knowledge, which we call expert knowledge in the following, is acquired under the form of diagrams built by the agronomists. These diagrams can be easily transcribed in conceptual graphs [Chein and Mugnier, 2009] using the graphical editor Cogui[3]. Conceptual graphs have the advantage of being both close to the expert diagrams and equipped with a translation in logics.

The chosen KR language is based on logical rules, a formalism well suited to the representation of expert knowledge. While being syntactically simple, these rules naturally allow for the representation of complex relationships between entities. They furthermore include computed functions (in the sense of programming), which are in particular used to calculate aggregations of trait values. Since existing OBDA systems do not offer the desired expressivity, we could not use them. Instead, we developed our own prototype based on the software Graal[4] dedicated to query answering with existential rule knowledge bases [Baget et al., 2015].

To study the feasibility of our approach, we focused on the issue of installing service herbaceous species in vineyards (aka *vine grassing*), see Figure 1. We specifically detail in this paper the case of the green manure service, i.e., nitrogen supply to the soil. Note that, beyond this specific case study, our approach is in principle applicable to any use case targeting the selection of plant species based on the relationships between functional traits and ecosystem functions and services.

Next, we present the following contributions:

- a system architecture inspired by the OBDA paradigm, which allows to combine data and knowledge

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[3] `https://www.lirmm.fr/cogui/`.

[4] Last beta version: `https://gitlab.inria.fr/rules/graal-v2/`.

in a principled way;

- a methodology to acquire scientific knowledge following the trait-function-service approach and link it to relevant data sources;
- a formalization in a rule-based language, in which rules are independent from specific diagrams and data sources, in order to ensure genericity and facilitate the evolution of the system;
- the detailed description of the knowledge base built for the vine grassing use case, with a focus on the difficulties encountered to exploit TRY data and choices made;
- an evaluation of the quality of the obtained results, and a discussion on the lessons learned and further challenges to be met.

The next sections are respectively devoted to an overview of our system (Section 2), the acquisition and formalization of expert knowledge (Section 3), the selection and transformation of data (Section 4), reasoning and querying (Section 5), the evaluation of the system's results (Section 6) and a discussion (Section 7).

2 Overview of the System

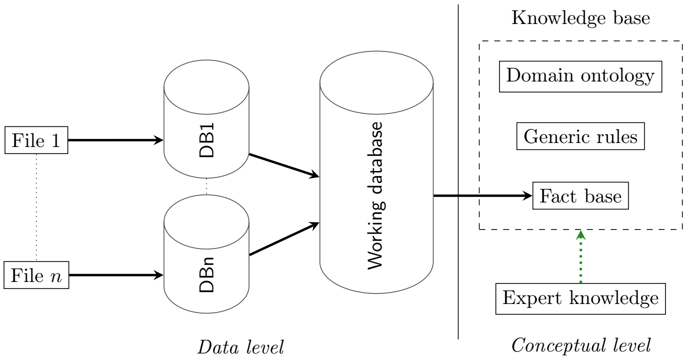

Figure 2: Overview of the global architecture. Cylinders depict databases, black arrows mappings and the green dotted arrow the formalization of expert knowledge.

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Our goal was to provide a tool that fulfills the following requirements:

1. integrating data, which may come from heterogeneous and independent sources,
2. combining data with a formal representation of expert knowledge that enables reasoning,
3. answering user queries while taking into account reasoning,
4. allowing an end-user to formulate queries in a familiar vocabulary,
5. being generic enough to be applicable to other use cases following the trait-function-service approach,
6. allowing for an easy evolution in terms of data sources or expert knowledge,

7. allowing to explain answers to queries.

The architecture of our system, presented next, meets requirements (1) to (4). Requirements (5) to (7) will be discussed in the last section.

Architecture of the system As explained in the introduction, the system's architecture is inspired by *ontology-based data access* (OBDA). Its main components are pictured in Figure 2. A global working database is obtained by integrating several data sources, which may themselves have required some preliminary cleaning steps. The data integration step selects and aggregates relevant data from the data sources, and translates it according to the global database schema, while keeping track of the data source provenance. The conceptual layer is made of a *knowledge base* (KB), expressed in a rule-based knowledge representation and reasoning language. The KB comprises two kinds of knowledge: *facts*, which are assertions about specific entities (together forming the fact base) ; and *rules*, which express general knowledge that can be applied to facts to infer/create new facts. We further distinguish between two kinds of facts: *data facts* obtained from the working database via mappings (e.g., the fact that some functional trait for a given species has some value according to a certain data source) and *expert facts* obtained from expert knowledge (e.g., the fact that a given ecosystem service relies on some ecosystem functions, which themselves are supported by some functional traits).

The *domain ontology* provides a vocabulary in terms of concepts and relations that are meaningful to a user (an expert in agroecology or an end-user). The semantic relationships between the elements of this vocabulary are specified by simple rules expressing concept/relation inclusions as well as signatures of relations. More complex relations and rules are used to process data facts and combine them with expert facts to evaluate the contribution of species to ecosystem functions and services. The latter rules are called *generic* in the figure, to emphasize that they are independent from specific functional traits, nor ecosystem function and services.

Mappings (black arrows in Figure 2) allow to select and aggregate information from a structure (a formatted text file, like a .csv file, or a database) and to translate the resulting information into the vocabulary of another structure (a database or a fact base). Mappings are specified in a declarative way. Different types of mappings are used in the system: *cleaning mappings* from a formatted text file to a database ; *database mappings* from a database DB_i to the working database ; and *data-to-knowledge mappings* from the working database to the fact base.

Queries from an end-user are formulated using the domain ontology vocabulary. This allows queries to be formulated at a high level of abstraction, regardless of how the data is actually stored (e.g., "select the k best species for the improvement of the soil structure, together with their score and the reliability of this score"). The answers to such queries are inferred from the KB, i.e., using facts and rules.

The KR language Most KR languages are based on (first-order) logic, even if they often have a dedicated syntax. This is the case of description logics [Baader et al., 2017], specially designed for the representation of ontologies, W3C semantic web languages like RDFS and OWL 2, and rule-based languages like Datalog [Abiteboul et al., 1994], existential rules (e.g., [Mugnier and Thomazo, 2014]) or Answer Set Programming [Lifschitz, 2019]. We did not make any *a priori* choice of a KR language, but rather started by eliciting expert knowledge to identify an appropriate language. By appropriate language, we mean a language allowing to express domain knowledge in a natural way, while having a minimal expressivity in order to avoid needlessly

```
% 3 data facts
hasTraitValue("specific root length","dactylis glomerata",0.72).
hasTraitValue("root length density","dactylis glomerata", 0.38).
hasTraitValue("relative growth rate","dactylis glomerata", 0.54).
% 2 expert facts
ecoSystemFunction("soil exploration and competition with vines").
isLinkedTo("soil exploration and competition with vines",
"specific root length","root length density","relative growth rate",fct:mean).

% Rule 1:  all traits filled, 100% reliability
isLinkedTo(EcoSystFunction,Trait1,Trait2,Trait3,Aggregation),
hasTraitValue(Trait1,Species,V1), hasTraitValue(Trait2,Species,V2),
hasTraitValue(Trait3,Species,V3)
→ hasFctValue(EcoSystFunction,Species,fct:aggreg3(Aggregation,V1,V2,V3), 100).

% Rule 2:  first trait not filled, 66 % reliability
isLinkedTo(EcoSystFunction,Trait1,Trait2,Trait3,Aggregation),
not hasTraitValue(Trait1,Species,V1), hasTraitValue(Trait2,Species,V2),
hasTraitValue(Trait3,Species,V3)
→ hasFctValue(EcoSystFunction,Species,fct:aggreg2(Aggregation,V2,V3), 66).
```

Figure 3: Five facts and two rules. Lines starting with % are comments.

costly inferences. Rule-based formalisms were found to be well-suited, as expert knowledge is often expressed under the form "if condition then conclusion" and complex relationships between entities can be represented. Another important feature was the ability to incorporate computed functions (in a programming sense, i.e., a function outputs a value given a list of parameters) into the logical formalism.

We do not give a full definition of our KR language in this paper but rather illustrate it on the example of Figure 3, composed of five facts and two rules. In short, we consider plain Datalog rules, extended with computed functions and stratified default negation [Abiteboul et al., 1994], which can also be seen as a specific case of Answer Set Programming.

We recall that an *atom* in first-order logic is of the form *predicate(list of arguments)*, where each argument is either a variable, a constant (a specific object or a value), or a function, i.e., a functional symbol with a list of arguments. A *fact* is an instantiated atom of the form *predicate(list of constants)*. In Figure 3, the first three atoms are data facts, which specify values of the traits "specific root length", "root length density" and "relative growth rate" for the species *dactylis glomerata*. Note that values have been normalized here and range on the interval $[0, 1]$. The next two atoms are expert facts and specify that "soil exploration and competition with vines" is an ecosystem function, which is linked to traits "specific root length", "root length density" and "relative growth rate", with the method of aggregation of these trait values being the mean, denoted here by "fct:mean".

A rule has the form $B \rightarrow H$, where B, the body of the rule, is a conjunction of (possibly negated) atoms and H, the head of the rule, is a single atom, whose variables already occur in the body. In our examples, strings starting with a capital letter denote variables, `not` denotes the negation and commas stand for conjunctions; furthermore lines beginning with % are comments. The rules from Figure 3 both consider an ecosystem function EcoSystFunction linked to traits Trait1, Trait2 and Trait3 with Aggregation as the aggregation method of these trait values. The first rule deals with the case where all traits have a value: if Trait1, Trait2 and Trait3 have values V1, V2 and V3, respectively, for a species Species, then the score of Species for EcoSystFunction is the aggregation of V1, V2 and V3 with method Aggregation, and the reliability of this score is 100%; the second rule deals with the case where Trait1 has no value for a species Species, while Trait2 and Trait3 respectively have values V2 and V3: then the score of Species for EcoSystFunction is the aggregation of V2 and V3 with method Aggregation, and the reliability of this score is 66%. Note that, in the 5th fact, fct:mean is a logical constant, denoting the mean function, while in the rules fct:aggreg3 and fct:aggreg2 are functional symbols whose first parameter is a variable acting as a placeholder for an aggregation method. Note also that this is a simplified example intended to illustrate the KR language; the actual atoms have additional arguments to specify the data source and the plant growing conditions for trait values, as well as weights expressing the strength of the participation of a trait to an ecosystem function.

Given a rule $B \rightarrow H$, its positive body B^+ (respectively, negative body B^-) is the subset of B that occurs positively (respectively, negatively) in B. We recall the classical notion of a homomorphism: a homomorphism h from a set of atoms B to a set of facts F is a substitution of the variables in B to the constants in F such $h(B) \subseteq F$, where $h(B)$ denotes the set of atoms obtained from B by substituting each variable according to h. A rule $B \rightarrow H$ is applicable to a set of facts F if (1) there is a homomorphism h from B^+ to F, and (2) there is no homomorphism extending h that maps an atom $a \in B^-$ to F. The application of the rule according to h yields the fact $h(H)$, obtained by substituting each variable X in H by $h(X)$, then evaluating computed functions. Note that negation is interpreted as default negation, i.e., a fact `not` a is entailed by the KB if a is not entailed by the KB.

In Figure 3, the first rule can be applied on the facts by the following homomorphism:

```
EcoSystemFunction ↦ "soil exploration and competition with vines",
Trait1 ↦ "specific root length",
Trait2 ↦ "root length density",
Trait3 ↦ "relative growth rate",
Aggregation ↦ fct:mean,
Species ↦ "dactylis glomerata",
V1 ↦ 0.72,
V2 ↦ 0.38,
V3 ↦ 0.54.
```

This rule application leads to evaluate the function fct:aggreg3(fct:mean,0.72,0.38,0.54), i.e., to execute the associated program code, and produces the new fact `hasFctValue("soil exploration and competition with vines", "dactylis glomerata", 0.55, 100)`. The second rule cannot be applied on the facts because the only homomorphism from its positive body to the facts can be extended to also map the atom `hasTraitValue(Trait1,Species,V1)` that belongs to its negative body.

The *saturated* fact base is obtained from the initial fact base by applying rules until a fixpoint is reached. A condition on the set of rules (known as stratifiability) ensures that a unique saturated fact base is obtained [Abiteboul et al., 1994].

Query Answering Query answering is performed on the saturated fact base. E.g., on the example from Figure 3, a query asking for all species with a value greater than 0.5 for the ecosystem function "soil exploration and competition with vines" will admit *dactylis glomerata* as an answer.

It should be mentioned that query answering in OBDA usually follows a mediating (aka virtualization) approach, i.e., the fact base remains virtual, and user queries are first reformulated with the ontology, then rewritten with the mappings, to yield queries that are directly evaluated on the data [Poggi et al., 2008, Calvanese et al., 2015, 2011, Buron et al., 2020, Michel et al., 2019]. In contrast, we follow here a materialization approach: the fact base is first materialized (by triggering the mappings to materialize data facts), then saturated by rule applications. Moreover, we finally store the part of the saturated fact base that is relevant to the end-user as a relational database, in order to benefit from the whole expressive power of SQL. There are several reasons for the choice of materialization: first, mediation has been mainly developed for simple queries (essentially unions of conjunctive queries), while our user queries are more complex (e.g., may involve aggregations); second, some features of our KR language (computed functions, default negation) do not allow to use off-the-shelf query reformulation techniques; third, most queries of interest require to rank species (e.g., find the k-best species for some service) and materialization is more appropriate to answer such queries efficiently. Finally, the main advantage of virtualization is the independence with respect to data updates, yet this is not an issue in our use cases, where it is not necessary to take into account data evolution in real time.

3 Acquisition and Formalization of Expert Knowledge

In this section, we present the methodology to get formalized expert knowledge. Briefly, expert knowledge is acquired by means of diagrams, which are linked to data sources, then formalized as conceptual graphs, which are automatically translated into logical facts.

3.1 Expert diagrams

Expert knowledge is acquired through the construction of diagrams structured in 3 levels: *traits*, *functions* and *services*, with links between elements of successive levels, as illustrated by Figure 4, which depicts the diagram for the *green manure* service, i.e. nitrogen supply to the vine [5] A green arrow denotes a positive correlation between the trait value (resp. function value) and the targeted function (resp. service). A red arrow on the contrary indicates a negative correlation between the trait value (resp. function value) and the function (resp. service).

To define services relevant to agroecosystems, the agronomists relied on the reference study EFESE[6]. Then, for each service they defined the underpinning functions and, for each function, relevant functional traits. These elements as well as arrows are based on scientific papers as well as grey literature.

To illustrate, let us comment on the construction of the diagram in Figure 4. One of the main ecosystem services expected by farmers from service plants is the regulation of nutrient availability to crops [Garcia et al., 2018a]. With respect to nitrogen, it can be provided by cover crops through two functions: the mineralization of their biomass when buried in the soil, and the symbiotic fixation of atmospheric nitrogen [Cherr et al., 2006, Thorup-Kristensen et al., 2003]. A third function plays an additional role in nitrogen availability, namely the exploration of soil by the root system of cover crops, which determines the level of competition for soil resources with the grapevine. The level of activation of these functions correlates to the

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[5] Diagrams for two other services (soil structuration, water storage and supply to the vine) can be found in the file "TFS-diagrams.pdf" at `https://drive.google.com/drive/folders/1srgjT6AoH9PktaniqtbwYwCXXNr7_z4q?usp=share_link`.

[6] EFESE is a French national initiative to assess ecosystems and ecosystem services: `https://www.inrae.fr/en/news/assessing-services-provided-agricultural-ecosystems-improve-their-management`.

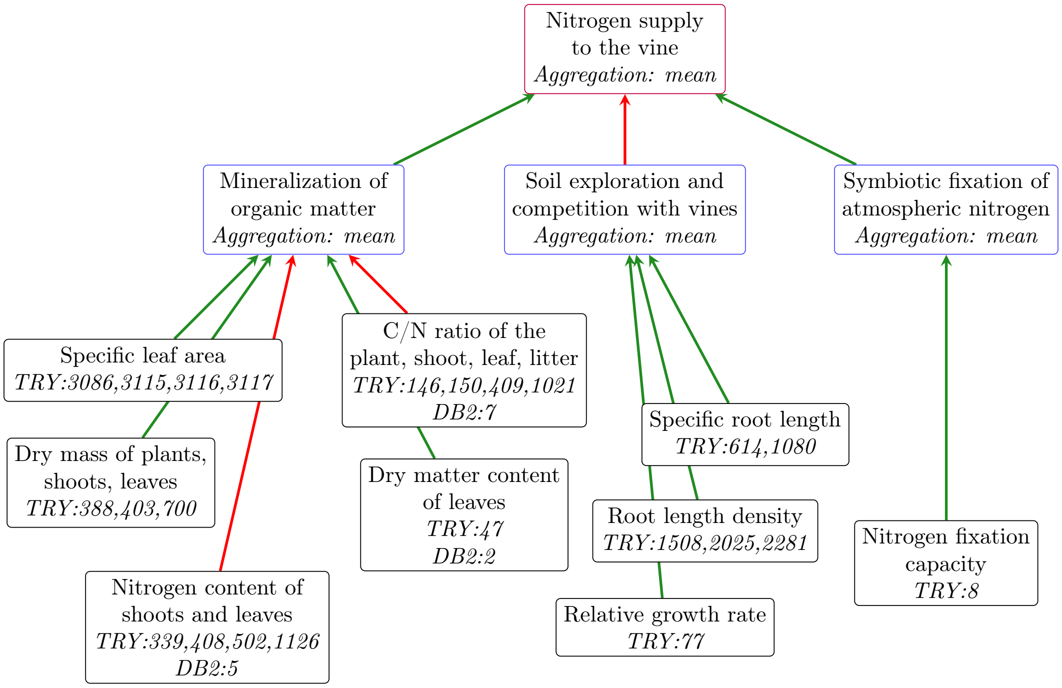

Figure 4: Trait-Function-Service diagram for the service "Nitrogen supply to the vine". Traits, functions and service are surrounded in black, blue and purple, resp. Green and red arrows indicate positive and negative impact, resp. Numbers are identifiers of traits in databases TRY and DB2.

values of some traits of plant species. High nitrogen release by mineralization is associated with high values of specific leaf area, biomass and nitrogen content of plants, and low values of leaf dry matter content and carbon to nitrogen ratio [Abalos et al., 2019], [Damour et al., 2015], [Hanisch et al., 2020]

An efficient exploration of the soil by roots and therefore a high competition with the grapevine is associated with high values of specific root length and root length density [Damour et al., 2015, Funk and Wolf, 2016, Freschet and Roumet, 2017]. At last, the symbiotic fixation of nitrogen is associated with a functional trait that is specific to legumes, the ability to fix atmospheric nitrogen ([Abalos et al., 2019]; [Damour et al., 2015]).

Next, the agronomists were asked to specify *methods of aggregation* to pass from traits to functions (resp. from functions to services). Since no precise criteria could be derived from state-of-the-art domain knowledge, they decided to consider the mean of the normalized trait values (see Section 4.3 about normalization), hence giving the same importance to all traits and functions. Note however that our formalization allows one to weight traits' and functions' contribution and to specify any method of aggregation.

3.2 Matching diagram traits to database trait IDs

In its current state, the prototype is mainly based on the large plant trait database TRY presented in the introduction. It also uses a second database built within a French study on the interests of intermediate crops[7], which provides records for 58 species according to 7 traits. Although it is very small, this database

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[7] `https://methode-merci.fr`

has the advantage of being devoted to herbaceous species grown in agroecosystems (relevant to the use of service crops in vineyards), and most trait values provided for these species are not filled in TRY. Moreover, it allows us to implement the principle of a multi-database setting. Next, this database is called DB2 as it is confidential. Note that both databases use the same standard names for plant species, as defined in *The Plant List*[8] [Kalwij, 2012] and with the help of the *Taxonomic Name Resolution Service*[9] [Boyle et al., 2013].

Hence, each trait in a diagram is associated with one or several trait IDs in the databases TRY and DB2. To illustrate, let us consider again Figure 4. Some traits are associated with a single database trait ID, like "Relative growth rate" associated with ID 77 in TRY, or with a single ID in each database, like "Dry matter content of leaves" associated with ID 47 in TRY and ID 2 in DB2. However, most traits have more than one match in TRY. The reason for this is that traits can be measured according to different techniques, which are reported in TRY. Hence, the same trait for the same observed individual plant may have different values depending on the measurement techniques. For instance, the trait "Specific leaf area" is linked to four traits in TRY, which are all deemed relevant:

- ID 3086: Leaf area per leaf dry mass: petiole, rhachis and midrib excluded,
- ID 3115: Leaf area per leaf dry mass: petiole excluded,
- ID 3116: Leaf area per leaf dry mass: petiole included,
- ID 3117: Leaf area per leaf dry mass: undefined if petiole is included or excluded.

Trait IDs associated with the same expert trait are called *exchangeable*. Since there is no universally preferred measurement technique and since we normalize trait ID values, it is pertinent to aggregate the values of exchangeable trait IDs for a species, regardless of the measurement technique. This aggregation is useful to mitigate the impact of missing values in databases. To perform this aggregation, the agronomists chose to uniformly consider the maximum value among the normalized values of exchangeable IDs in a given database (and for the same growing condition of plants, see Section 4.1).

Finally, our modeling includes *preferences* between databases: there is a global default total order, which can be overwritten for specific traits (here, TRY is globally preferred to DB2). This allows to give a higher priority to a more reliable source. Then, the value of a trait for a species is given by the highest priority data source that provides such value.

To summarize, our methodology for the acquisition of expert knowledge consists of the following main steps:

1. Build trait-function-service diagrams, based on the scientific and the grey literature.
2. Identify relevant databases and associate diagram traits with relevant trait IDs in these databases, with the choice of an aggregation technique if there are exchangeable IDs.
3. Define priority among databases, globally and possibly for specific traits.

Back and forth between the steps (1) and (2) is necessary, as traits in the diagrams have to find counterparts in the databases.

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[8] `http://www.theplantlist.org`.

[9] `https://tnrs.biendata.org/`.

1. **Relations common to expert diagrams and end-user queries**

```
isLinkedToFunction(Trait,Function)
  % specialisations
    % equivalent to isWeightedLinkedToFunction(Trait,Function,1):
    isPositivelyLinkedToFunction(Trait,Function)
    % equivalent to isWeightedLinkedToFunction(Trait,Function,-1):
    isNegativelyLinkedToFunction(Trait,Function)
isWeightedLinkedToFunction(Trait,Function,Weight)
isLinkedToService(Function,Service)
  % specialisations
    % equivalent to isWeightedLinkedToService(Function,Service,1):
    isPositivelyLinkedToService(Function,Service)
    % equivalent to isWeightedLinkedToService(Function,Service,-1):
    isNegativelyLinkedToService(Function,Service)
isWeightedLinkedToService(Function,Service,Weight)
hasAggregationMethod(TFSObject,Aggregation)
```

2. **Relations used solely in expert diagrams**

```
hasMatchingTraitID(Trait,TraitID,DataSource)
hasGlobalPriority(DataSource,DataSource)
hasPriorityForTrait(Trait,DataSource,DataSource)
```

3. **Relations used solely in end-user queries**

```
hasSingleDBTraitValue(Trait,Species,GrowingCondition,Value,Source)
hasTraitValue(Trait,Species,GrowingCondition,Value)
hasFunctionValue(Function,Species,Value,Reliability,GrowingCondition)
hasUserValueOfFunction(Function,Species,Value,Reliability,GrowingCondition)
hasComputedValueOfFunction(Function,Species,Value,Reliability,GrowingCondition)
hasServiceValue(Service,Species,Value,Reliability,GrowingCondition)
```

Figure 5: Relations of the domain ontology. The names given to the relation arguments reflect the relation signatures (i.e., concepts that type the arguments), except for literal values: Weight, Value and Reliability are decimal numbers and TraitID is a string.

3.3 From diagrams to formal conceptual graphs

Conceptual graphs are a KR language in which knowledge is encoded as labeled graphs (in the sense of graph theory) provided with a translation in first-order logic [Sowa, 1984, Chein and Mugnier, 2009]. We used them as an intermediate representation between expert diagrams and logics, which has the advantage of being both easy to understand by domain experts and formal. To draw and manage conceptual graphs, we used the visual tool Cogui[10], which implements the framework developed in [Chein and Mugnier, 2009]. This framework allows to manage knowledge bases composed of an ontological vocabulary, facts and rules built on this vocabulary, and to do logically-founded reasoning based on graph mechanisms. It does however not provide negation nor computed functions, which is required in some of our rules, hence we only used Cogui to build the expert facts, then exported them into the logical framework (using Cogui export functionality).

The ontological vocabulary consists of a few concepts (mainly: `TFS object`—with subconcepts `trait`, `function` and `service`—, `aggregation`, and `source`—with subconcepts `dataSource` and `userSource`) as well as the relations depicted in Figure 5. To describe expert diagrams, only the relations listed in Points 1

---

[10] `https://www.lirmm.fr/cogui/`.

and 2 of the figure are used; relations listed in Point 3 are used in end-user queries (see Section 5.6).

A conceptual graph is made of two kinds of nodes: concept nodes with labels of the form $type : marker$, where *type* is a (list of) concept(s) and *marker* is a constant or the symbol $\star$ denoting an unknown entity (here, we only use constants); and relation nodes labeled by a relation. Each relation node labeled by a relation of arity k is incident to k edges, labeled from 1 to k, that link it to concept nodes.

Figure 6 depicts conceptual graphs that partially translate the diagram from Figure 4: the top graph describes the trait-function-service relationships and the bottom graph the links between the trait "nitrogen content of shoots and leaves" and the associated trait IDs in TRY and BD2. In the case of binary relations (see the top graph), Cogui replaces edges labels 1 and 2 by directed edges. Note that different conceptual graphs are implicitely joined on the nodes that share the same constant. Generally speaking, the ability to split graphs into several components facilitates the design activity and provides better readability.

3.4 From conceptual graphs to logical facts

A conceptual graph has a natural translation into a set of logical facts. Concepts and relations from the vocabulary are seen as predicates: unary predicates for concepts and predicates of the same arity for relations. Then, each concept node with label *type:constant* yields a fact of the form *type(constant)*, and each relation node with label r and arity k yields a fact of the form $r(c_1, ..., c_k)$, where c_i is the constant that labels its i-th neighbor. See Figure 7 for an example.

4 From Data to Facts

In this section we detail how facts are built from data using different kinds of mappings. Generally speaking, a mapping from a structure S_1 to a structure S_2 is a pair of queries: the first query on S_1 returns tuples of values selected from S_1, and the second query on S_2 inserts these tuples into S_2. As outlined in Section 2, we distinguish between three types of mappings: cleaning mappings from a formatted text file to a source database, database mappings from a source database to the working database, and data-to-knowledge mappings from the working database to the fact base.

4.1 From formatted text data to clean structured data

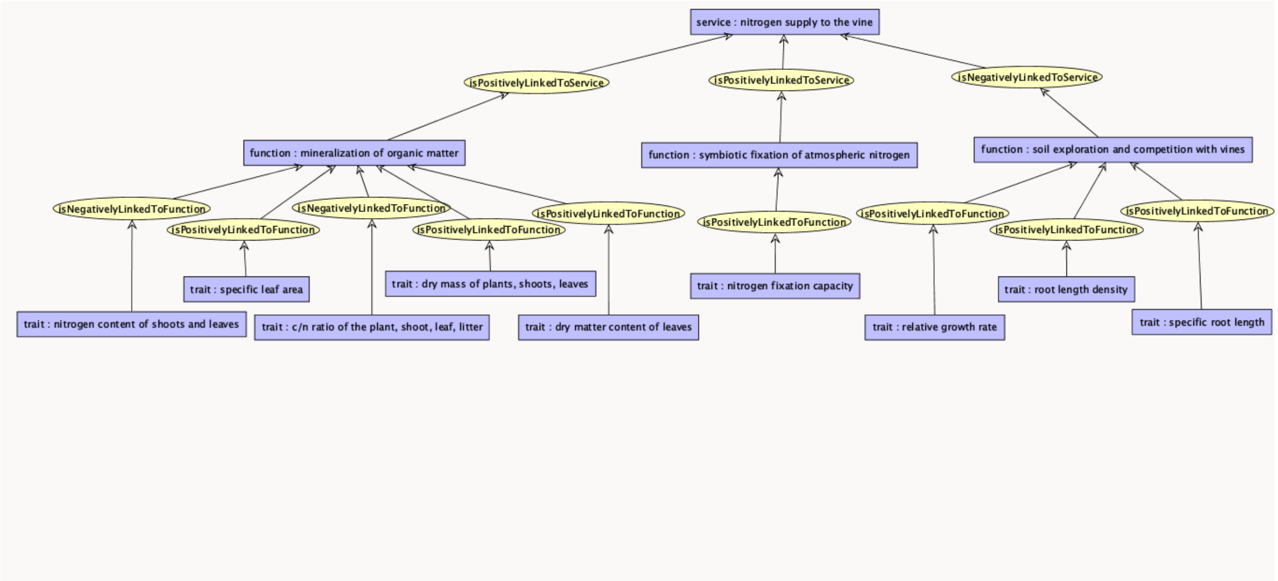
TRY data is available on request for specific traits (we asked for 52 traits, which yielded about 151k species)[11]and comes as a formatted text file (similar to csv). This file contains so-called *observations* (about 1.6M); each observation (identified by an ID) corresponds to measurements of traits (identified by IDs) on an individual plant (associated with a species or genus ID). [12]

An observation is described by several lines, which provide the measurements themselves and their units of measure, as well as contextual information (called covariates) and original dataset provenance. Furthermore, for quantitative traits with at least 1000 occurrences, some data quality checks and standardizations of measure units have been made; in particular an estimation of the (un)reliability of the values (called error risk) is given.

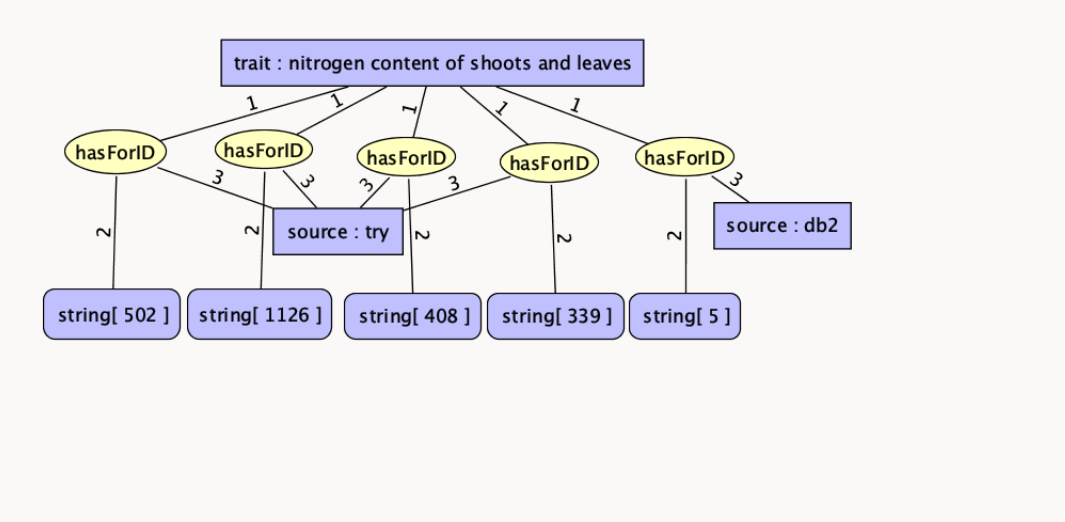
---

[11] The request to TRY was made in July 2021.

[12] Actually, a trait is itself divided into subgroups called "Data Names", identified by "Data ID"s. The measures are given for a subgroup. For the sake of simplicity, we ignore this level in our explanations.



(a) Trait-Function-Service



(b) Nitrogen content of shoots and leaves

Figure 6: Conceptual graphs associated with the expert diagram from Figure 4. Rectangles (in purple) denote concept nodes and oval shapes (in yellow) relation nodes. Numbers on edges specify the order of arguments for non-binary relations.

```
% Top graph (A)
service("nitrogen supply to the vine").
function("mineralization of organic matter").
function("soil exploration and competition with vines").
function("symbiotic fixation of atmospheric nitrogen").
isPositivelyLinkedToService("mineralization of organic matter","nitrogen supply to the
vine").
isNegativelyLinkedToService("soil exploration and competition with vines","nitrogen
supply to the vine").
isPositivelyLinkedToService("symbiotic fixation of atmospheric nitrogen","nitrogen supply
to the vine").
hasAggregationMethod("nitrogen supply to the vine", fct:mean).
...
% Bottom graph (B)
trait("nitrogen content of shoots and leaves").
dataSource(try).
dataSource(db2).
hasMatchingTraitID("nitrogen content of shoots and leaves","339",try).
hasMatchingTraitID("nitrogen content of shoots and leaves","408",try).
hasMatchingTraitID("nitrogen content of shoots and leaves","502",try).
hasMatchingTraitID("nitrogen content of shoots and leaves","1126",try).
hasMatchingTraitID("nitrogen content of shoots and leaves","5",db2).
```

Figure 7: (Partial) logical translation of the conceptual graphs from Figure 6

However, among our 52 traits, only 8 have all their values expressed in a standardized measure unit. In general, cells have heterogeneous contents in terms of measure units, values taken by a non-numerical field, kind of contextual information, etc. To illustrate, the trait Plant Life Span takes string values among ["Bisannual", "Annual", "Biennial", "Perennial"] but one also finds a lot of other values like "perennial < 20 years", "biasannual", "pere", "nope", "from few decades to more than 60 years", "1", "2", "3", "winter annual", "shrub", "woody", etc. Hence, a step of cleaning is mandatory before this rich source of information can be exploited in an automated way. This step, mainly based on string search, discards irrelevant, doubtful (according to the error risk when available) or unusable information, and transforms values for the retained fields.

We also observed that the growing conditions of the observed plants may lead to large variations of trait values, hence, again by string search, we made the distinction between “natural growing conditions” and “experimental growing conditions”.

The abstract form of our cleaning mappings is $q_{\text{csv}} \rightarrow q_{\text{DB}}$, where

$$q_{\text{csv}} = \text{SELECT } \overrightarrow{X} \text{ FROM line}(\overrightarrow{Y}), \text{ valid}_1(\overrightarrow{Y_1}), \ldots, \text{valid}_k(\overrightarrow{Y_k}),$$
$$q_{\text{DB}} = \text{INSERT } (f_1(\overrightarrow{X_1})), \ldots, f_p(\overrightarrow{X_p})),$$
$$\overrightarrow{X}, \overrightarrow{Y_1}, ..., \overrightarrow{Y_k} \text{ are sublists of } \overrightarrow{Y} \text{ and } \overrightarrow{X_1}, ..., \overrightarrow{X_p} \text{ are sublists of } \overrightarrow{X}.$$

The query q_{csv} reads each line of the csv file, where $\overrightarrow{Y}$ is the list of values in this line, then checks if the line satisfies all the validity tests expressed by Boolean functions $valid_1(\overrightarrow{Y_1}), \ldots, valid_k(\overrightarrow{Y_k})$, where each $\overrightarrow{Y_i}$ is a sublist of $\overrightarrow{Y}$. If the validity check succeeds, the sublist of values $\overrightarrow{X}$ is passed to the query q_{DB}, which inserts a list of p values in the database DB, each of these values being built from a sublist $\overrightarrow{X_i}$ of $\overrightarrow{X}$ using a transformation function f_i.

At the end of this step, each tuple (observation ID, species ID, trait ID, growing conditions) occurring in the obtained database is associated with a single trait value expressed in a standardized unit (i.e., we chose a unit of measure for each trait).

Although cleaning could have comprised the whole data received from TRY and be independent of the specific vine grassing use case, we performed some selective cleaning for time reasons. In particular, only herbaceous species are relevant for the use case; we constructed this category (which is not a well-defined category with respect to plant taxonomy) from specific values of trait IDs, in order to distinguish species that are herbaceous from the others. Finer categories could be built for other use cases.

The data source DB2 considers solely herbaceous with natural growing conditions and required no cleaning.

4.2 From databases to the working database

To build the working database, we selected the herbaceous species from our local TRY database (about half of the species) and aggregated all the trait values coming from different observations for a given tuple (species ID, trait ID, growing conditions, source database). Aggregation is performed by taking the mean of the values. DB2 is just imported in the working database. The general form of a database mapping is $q_{\mathrm{DB}_i} \rightarrow q_{wDB}$, where q_{DB_i} is a selection query on database DB_i and q_{wDB} inserts the tuples returned by q_{DB_i} into the working database (wDB).

At the end of this step, the working database contains a single trait value for each tuple (species ID, trait ID, growing condition, source database).

4.3 From the working database to logical facts

The computation of species' score for ecosystem functions and services, which is performed at the conceptual level, requires to aggregate values of different traits. To do so, we turn each value associated with a trait ID into a normalized value ranging over the interval $[0, \ldots, 1]$. This is done by the formula $\frac{v - min}{max - min}$, where v is the value of the trait to be normalized for one species and min (resp. max) is the minimum (resp. maximum) value of the trait for all species in the working database. [13]

A data-to-knowledge mapping is of the general form $q_{wDB} \rightarrow q_{FB}$, where q_{wDB} is a selection query on the working database (wDB) and q_{FB} inserts the facts obtained from the tuples returned by q_{wDB} into the fact base.

Finally, the data-to-knowledge mappings yield facts of the following shape:

```
hasInitialValue(TraitID,SpeciesID,GrowingCondition,NormalizedValue,DB).
hasSpeciesID(Species, SpeciesID, Database).
```

Note that the facts with predicate `hasInitialValue` still consider trait IDs and not the traits defined by the agronomists. It will be the role of rules to associate values to expert traits.

---

[13] With respect to the preceding note: v is actually the value for a Data Name of the trait, and we take for the trait value the mean of the normalized values of its Data Names.

5 Reasoning and Querying

So far, we explained how to build the initial fact base, composed of expert facts and data facts. This section is devoted to reasoning and querying.

The domain ontology (see Figure 5 for its set of relations) provides the vocabulary for expert users (formalization of diagrams) and end-users (formulation of queries). It contains simple rules that express the relationships between its concepts and relations (inclusions, relation signatures). This vocabulary is extended by other predicates used to express data facts as well as the different kinds of rules described in this section. [14]

5.1 Rules to group expert facts

To reason about facts, in particular to compute various aggregations, we need to know the set of traits (resp. functions) linked to a function (resp. service) and its cardinality. The same holds for the set of trait IDs associated with an expert trait. That is why some rules operate on expert facts to produce facts of the following shape:

- `isLinkedTo`k`Traits(Function,Trait1,Weight1,...,Trait`k`,Weight`k`,Aggregation)` to link an ecosystem function (Function) to its k underlying traits (Trait1 ... Trait$k$), with associated weights (Weight1 ... Weight$k$) and the method of aggregation of these trait values (Aggregation). Here, the predicate has arity $2k + 2$.
- `isLinkedTo`k`Functions(Service,Function1,Weight1,...,Function`k`,Weight`k`,Aggregation)`, built similarly to link a service to its k underlying functions.
- `has`k`TraitIDs(Trait, TraitID1, ..., TraitID`k`, DataSource, Aggregation)` to link a trait to its k exchangeable trait IDs in a data source.

Note that these relations of high arity could have been directly encoded in the conceptual graphs associated with expert diagrams, however we preferred to keep conceptual graphs simple and as close as possible to the diagrams.

5.2 The issue of missing values

Before presenting rules that combine expert and data facts, we point out the major issue of missing values, which explains some of the choices made.

Despite TRY is a very large data source, missing values appeared to be a crucial issue. More precisely, the three modeled services involve 52 traits and the associated observations concern $n = 150976$ species, among which $n_h = 70152$ are herbaceous species. One trait, namely “Plant growth form”, has a value for 97% of the n species and almost 100% of the n_h herbaceous species. However, the other traits are only filled for few species: the best case is for the trait “nitrogen fixation capacity”, which takes a Boolean value, and is filled for 8,8% of the n species and 6,4% of the n_h species; the worst case is for a trait filled for a single non-herbaceous species. Note that herbaceous are not a disadvantaged category, as for most traits the proportion of species with a trait value is higher among herbaceous than in the global set.

As will become clear below, we had to make choices to face this issue of missing values.

---

[14] The full list of rules, including the domain ontology, can be found in the folder “Rules” at `https://drive.google.com/drive/folders/1srgjT6AoH9PktaniqtbwYwCXXNr7_z4q?usp=share_link`. (in French).

5.3 Rules to consolidate trait values

As seen in Section 3.2, a trait (from an expert diagram) can be associated with several exchangeable trait IDs in each database. The aggregation of their normalized values for a species S yields the trait value for S according to the considered database.

The interest of this aggregation is that it yields more observations for a species, hence leads to retrieve more species. Consider for instance the service "nitrogen supply to the vine" (Figure 4), which involves nine traits. Among these nine traits, six have several exchangeable trait IDs. Table 1 shows the number of retrieved species for each exchangeable trait ID (third column) and for the set of all trait's exchangeable IDs (last column). Clearly, considering exchangeable traits increases the number of retrieved species. For instance, the trait "specific leaf area" is associated with four IDs in TRY, which are filled in for respectively 403, 7485, 6705 and 12584 species, which at the end yields 16006 species with a value for this trait, that is about 3500 more species than with the most favourable trait ID.

Experts traits	TRY IDs	# species	# species
Specific leaf area	3086	403	16006
	3115	7485	
	3116	6705	
	3117	12584	
Dry mass of plants, shoots, leaves	388	68	883
	403	750	
	700	227	
Nitrogen content of shoots and leaves	339	196	333
	408	126	
	502	2	
	1126	115	
C/N ratio of the plant, shoot, leaf, litter	146	4717	6205
	150	155	
	409	2050	
	1021	16	
Root length density	1508	24	80
	2025	51	
	2281	27	
Specific root length	614	1062	1369
	1080	494	

Table 1: Number of species per trait for each exchangeable ID (3rd column) and for the aggregation of all exchangeable IDs (4th column).

Figure 8 depicts rules dealing with the case where a trait has two matching IDs in a database. For a given trait Trait that matches two IDs (TraitID1 and TraitID2), a species SpeciesID, a growing condition GrowCond, all from the same database DB, two cases are considered: either both database traits have values, and the computed value is the aggregation of these values (Rule R1); or only one of the database traits has a value, which is then retained (Rule R2).

This step produces facts of the following form:

`hasSingleDBTraitValue(Trait,Species,GrowCond,NormalizedValue,DB).`

Finally, another set of rules enables one to exploit the preference order on databases to retain the first available trait value and compute facts of the following form:

```
(R1):  has2TraitIDs(Trait, TraitID1,TraitID2, DB, Aggregation),
hasSpeciesID(Species,SpeciesID,DB),
hasInitialTraitValue(TraitID1,SpeciesID,GrowCond,V1,DB),
hasInitialTraitValue(TraitID2,SpeciesID,GrowCond,V2,DB)
→ hasSingleDBTraitValue(Trait,Species,GrowCond,fct:aggreg2(Aggregation,V1,V2), DB).
```

```
(R2):  has2TraitIDs(Trait, TraitID1,TraitID2, DB, Aggregation),
hasSpeciesID(Species,SpeciesID,DB),
hasInitialTraitValue(TraitID1,SpeciesID,GrowCond,V1,DB),
not hasInitialTraitValue(TraitID2,SpeciesID,GrowCond,V2,DB)
→ hasSingleDBTraitValue(Trait,Species,GrowCond,V1,DB).
```

Figure 8: Rules to aggregate trait values coming from a single database.

`hasTraitValue(Trait,Species,GrowCond,NormalizedValue).`

5.4 Rules to compute ecosystem function and service values

The aim of these rules is to express that the score of a species for an ecosystem function is the aggregation of its values for all traits participating to the function. And similarly to go from ecosystem functions to services. However, we face again here the problem of missing values: it often happens that not all the values of traits participating in a function are filled for some species. The natural way of doing, first recommended by the agronomists, was to discard species for which a required trait value was missing. However, this made almost all the species disappear when coming to ecosystem services.

Therefore, we decided to add a parameter to specify the *reliability* of the computed value of a function (respectively of a service). This allows one to return more species, which is in line with the objective of "widening the space of possibilities". The reliability parameter indicates the proportion of valued traits among all the traits associated with the function (resp. service), i.e., $\frac{n_r}{n_t}$ where n_r is the number of traits with a value and n_t the total number of traits attached to the function (resp. service). To illustrate, Figure 9 depicts the rules allowing to compute the value of an ecosystem function linked to 2 traits: (R1) considers the case where both traits are filled (then the reliability of the result is 100%) and (R2-R3) the case where only one trait is filled (then the reliability is 50%). The produced facts have the shape `hasCalculatedValueOfFunction(Function,Species,Value,Reliability)`.

5.5 Rules to account for user feedback

Finally, feedback from the end-user may palliate missing values for traits or dispute the value assigned to an ecosystem function for a specific species. In the case of traits, the user is simply considered as a data source that has the highest priority, associated with trivial mappings. Facts coming from the user have the following shape: `hasSingleDBTraitValue(Trait,Species,GrowCond,Value,User)`, where the variable `User` denotes the source associated with the user. Then, facts with predicate `hasTraitValue` are produced as previously. In the case of functions, facts coming from the user have the following shape: `hasUserValueOfFunction(Function,Species,Value,Reliability)`. Rules that compute the value of a function give priority to facts with that predicate over those with predicate `hasCalculatedValueOfFunction`, as illustrated by Figure 10.

```
% (R1): both traits filled, 100% reliability
isLinkedTo2Traits(Function,Trait1,Link1,Trait2,Link2,Aggregation),
hasTraitValue(Trait1,Species,V1,GrowCond),
hasTraitValue(Trait2,Species,V2,GrowCond)
→ hasCalculatedValueOfFunction(Function,Species,
      fct:aggreg2Links(Aggregation,V1,Link1,V2,Link2),100,GrowCond).

% (R2): first trait filled, 50% reliability
isLinkedTo2Traits(Function,Trait1,Link1,Trait2,Link2,Aggregation),
hasTraitValue(Trait1,Species,V1,GrowCond),
not hasTraitValue(Trait2,Species,V2,GrowCond)
→ hasCalculatedValueOfFunction(Function,Species,V1,50,GrowCond).

% (R3): second trait filled, 50% reliability
% similar to (R2)
```

Figure 9: Rules to compute the value of an ecosystem function (first step)

```
% if there is a user value for the function
hasUserValueOfFunction(Function,Species,V,Reliability,GrowCond)
→ hasFunctionValue(Function,Species,V,Reliability,GrowCond).
% if there is no user value for the function
hasCalculatedValueOfFunction(Function,Species,V,Reliability, GrowCond),
not hasUserValueOfFunction(Function,Species,V2,Reliability2,GrowCond).
→ hasFunctionValue(Function,Species,V,Reliability,GrowCond).
```

Figure 10: Rules to compute the value of an ecosystem function (second step)

5.6 Querying the system

End-user queries are formulated in a privileged way using the vocabulary of the domain ontology, particularly the relations listed in Points 1 and 3 of Figure 5. This vocabulary allows to query the expert diagrams (e.g., which traits are negatively linked to an ecosystem function that underlies the service "nitrogen supply to the vine"?) as well as the contributions of species to ecosystem functions and services (e.g., which are the 10 best species for the service "nitrogen supply to the vine" with a reliability of the result at least 60%?).

Although we distinguish the vocabulary relevant to an end-user, the whole saturated fact base can be queried. As already mentioned, the saturated fact base is stored in a relational database, which allows to benefit from the whole power of SQL.

6 Evaluation

In order to assess the applicative validity of the approach, we carried out an evaluation on a specific ecosystem service for a selected set of species, and compared the scores provided on the one hand by the tool and on the other hand by the domain literature.

Specifically, we proceeded as follows:

1. *Selection of a service*: we chose the service of "nitrogen supply to the vine" (Figure 4), since it is one of the most documented ecosystem services regarding the use of service crops in viticulture.

2. *Selection of species*: Based on a literature search, we selected a set of 23 herbaceous species commonly used as service crops in agriculture, and considered to be well-documented in the scientific and grey literature (see the list of species in Table 2).

3. *Species ranking from the literature*: we retained 16 papers from the literature, each one providing a comparison between some of the selected species for the selected service. Note that each paper covers only some of the selected species (from 2 to 8 species). From each paper, we extracted an ordering on the species covered by the paper.[15]

Given two species s_i and s_j, let us note $s_i > s_j$ if s_i is deemed (strictly) better than s_j for the service according to at least one document. To obtain a global ranking, we built a directed graph, whose nodes are the species s_i and there is an edge (s_i, s_j) if $s_i > s_j$ holds for at least one document. This graph is depicted in Figure 11, after removal of all redundant edges for the sake of clarity (an edge (s_i, s_j) is redundant if there is already a path from s_i to s_j in the graph). We can see that the results in the literature are remarkably coherent, since the graph is circuit-free. Hence, the graph provides a partial order on the whole set of species. We then considered all the linear extensions of this partial order (i.e., all the total orders compatible with this partial order), and assigned to each species a score equal to the average of its ranks in the extensions.

For instance, if we only consider the subgraph induced by nodes 21, 19 and 23, we have $21 > 23$ and $19 > 23$, hence 2 linear extensions: $21 > 19 > 23$ and $19 > 21 > 23$. The whole graph admits more than 44 millions linear extensions. The obtained scores are shown in Table 2, column "Expert ranking". Note that species 21 and 19 obtain the same score, whereas they are incomparable in the graph. The service value computed by the tool for each species, and the reliability of the computation are shown in columns "Tool's value" and "Tool's reliability", respectively. We recall that the reliability depends on the proportion of traits for which a value could be computed.

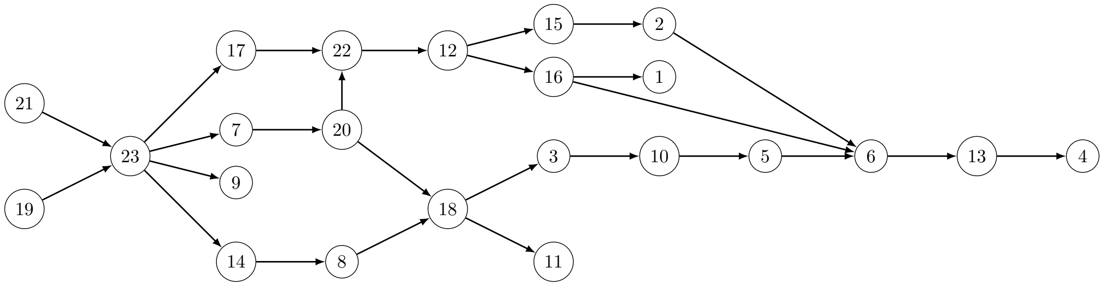


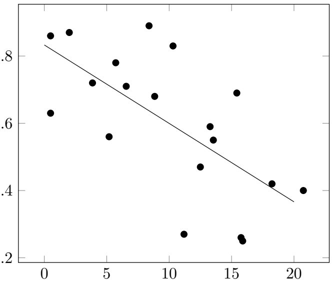
Figure 11: Ranking graph of species for the service of "nitrogen supply to the vine", based on the literature.. Each node represents a species and is labeled by the corresponding species# from Table 2. An edge from s_i to s_j means that $s_i > s_j$.

Finally, we studied the correlation between the expert and tool scores, according to Pearson correlation coefficient r. In our case, a perfect correlation is reflected by $r = -1$ (as the tool and the expert rank species in opposite orders), a perfect inverse correlation by $r = 1$, and an absence of correlation by $r = 0$. The correlation is considered good if $r \leq -0.5$.

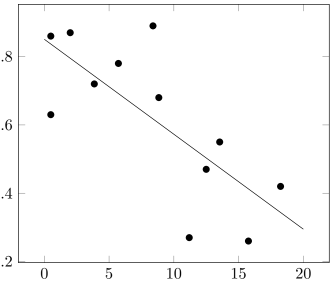
When considering the whole set of species (Graph 12a), the correlation coefficient is already significant ($r = -0.67$). We furthermore observe that the reliability of the tool's score is a crucial parameter. Indeed,

---

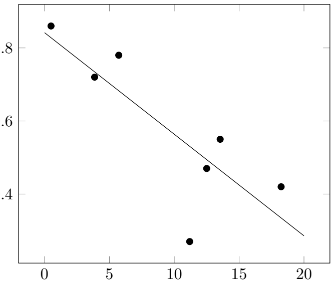
[15] For details, see the file "literature-ranking.pdf" at `https://drive.google.com/drive/folders/1srgjT6AoH9PktaniqtbwYwCXXNr7_z4q?usp=share_link`.



(a) All reliabilities



(b) Reliability ≥ 50



(c) Reliability ≥ 60

Figure 12: Correlation between expert scores (x axis) and tool scores (y axis); each point denotes a species. The line is a linear regression line.

Species#	Species	Experts' ranking	Tools' value of service	Tools' Reliability
1	*Avena sativa*	18.55	—	—
2	*Brassica napus*	16.45	0.26	56
3	*Dactylis glomerata*	11.65	0.27	78
4	*Fagopyrum esculentum*	21.68	0.40	44
5	*Hordeum vulgare*	16.58	0.25	44
6	*Lolium multiflorum*	19.05	0.42	67
7	*Lotus corniculatus*	3.95	0.72	67
8	*Lupinus albus*	6.79	0.71	33
9	*Medicago lupulina*	12.5	0.47	67
10	*Medicago sativa*	14.12	0.55	67
11	*Melilotus officinalis*	16.09	0.69	33
12	*Pisum sativum*	10.73	0.83	44
13	*Raphanus sativus*	20.37	—	—
14	*Rumex acetosa*	4.4	—	—
15	*Secale cereale*	13.84	0.59	44
16	*Sinapsis alba*	14.1	—	—
17	*Trifolium alexandrinum*	5.35	0.56	44
18	*Trifolium incarnatum*	9.19	0.68	55
19	*Trifolium pratense*	0.5	0.86	78
20	*Trifolium repens*	5.9	0.78	78
21	*Trifolium subterraneum*	0.5	0.63	55
22	*Vicia faba*	8.71	0.89	56
23	*Vicia villosa*	2	0.87	55

Table 2: Expert and tool rankings for the service of "nitrogen supply to the vine". The 3rd column gives the expert score. The 4th and 5th columns give the value output by the tool and its reliability, resp. Some species do not occur in the databases, hence the —.

the correlation coefficient drops to -0.74 when the set of species is restricted to those whose computed value has reliability at least 50% (Graph 12b) and to -0.81 for reliability at least 60% (Graph 12c). In the case of this service, a reliability higher or equal to 60% for a species means that at least 6 of the 9 traits actually have a value by the predicate `hasTraitValue` on this species. On the graph associated with reliability at least 60% (Graph 12c), we can see that only one species (*dactylis glomerata*) is quite far from the regression line. If we go back to the TRY data, we notice that for this species several traits have important value variations, which might be explained by variations of the observation contexts (e.g., elevation and phosphorus content of the soil in this case).

7 Discussion and Perspectives

In this paper, we studied the feasibility of an original approach for the selection of service plant species in agroecology. The main idea is to combine a formal representation of scientific knowledge in agronomy on the relationships between functional traits, ecosystem functions and services, with independently-built data sources, in particular the database TRY that integrates the main data sets about functional traits collected by the research community in ecology. To implement this approach in a principled manner, we followed the principles of so-called OBDA paradigm. As argued in the introduction, this is, to the best of our knowledge, a novel approach in agroecological engineering.

OBDA allows one to query data at a conceptual level, while taking reasoning into account. Further requirements were the genericity of the formalization, the evolutivity of the system and the explanability of query answers (i.e., items (5) to (7) listed at the beginning of Section 2). Regarding genericity, expert knowledge about traits, functions and services is formalized as two types of objects:

- *Rules* handling the passage from database values to trait, function and service values. Importantly, these rules are generic in the sense that they do not consider specific traits, functions or services, nor specific aggregation methods, hence they are not tied to specific diagrams, nor to specific data sources.
- *Facts* that describe specific diagrams, including their links to database IDs.

Whereas rule-based expert systems often rely on carefully crafted rules that are tailored for a specific use-case, our rules could in principle be applicable to any use-case that follows the trait-function-service framework [Damour et al., 2018].

This formalization moreover allows for a smooth evolution of expert knowledge encoded in diagrams, without impact on the rules. Indeed, updates in diagrams, including the introduction of new diagrams, only leads to updates in expert facts. Similarly, updates in the content of a source file or a database only leads to trigger again the associated mappings. The introduction of a new data source requires to add adequate mappings, independently from those already associated with the other sources, and to link functional traits in expert diagrams to this new data source by identifying relevant trait IDs and establishing priorities among data sources. Obviously, the saturation of the fact base has to be updated when the fact base is updated.

Explanability of answers to queries directly follows from the chosen KR language. More precisely, the successive rule applications can be recorded, so that the way each derived fact has been obtained can be traced back to initial facts. However, we want explanations that are intelligible to an end-user, which means that they must be structurally simple, short and rely on a vocabulary that is meaningful to her. As we have seen, rules may use predicates that do not belong to the ontological vocabulary. Hence, further work is required to define an adequate way of composing successive rule applications in order to “forget” such intermediate predicates, an issue related to both axiom pinpointing and forgetting in ontologies (see e.g., [Peñaloza, 2020, Eiter and Kern-Isberner, 2019] for surveys). On the other hand, the main queries of interest are about the contributions of species to services: here, expert diagrams (which are formally described using the ontological vocabulary) naturally provide a view of how the values associated with a given species are computed, from its trait values to its service score. Such visualization is synthetic and understandable by an end-user. The development of a graphical query interface dedicated to end-users and provided with explanation facilities is part of our agenda.

To put our approach in practice, we first had to undertake significant efforts to clean the data from TRY. This was a mandatory step before any automated exploitation of the data. We then faced the crucial issue of missing values. This issue, extensively analyzed in [Kattge and al., 2020], is probably exacerbated by the fact that data was collected for research in ecology, which focuses more on natural and spontaneous species than on species bred for agricultural purposes.

To mitigate the impact of missing values, we exploited exchangeable traits IDs and we introduced a reliability parameter, which allows to consider species for which not all relevant traits have values. The evaluation carried out (Section 6) shows that very satisfactory results can be obtained as long as the proportion of missing values is not too high. Since the TRY initiative is developing, in both volume and standardization of the data, and there is a growing effort to produce trait data in agronomy [Blesh, 2018, Garcia et al., 2020, 2019, Wood et al., 2015, Martin and Isaac, 2015, 2018], one can only expect more accurate results in the next years.

Outside missing values, a reason for observed discrepancies between the tool’s results and results from the literature seems to be, for some traits, a high variation of the values measured for individual plants of the same species. Besides potential problems of reliability of some observations, it is likely that such variations are related to differences in the contexts of the observations, be it the cultivation context (like characteristics of the soil, climate and plant management, ...) or the plant growth stage. Apart from the growing conditions of plants, we did not take context into account for two reasons: first, it would have reduced the number of relevant observations, hence worsen the problem of missing values; second, many observations in TRY are not provided with adequate context information (beyond the problem of automatically exploiting such information). Once again, the development of data on traits should allow to leverage contextual information in the near future.

Contextual information could be considered to homogenise the conditions of the measurements themselves, like the plant growth stage. More importantly, it could be considered in relationship with information about the soil properties and climate, and/or cropping practices: if the context of measurement of functional traits in the databases is important to limit the variability of their values, the context of installation of service plants in the field (soil, climate, cropping practices) is also important to ensure that they will actually provide the expected functions and services. As already mentioned, functional traits are relevant to the effects of plants on ecosystem properties (effect traits) and/or the response of plants to the environment (response traits) [Damour et al., 2018]. In other words, traits also give us information about the ability of a species to grow in a specific environment. Our expert diagrams involve effect traits: for these traits, the pedoclimate can be considered in order to restrict relevant data observations. Technically, this requires to specialize mappings so that contextual information of interest is imported into the working database, and to extend the logical vocabulary to represent it (for instance, by increasing the arity of predicates to include new parameters, as we did for the plant growing conditions). Response traits (like resistance to frost or drought, or the ability to grow in a nutrient-poor soil) can be taken into account *a posteriori* to filter species returned as answers. To conclude, our framework allows for such extensions, the limiting factor being the availability of data.

Similarly, our modeling allows to refine expert diagrams, in particular by weighting traits' participations and making aggregation methods more complex, the limiting factor being whether state-of-the-art domain knowledge enables such refinements.

Finally, this work also supports future research about the combination of various plant species to provide the expected functions and services, in comparison to single species [Storkey et al., 2015, Finney et al., 2017].

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