



A Semantic-Based Framework for Rice Plant Disease Management

Identification, Early Warning, and Treatment Recommendation Using Multiple Observations

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Abstract

Rice plant diseases can cause damages and yield losses. To reduce the productivity losses, farmers need to observe and decide suitable treatments for the diseases recognized from the abnormal characteristics appeared in their farms. Traditionally, farmers identify potential diseases from their experiences or by consulting other experts. However, this approach has certain disadvantages due to varying knowledge, and at times unreliable experience and perception of different farmers. Externalization of knowledge from existing reliable sources and utilization of multiple farmer's observations can overcome such problems. Thus, this study presents the design and development of RiceMan, a semantic-based framework in agriculture for rice plant disease management using multiple observations. The framework not only manages observations within a single farm, but also integrates with neighborhood observations to cope with spreadable rice diseases. In addition, with proper design of Rice Diseases Ontology (RiceDO) and Treatment Ontology (TreatO), the framework can identify possible diseases and give early warnings to farmers for their appropriate actions. Based on realistic situations, the paper also illustrates how the proposed framework can help farmers to better: (1) identify rice diseases, (2) prepare for the early warnings, and (3) obtain recommended treatments.

Keywords Knowledge representation · Multiple observations · Ontologies · Semantic-based recommendation

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Introduction

Dealing with rice diseases is one of the important challenges during rice cultivation. Rice plants can be damaged from abiotic and biotic factors. Abiotic factors can be drought, cold, heat, phosphorus deficiency, and others. On the other hand, biotic factors can be classified into animals, bacterial, fungal, and viral. Traditionally, farmers observe abnormalities that appear on rice plants and manage the damaged rice plants based on their personal knowledge and experience. Some farmers may consult experts such as experienced farmers and agronomists for advices.

Fortunately, numerous knowledge related to rice cultivation have been written and published widely especially in the online platform. This can help farmers to seek for desirable knowledge by searching through websites including how to identify a disease, why does it occurs, and how to manage it. However, farmers need to read a lot of contents to find out the desired information. This problem is a motivation of this research, which aims at developing an expert system for farmers to deal with observations in agriculture. Based on [12, 16, 20], modeling knowledge base related to rice plants has gained attention these days. Such works have attempted to capture the knowledge from different sources and formats into a knowledge base. A number of rice plant knowledge base have been modeled as an ontology in the Web Ontology Language (OWL) [11, 18]. Modeling a knowledge base as an ontology can enable several reasoning tasks. Thus, it provides benefits to an expert system in terms of exposing the implicit knowledge.

This work not only focuses on modeling an ontology related to rice plant knowledge, but also focuses on applying the ontology to help farmers examining rice plant by themselves. In fact, most rice diseases can spread from farms to farms. Hence, knowing that the neighborhood surrounding our farm has been infected with any disease is beneficial. This points out a crucial issue of considering neighborhood's situation through their observation data. Thus, this research also considers the nearby observation data and provides warning messages if a spreadable disease is suspected. The warning messages help farmers to detect possible transmission of diseases.

More specifically, this research aims at developing a semantic-based framework, namely RiceMan, to manage observation data collected by farmers. RiceMan is based on the conceptual model and the formalism for managing multiple observations, introduced in [10]. The framework enables farmers to make and share their observations, and hence supports: (1) possible rice diseases and early warning identification based on multiple observation data, and (2) treatment suggestion based on the possible diseases.

The rest of this paper is organized as follows: Sect. "[Preliminary](#)" discusses a background in observation management and related works. Section "[Proposed Framework: RiceMan](#)" introduces the proposed framework and system architecture. Section "[Ontology Model](#)" presents the developed Rice Disease Ontology and Treatment Ontology. Section "[Semantic-Based Recommendation Approach](#)" explains the proposed semantic-based recommendation approach. Section "[Practical](#)

[Use Case and Usages](#)” discusses the practical use case of various situations. Finally, Sect. “[Conclusion](#)” concludes and outlines future research direction.

Preliminary

This section provides background related to the formalism for managing observations from farmers and discusses the related works.

Formal Representation of Observations

In [10], the authors introduced a conceptual model and a formalism to manage observation data in agriculture and to recommend an advice based on corresponding observation data. The formalism described the representation of an observation data, the similarity among different observations, the composition of similar observations, the representation of an advice, and advice retrieving. The following are the important terms and definitions that are reused and modified to develop RiceMan.

1. *Observation* An observation is represented as a vector called *warncons*. A *warncons* is defined as the following formalism.

Definition 1 A *warncons* (denoted by w^m) is defined as an m -dimensional feature vector: $w^m = \langle wf_1, wf_2, \dots, wf_x, c_1, c_2, \dots, c_y \rangle$, where $m = x + y$, wf_i (where $1 \leq i \leq x$) represents a feature characterizing a set of contextual information from the user, and c_j (where $1 \leq j \leq y$) represents a feature characterizing a set of contextual information from the sensors.

Example: Assume that a farmer found “a brown spot on a leaf” and a sensor provided the latitude (e.g., 30) and longitude (e.g., 59) coordinates, and the observation date and time (e.g., Monday, May 26, 2018, 15:30). According to Definition 1, the contextual information from the farmer can be represented as wf_1 where wf_1 characterize a set of abnormal characteristics obtained by a farmer. Note that an *abnormal characteristic* in this work means a visible sign and symptom of a disease appearing on a rice plant. Thus, $wf_1 = \{Spot, Leaf, Brown\}$. The contextual information from the sensor can be represented as $c_1 = \{30, 59\}$ and $c_2 = \{Monday, May 26, 2018, 15:30\}$. Therefore, this *warncons* contains three features and expresses as follows:

$$w^3 = \langle \{Spot, Leaf, Brown\}, \{30, 59\}, \{Monday, May 26, 2018, 15:30\} \rangle.$$

To develop RiceMan, we adopt the idea of *warncons* and call it as ‘observation’ O . Hence, O_1, O_2 , for example, denote the first and second observations, respectively.

2. *Composition* Composition is a method used to combine different observation data. Important concepts related to observation composition are: (1) composable observations, which refer to relevant observations that can be composed with the considering observation, and (2) composed observation, which refers to the results of the composition.
3. *Treatment* This work focuses on treatment retrieval based on the identified diseases from an observation.

Related Works and Existing Ontologies

Various techniques to identify plant diseases were classified into direct methods and indirect methods [21]. The direct methods focused on an experiment (e.g., proteins and enzymes) in a laboratory, and were called traditional molecular methods in [15]. On the other hand, the indirect methods were called innovative detection methods which includes biomarker-based, image-based, and remote-sensing technologies. Recently, the work of [9] introduced an ontology-based approach to detect plant diseases.

Image-based approaches that employed image processing techniques were widely used for detection and classification of plant diseases [4, 14, 22]. In [4], an image processing algorithm was proposed and used for segmentation of leaf rot in a betel vine leaf. In [14], the authors introduced the use of image processing for plant disease detection. In [22], several image segmentation methods for detection of leaf diseases on banana, bean, lemon, and rose were proposed and compared.

A knowledge-based approach, especially an ontology-based, indicated the utilization of knowledge such as sharing, reusing, and inference. Many works presented knowledge-based expert systems for agricultural domain. In [1], the authors developed an ontology related to agricultural data (e.g., crops and products, farm, and agricultural activities), to use in the data integration model. In [3, 12, 16], rule-based expert systems were proposed for detection of rice diseases and coffee diseases. A decision tree was constructed from the facts about coffee diseases and symptoms, which was used to create if-then rules for detecting coffee disease [3]. A similar approach was developed for rice plant diseases [16].

Consider existing ontologies related to rice domain. Various rice ontology developments were proposed for different purposes [2, 11, 13, 20, 24]. A rice ontology-based Q&A system was presented in [13]. The ontology supports querying knowledge related to a disease such as “what it is?”. The returned results were retrieved from various knowledge sites. The Thailand Rice Production Ontology, which provide searching research works w.r.t. rice production knowledge, was modeled in [24]. Another approach to automatically constructing Thai Rice Ontology from data in a web portal was presented in [20]. This ontology was modeled from semi-structured data in Thai rice knowledge web portal published by Rice Department of Thailand. Unfortunately, in this web portal, the data about the characteristics of rice were unstructured-data.

In this work, we focus on modeling an ontology of rice diseases w.r.t. the characteristics and abnormality of rice plants infected with rice diseases. The following

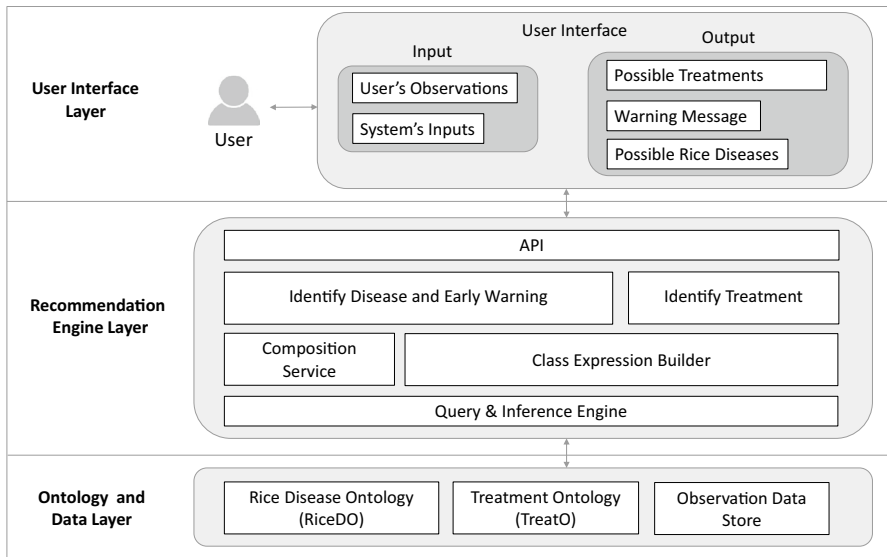


Fig. 1 RiceMan system architecture

four existing ontologies were reused and extended: Rice Ontology [11], Plant Disease Ontology [18], Plant Protection Ontology [17], and Rice Disease Ontology [9]. First, Rice Ontology (RO) consisted of rice trait knowledge in terms of phenotype and genotype. The class hierarchy classified rice diseases into abiotic and biotic stresses. The details of each disease were described in text as an annotation. Second, Plant Disease Ontology (PDO) only focused on biotic stress and classified rice diseases into bacterial, fungal, and viral diseases. Third, Plant Protection Ontology (PPO) classified disorder of plant into abiotic and biotic disorders, which was similar to RO. The authors also classified biotic damage as same as PDO. However, PPO focused on barley disorders. Finally, Rice Disease Ontology (RDO) combined RO, PDO, and PPO under the domain of rice diseases. The proposed class hierarchy described the characteristics of rice diseases in terms of symptom, shape, and color. An object property called 'roleGroup' was proposed to group characteristics of rice diseases that appear together such as "having blight symptom and having yellow color". RDO was used to identify rice diseases based on a class expression of a single observation only.

Proposed Framework: RiceMan

RiceMan is a framework and a mobile web application for managing observation data from farmers. It employs a semantic-based approach for identifying rice diseases, providing warnings, and giving relevant treatments. The developed application is used by farmers to enter abnormal characteristics that they observe. The

application can then identify rice plant diseases, alert a possible spread of diseases, and/or recommend treatments accordingly.

Figure 1 depicts RiceMan's system architecture which is classified into three layers: user interface, recommendation engine, and ontology. Each layer contains necessary components discussed as follows:

1. *User interface layer* In Fig 1, user interface layer handles inputs and outputs of the framework. It is responsible for gathering input from users and displaying output to them. There are two types of inputs: user's input and system's input. Regarding a user's input, user (e.g., farmer) observes a rice plant in the field and enters an observation using the developed mobile web application. The application's user interface enables a farmer to specify observed abnormalities of rice plant in terms of symptom, shape, color, plant part, and growth stage. Practically, multiple symptoms may occur at the same time. Therefore, the designed user interface supports the description of an observation having multiple characteristics and abnormalities. On the other hand, the system's input is automatically recorded by the application when a user performs each observation including the latitude and longitude coordinates, date and time, wind speed and direction, temperature, and humidity. To elaborate our approach here, in the system's input, we exclude the wind speed, temperature, and humidity; and, we only focus on latitude, longitude, date, and time for simplification. Furthermore, a user can also interact with the user interface's output by obtaining the possible rice diseases, warning messages, and possible treatments.
2. *Recommendation engine layer* This layer contains an API to provide the following two services: (1) disease identification and early warning service, and (2) treatment recommendation service.
 - *Disease identification and early warning service* This service provides two types of responses. First, we use OWL API [7] to provide Disease Identification Service. OWL API is a Java API for parsing ontologies to the application and enabling reasoning services on the ontologies. In this part, we use OWL API to connect with our OWL ontology, i.e., RiceDO. The inference engine (reasoner) used in this work is HermiT [5]. We use HermiT reasoner to identify diseases based on subsumption relationships between classes. Second, this service returns helpful messages which may relate to the current observation. These messages are called 'early warning'. A warning message contains warning of possible spreadable diseases and knowledge of possible abnormal characteristics that are related to them. Hence, farmers are notified and then can better prepare to cope with the possible transmission.
 - *Treatment recommendation service* This service provides treatments related to the results returned from the Disease Identification Service. To recommend reasonable treatments, this service also employs the inference engine, i.e., HermiT on our ontology TreatO which is connected with the application via OWL API.
3. *Ontology and data layer* This layer consists of two ontologies: Rice Disease Ontology (RiceDO) and Treatment Ontology (TreatO), and Observation Data

store. RiceDO captures knowledge related to rice diseases, especially the characteristics of rice plant damaged with diseases. On the other hand, TreatO captures knowledge related to biological and chemical treatments to the corresponding rice plant diseases in RiceDO. Each observation is recorded into the Observation Data Store. More details about the design and usage of both ontologies are discussed in the next section.

Ontology Model

Rice Disease Ontology (RiceDO)

RiceDO¹ extends RDO [9] with some necessary classes imported from PDO [18] and PPO [17]. Important classes and object properties are modeled to describe and represent the observable abnormal characteristics of rice plant infected with diseases. In this work, we focus on 23 rice diseases that occur in Thailand, 19 of which are caused by bacterial, fungal, and viral, while the remaining 4 of which are caused by animals. These 4 diseases caused by animals are categorized into 3 insects (which are carriers of rice diseases) and 1 insect (whose damage is similar to rice blast disease and brown planthopper).

Currently, RiceDO is designed to consider the characteristics of a rice plant that is infected with biotic factors, viz., bacterial, fungal, and viral, and is damaged from animals, e.g., brown planthoppers. As for future directions, the scope of diseases can be extended with more factors such as soil nutrients, weeds, and other animals. Three important knowledge sources used to model RiceDO include: (1) Rice Knowledge Bank (Thai-RKB) [19] by the Rice Department of Thailand, (2) fact sheets of Rice Knowledge Bank (RKB) by International Rice Research Institute (IRRI) [8], and (3) Rice Ontology (RO) [11]. RiceDO mainly focuses on rice disease knowledge that is available on Thai-RKB. These knowledge sources provide the validated and reliable knowledge about rice diseases, and explain the abnormalities of each disease in terms of contagion, symptom, shape, color, growth stage, and the position of damaged on a plant.

Figure 2 depicts the design of RiceDO with its class hierarchy consisting of seven top-level classes, and its object property hierarchy consisting of seven object properties. The class **PlantDisease** contains 23 diseases, while other classes, including **Abnormality**, **Distribution**, **GrowthStage**, and **PlantPart**, are used to model the characteristics of a disease. The class **Abnormality** contains necessary subclasses to explain the abnormality of rice plants as follows: **Color**, **Shape**, and **Symptom**. These subclasses can be used together with the object properties **hasColor**, **hasShape**, and **hasSymptom**, respectively. For instance, the abnormal characteristic “curly leaf” can be described using the class **Curl** and **Leaf**, and the object property

¹ The OWL file is available at <https://webprotege.stanford.edu/#projects/56da2650-9804-4e71-9207-514760e92a30/edit/OWL%20Classes> and <https://github.com/RiceManFramework/riceman/blob/master/RiceDO.owl>.

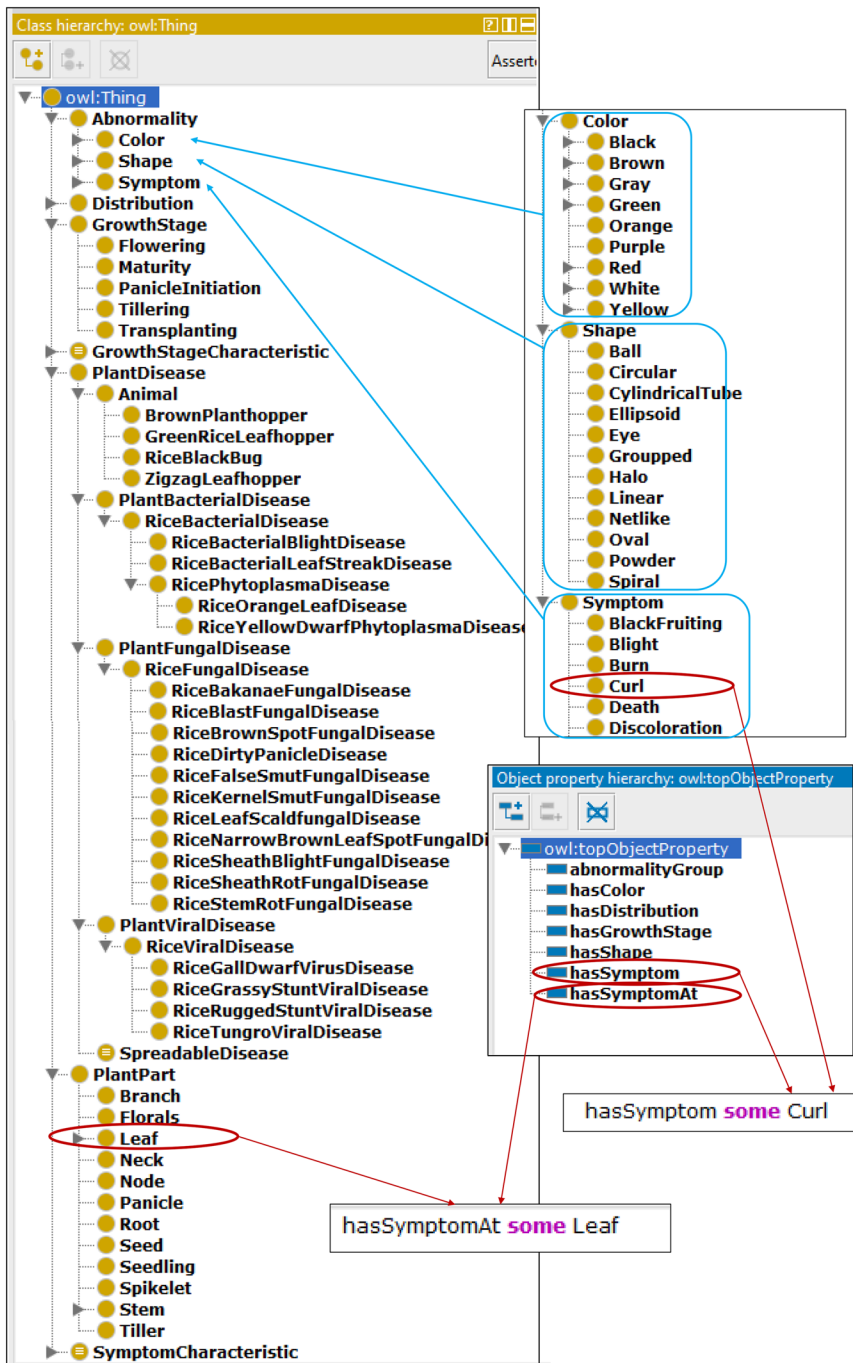


Fig. 2 Class hierarchy and object properties of RiceDO

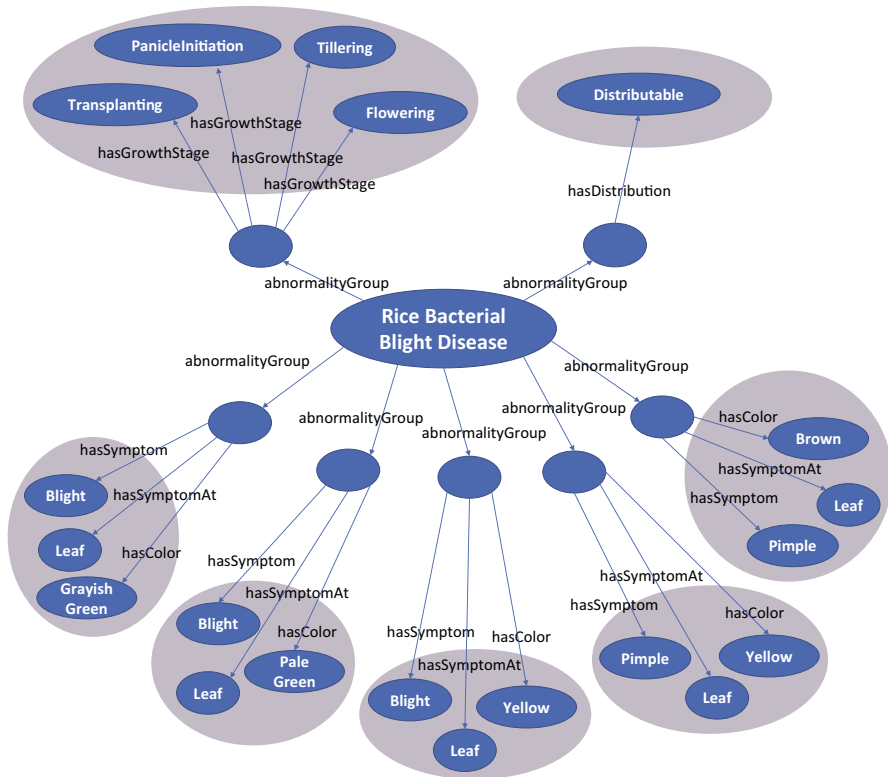


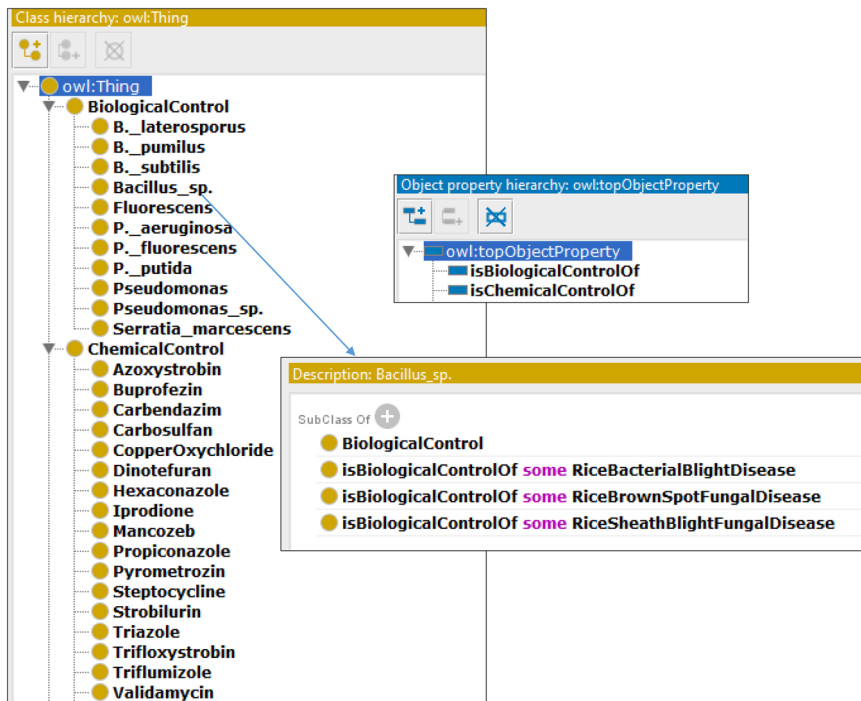
Fig. 3 A knowledge graph represents a rice bacterial blight disease

hasSymptom and hasSymptomAt, i.e., “hasSymptom some Curl” and “hasSymptomAt some Leaf”, as shown in Fig. 2. The class Distribution is used to define the disease that can and cannot propagate. The class GrowthStage is used to describe which growth stage of rice plant that can be infected with each disease. It is able to explain the abnormality of infected rice plants in different growth stages. Besides, the class PlantPart is used to specify where the abnormality happens.

In this work, we model each disease by providing the description using SubClassOf relationship. For example, the description of rice bacterial blight disease is shown in Fig. 3. A schema of rice bacterial blight disease is represented as a knowledge graph. The graph contains seven abnormalityGroup. Rice bacterial blight disease is defined as a subclass of each abnormalityGroup. The abnormalityGroup is previously introduced in RDO and is called roleGroup. For ease of understanding, it is renamed to abnormalityGroup. Here, abnormalityGroup is defined to group various characteristics that occur together into the same group. For example, considering the two facts that “infected leaf has yellow blight” and “infected leaf has brown pimple” can refer to rice bacterial blight disease, we use abnormalityGroup to represent each fact. As seen in Fig. 3, seven abnormalityGroup are used to group and represent seven different group of characteristics that can be emerged in the rice

Table 1 The statistical information of RiceDO and TreatO

Metrics	RiceDO	TreatO
Class count	187	63
Number of rice diseases	23	23
Number of biological control	0	11
Number of chemical control	0	18
Object property count	8	3
SubClassOf axioms	284	132
EquivalenceClasses axioms	3	0

**Fig. 4** Class hierarchy and object property hierarchy of Treatment Ontology (TreatO)

bacterial blight disease. Table 1 summarizes the important statistical information of RiceDO including the total number of classes, object properties, and subclass of relations.

Treatment Ontology (TreatO)

There are four important approaches to rice disease management [23]: physical practices, host resistance, biological control, and chemical control. Our work models TreatO by focusing on biological and chemical control. Chemical control (a.k.a. chemical pesticides) can be applied to plants to control the diseases and pests. Biological control is an alternative approach that is more environmental-friendly and is less harmful to both plants and human. The idea is to use the antagonism agents against the plant disease pathogens. Table 1 shows the statistical information of TreatO, and Fig. 4 illustrates the classes and subclasses of biological control and chemical control, respectively. Figure 4 also shows a relationship between a biological agent and rice diseases. The knowledge sources for modeling TreatO² are IRRI's fact sheets [8] and plant disease management knowledge from [6, 23]. Note that other disease management approaches (e.g., physical practices and resistance control), instructions of usage, restriction of the usage, and the usage's quantity are not modeled in TreatO yet. These issue can be further investigated and consulted with the domain expert such as agronomists and chemists.

Semantic-Based Recommendation Approach

Based on the proposed framework and the designed ontologies discussed earlier, this section elaborates our approach to practically representing observations, identifying diseases, giving early warnings, and recommending treatments.

Observation Representation

Figure 5 presents several representations of an observation. First, farmers (or users) can use the RiceMan application to enter an observation, based on what they have seen during the field observation. Here, a user can explain abnormal appearances of rice plant by specifying a rice plant part, an appearing symptom, the shape and color of the symptom, and the rice plant growth stage. The *Add more* button of RiceMan enables the user to specify several abnormality groups within a single observation. Figure 5 depicts an example of user's interface which represents the user's inputs of an observation denoted by O_1 , whereas the system's inputs of O_1 including latitude, longitude, date, and time are given automatically. In addition, Fig. 5 shows the semantic representation of O_1 , which is modeled as a 3-dimensional vector of abnormality characteristics, geo-location, and date/time. Likewise, the corresponding syntactic representation of the found abnormality using an ontological class expression is also shown in the figure. Finally, a knowledge graph is illustrated. From the graph, it is seen that O_1 simply contains one abnormality group. Figure 6 depicts another

² The OWL file is available at <https://webprotege.stanford.edu/#projects/5751206f-64d7-415d-9fc1-981f0e2be923/edit/OWL%20Classes> and <https://github.com/RiceManFramework/riceman/blob/master/TreatO.owl>.

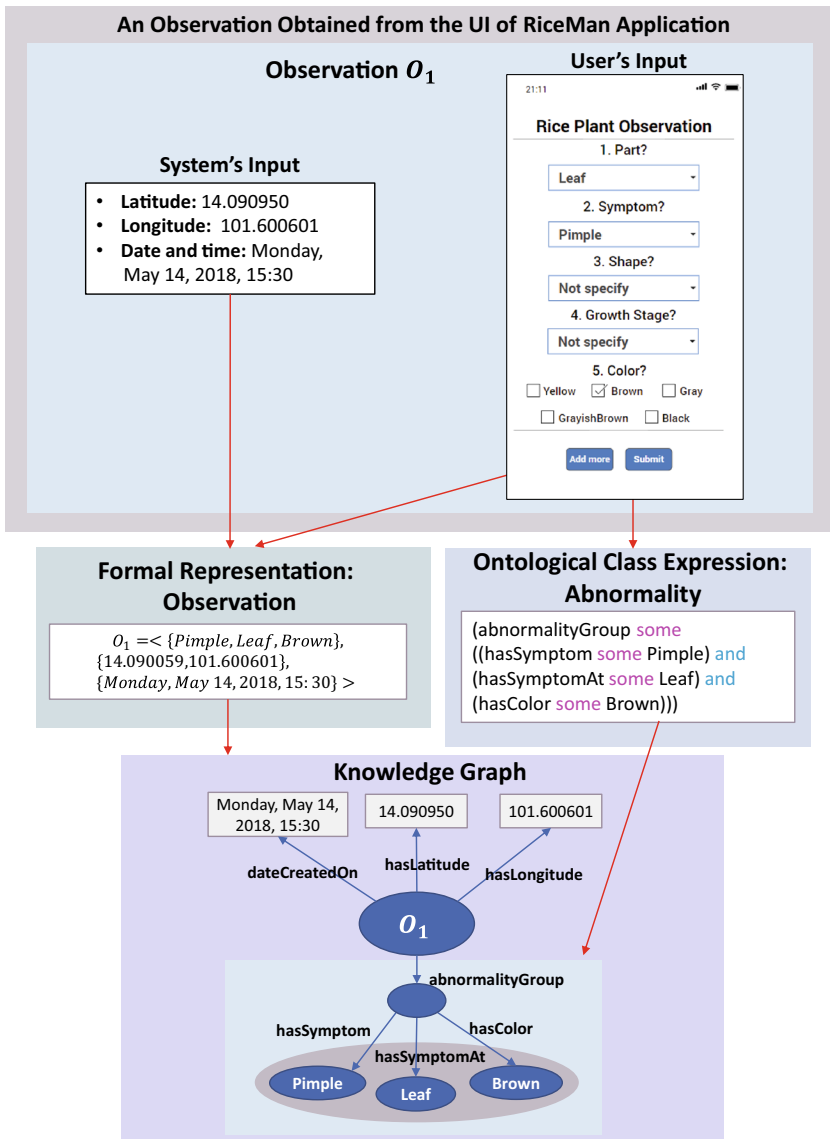


Fig. 5 Several representations of an observation

example Observation O_2 in which a user observes two abnormality groups: (1) a brown spot on a leaf and (2) a yellow halo spot on a leaf.

Disease Identification and Early Warning

Our approach focuses on the use of multiple relevant observations to identify possible rice diseases and give early warnings. Thus, current observation data will be

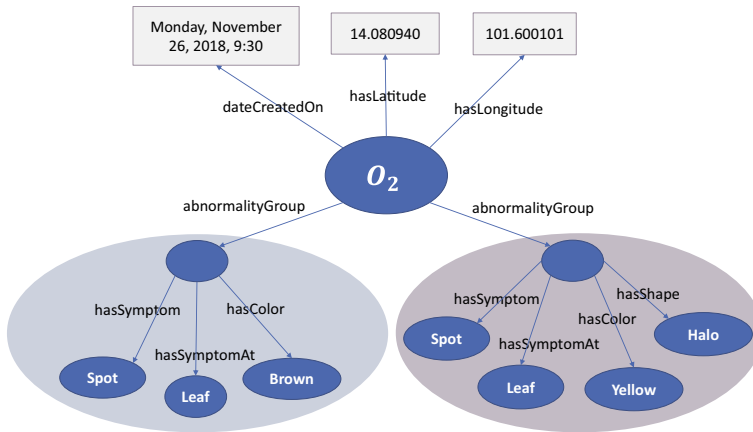


Fig. 6 An observation contains two abnormality groups

combined with other relevant observation data by the Composition Service. The result of the composition is called a *composed observation*, and is used to identify rice diseases. In this work, the existing relevant observations can be retrieved based on following three constraints: distance, duration, and disease spreadability. Next, the three steps to identify rice diseases and provide early warnings are elaborated:

1. *Finding nearby and recent observations with spreadable diseases* Some rice diseases are spreadable to the nearby areas. Hence, we consider this fact and propose to take into account previous observations which can yield spreadable diseases. More specifically, we should consider only the recent observations. Therefore, this step intends to find the existing observations under three constraints: distance, duration, and disease spreadability. These existing observations satisfying the three constraints are called '*composable observations*'. These constraints can be considered as selection criteria to select relevant observation data to be used as input data in the next step. Thus, when there are a large amount of observation data, the selection criteria can filter irrelevant data to be processed.

For this step, RiceMan allows farmers (or users) to adjust a threshold for determining the nearby and recent observations. Thresholds are classified into Distance Threshold and Duration Threshold. In general, time and location of an observation are automatically recorded as system's inputs. Hence, the latitude and the longitude coordinates are used to retrieve the existing nearby observations under the specified Distance Threshold, whereas the date and time are used under the Duration Threshold. Furthermore, we define the class 'SpreadableDisease' for any rice disease that can spread, and then, a subsumption reasoner is employed on each disease name and verify if 'SpreadableDisease' is its superclass or not. For instance, we can verify if a class 'RiceBlastFungalDisease' has a superclass-subclass relation to 'SpreadableDisease'. Since such relation exists, we can conclude

that rice blast fungal disease is spreadable. Therefore, the previous observation that is under the specified Distance Threshold and Duration Threshold, and can infer to ‘SpreadableDisease’, is a composable observation and is able to use in the Composition Service.

2. *Composition* Composition Service is a service for composing multiple observations into one observation called a ‘*composed observation*’. This service allows composition between a current observation and composable observations (Cf. Step 1). To compose, all composable observations represented as OWLClassExpression, are composed together using the operator ‘and’.

Example: O_1 and O_2 refer to the observations in Figs. 5 and 6, respectively. Assume that O_2 is the current observation and O_1 is an existing and composable observation (verified by Step 1). Hence, let us use the Composition Service to compose between O_2 and O_1 . As stated above, each observation must be first transformed into OWLClassExpression as follows:

- O_1 : “abnormalityGroup some (hasSymptom some Pimple and hasSymptomAt some Leaf and hasColor some Brown)”.
- O_2 : “abnormalityGroup some (hasSymptom some Spot and hasSymptomAt some Leaf and hasColor some Brown) and abnormalityGroup some (hasSymptom some Spot and hasSymptomAt some Leaf and hasColor some Yellow and hasShape some Halo)”.

The composition of O_2 and O_1 is a composed observation and is presented as follows:

- “(abnormalityGroup some (hasSymptom some Pimple and hasSymptomAt some Leaf and hasColor some Brown)) and (abnormalityGroup some (hasSymptom some Spot and hasSymptomAt some Leaf and hasColor some Brown) and abnormalityGroup some (hasSymptom some Spot and hasSymptomAt some Leaf and hasColor some Yellow and hasShape some Halo))”.

A composed observation plays an important role to identify ‘*relevant*’ possible diseases and provide early warnings, where using a single observation alone may not be sufficient in this task.

3. *Identification* In this step, the composed observation from Step 2 is used for disease identification and early warning recommendation. Its methodology is described as follows:

- (a) If there exist diseases that are subclasses of the composed observation using a subsumption reasoner (e.g., HermiT) on RiceDO. If so, we perform the following:
 - (i) The retrieved subclasses are possible identified diseases corresponding to the composed observation. In other words, these diseases cause the abnormality characteristics which appear in the composed observation;
 - (ii) The composed observation is a comprehensive consideration of related information to retrieve possible diseases. It may omit some diseases, which can be classified as possible diseases when considering a single observation separately, because they are not subclasses of the composed observation. To prevent loss of information, RiceMan categorizes those diseases, caused by a single observation, as early warnings. Each early warning includes a disease name, its abnormal characteristics as well as other useful knowledge such as possible treatments.
- (b) If there is no disease that is a subclass of the composed observation, we perform the following:
 - (i) We use the current observation to identify possible diseases using a subsumption reasoner. Intuitively, when there exists no disease related to the composed observation, RiceMan considers possible diseases according to the current observation.
 - (ii) Find the diseases that are subclasses of each composable observations and return them as early warnings. Again, each early warning includes a disease name, its abnormal characteristics, and other useful knowledge.

Note that the capability of identifying rice diseases of RiceMan relies on the following three points; (1) the completeness of users' input, e.g., whether they provide enough information covering the distinct features. If the users enter all data which they can observe, then our system can function well, (2) the appearing abnormal characteristics of the disease on a rice plant, and (3) the distinct characteristics of each disease in RiceDO. If diseases have uncommon characteristics, then it can be distinguished by their appearances easily.

Treatment Recommendation

Diseases identified by the previous subsection are used to retrieve treatments in this step. Since the current design of TreatO mainly emphasizes on the management of rice plant diseases based on the biological and chemical control, the recommended treatments consist of these two kinds of control methods. Moreover, we further

classify the returned treatments of each method into two sub-categories: (1) *Recommended treatments* that are suitable for a conjunction of the identified diseases, and (2) *Specific treatments* that are suitable for each individual disease. The recommended treatments are also computed using a subsumption reasoner.

Example: Suppose that there are two diseases identified by the Disease Identification Service: ‘Rice brown spot fungal disease’ and ‘Rice bacterial blight disease’. The following are the treatments retrieved from TreatO:

1. Recommended treatments for both diseases:
 - Biological controls: *Bacillus* sp.
 - Chemical controls: none
2. Specific treatments for Rice brown spot fungal disease:
 - Biological controls: *B. subtilis*, *Bacillus* sp., *P. aeruginosa*, and *Pseudomonas* sp.
 - Chemical controls: Azoxystrobin, Carbendazim, Iprodione, Propiconazole, and Trifloxystrobin.
3. Specific treatments for Rice bacterial blight disease:
 - Biological controls: *Bacillus* sp.
 - Chemical controls: Copper Oxychloride, Streptocycline, and Zineb.

Practical Use Case and Usages

This section discusses the results of RiceMan system to identify rice diseases, provide warnings, and recommend treatments by comparing between a single observation and multiple observations. Considering a single observation means that only the current observation is considered, whereas multiple observations mean that the current observation is considered together with the composable observations (i.e., using the Composition Service).

Let O_1, O_2, O_3 , and O_4 be the following observations:

$$\begin{aligned}
 O_1 &= \langle \{Pimple, Leaf, Brown\}, \{14.090950, 101.600601\}, \{Monday, \\
 &\quad May\ 14, 2018, 15:30\} \rangle \\
 O_2 &= \langle \{Spot, Leaf, Brown\}, \{Spot, Leaf, Yellow, Halo\}, \\
 &\quad \{14.080940, 101.600101\}, \{Monday, November\ 26, 2018, 9:30\} \rangle \\
 O_3 &= \langle \{Spot, Leaf, Brown\}, \{Spot, Leaf, Gray\}, \\
 &\quad \{14.082900, 101.550300\}, \{Monday, November\ 26, 2018, 9:40\} \rangle \\
 O_4 &= \langle \{Blight, Leaf, GrayishGreen\}, \{Pimple, Leaf, Yellow\}, \\
 &\quad \{14.090950, 101.600200\}, \{Tuesday, November\ 27, 2018, 13:30\} \rangle
 \end{aligned}$$

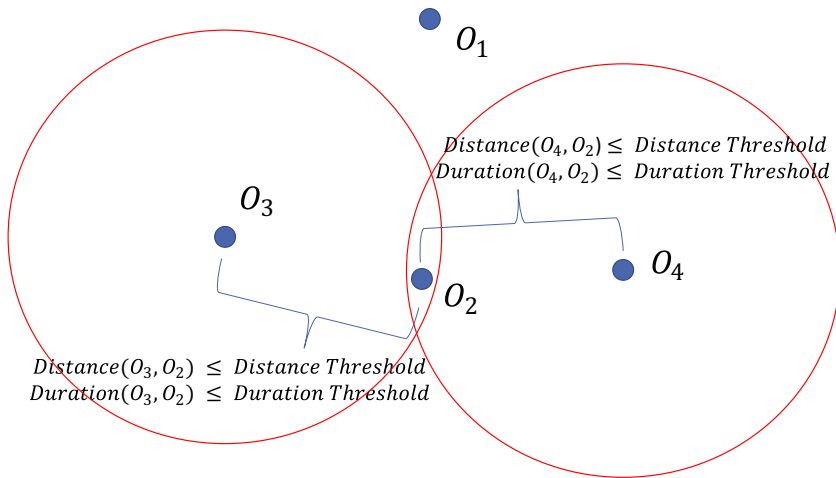


Fig. 7 Practical Observations O_1, O_2, O_3 , and O_4

Then, let A_1, \dots, A_6 denote abnormality groups appearing in O_1, \dots, O_4 as follows:

$$\begin{aligned} A_1 &= \{Pimple, Leaf, Brown\} & A_4 &= \{Spot, Leaf, Gray\} \\ A_2 &= \{Spot, Leaf, Brown\} & A_5 &= \{Blight, Leaf, GrayishGreen\} \\ A_3 &= \{Spot, Leaf, Yellow, Halo\} & A_6 &= \{Pimple, Leaf, Yellow\}. \end{aligned}$$

Figure 7 also illustrates the four observations O_1, O_2, O_3 , and O_4 in different geolocations. Table 2 provides the details of observations which are represented by a formal representation. Observation O_1 contains only one abnormality group, while other observations contain two abnormality groups. In this practical use case, O_1 was collected first, and followed by O_2, O_3 , and O_4 . Table 2 shows the corresponding results for each observation, when considering a single observation versus multiple observations. It can be seen that the results yielded by both cases have different possible identified diseases, early warnings, and treatments, which can be explained as follows:

1. *Observation O_1* : Since O_1 is the first observation, there exists no nearby or recent observation. O_1 consists of one abnormality group, i.e., A_1 . Hence, single and multiple observation-based approaches yield the same results. As aforementioned, RiceMan uses a subsumption reasoner to identify possible diseases from the observed abnormality groups and to recommend corresponding treatments accordingly.

As shown in Table 2, rice bacterial blight disease (denoted by ‘Blight’) is identified as a possible disease from the abnormality group A_1 . Using this disease,

Table 2 The results of identified diseases, corresponding warnings, and recommended treatments of O_1 , O_2 , O_3 , and O_4 based on a single observation and multiple observations approach

Approach	Observation	Abnormality group	Composable observation	Composed observation	Identified diseases	Warnings	Recommended treatments	Biological control	Chemical control
Single Observation-based	O1	A1	–	–	Blight		T (Blight)	<i>Bacillus</i> sp.	CopperOxyChloride, Streptocycline, Zineb
	O2	A2, A3	–	–	Brown spot		T (Brown spot)	<i>Pseudomonas</i> sp. <i>P. aeruginosa</i> <i>Bacillus</i> sp. <i>B. subtilis</i>	Azoxystrobin Carbendazim Iprodione Propiconazole Trifloxystrobin
	O3	A2, A4	–	–	Brown spot and blast		T (Brown spot) \cap T (Blast)	<i>Bacillus</i> sp.	None
	O4	A5, A6	–	–	Blight		T (blight)	<i>Bacillus</i> sp.	CopperOxyChloride, Streptocycline, Zineb

Table 2 (continued)

Approach	Observation	Abnormality group	Composable observation	Composed observation	Identified diseases	Warnings	Recommended treatments	Biological control	Chemical control
Multiple observation-based	O1	A1	–	–	Blight		T (Blight)	<i>Bacillus</i> sp.	CopperOxyChloride, Streptocycline, Zineb
	O2	A2, A3	–	–	Brown spot		T (brown spot)	<i>Pseudomonas</i> sp., <i>P. aeruginosa</i> , <i>Bacillus</i> sp., <i>B. subtilis</i>	Azoxystrobin, Carbendazim, Iprodione, Propiconazole, Trifloxystrobin
	O3	A2, A4	O2	A2 and A3 and A4	Brown spot	Blast	T (brown spot)	<i>Pseudomonas</i> sp., <i>P. aeruginosa</i> , <i>Bacillus</i> sp., <i>B. subtilis</i>	Azoxystrobin, Carbendazim, Iprodione, Propiconazole, Trifloxystrobin
	O4	A5, A6	O2	A2 and A3 and A5 and A6	Blight	Brown spot	T (Blight)	<i>Bacillus</i> sp.	CopperOxyChloride, Streptocycline, Zineb

Note the following abbreviations: ‘Rice bacterial blight disease’ is abbreviated by ‘Blight’, ‘Rice brown spot fungal disease’ is ‘Brown spot’, and ‘Rice blast fungal disease’ is ‘Blast’

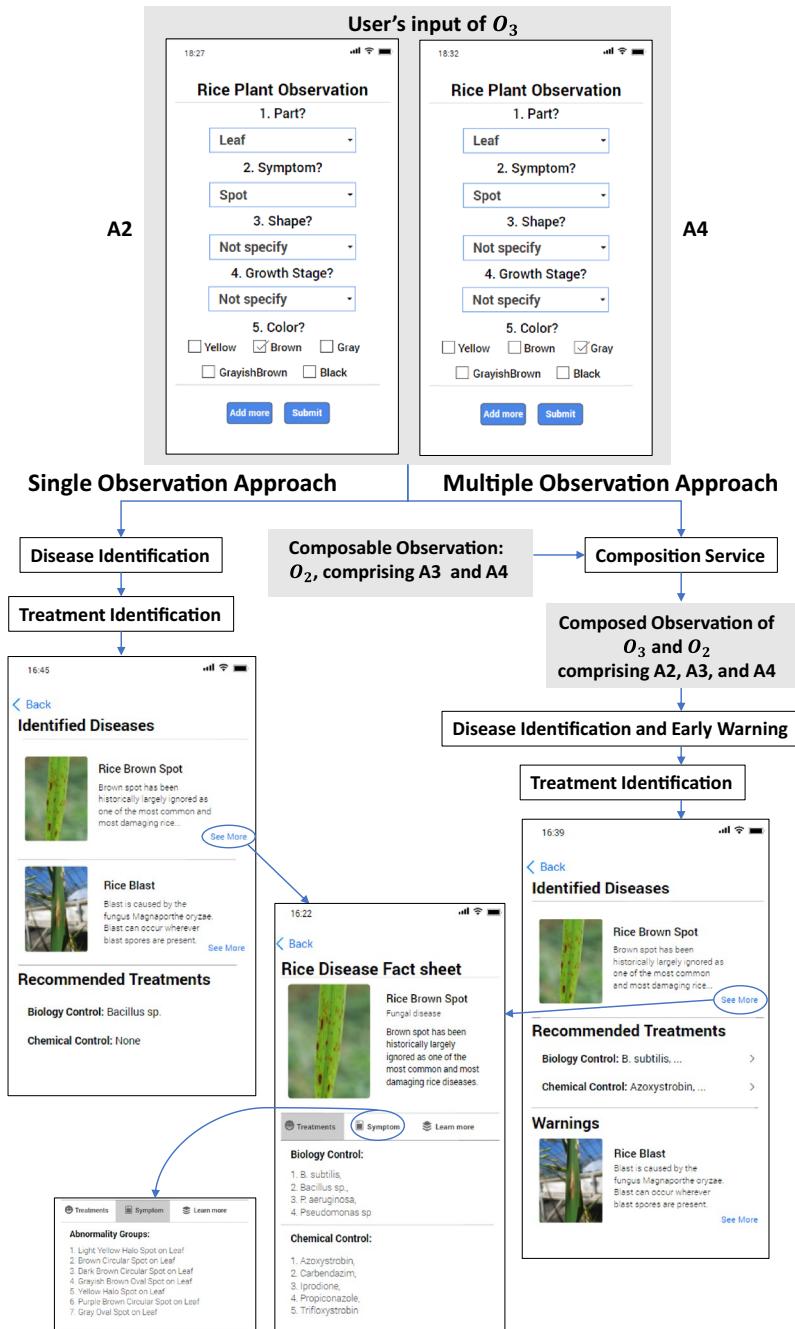


Fig. 8 Comparison between two approaches using observation O_3

RiceMan then recommends both biological and chemical control treatments of blight disease to the user.

2. *Observation O_2* : O_2 is the second observation and consists of two abnormality groups: A2 and A3. Regarding the single observation method, these two abnormality groups are used to infer possible diseases. Since **rice brown spot fungal disease** is a subclass of A2 and A3, it is obvious that this disease is inferred and indicated as a possible disease, as shown in Table 2. Next, corresponding treatments are determined and recommended.

When considering the multiple observations method, the first step is to find composable observations, and compose them with the current observation. As shown in Fig. 7, O_1 is an existing observation, but it is not a nearby nor recent observation. Thus, only the abnormality groups of O_2 (A2 and A3) are used to identify diseases, which results in the same identified diseases and treatments as in the single observation method.

3. *Observation O_3* : O_3 is the third observation and consists of two abnormality groups: A2 and A4. Figure 8 shows the user interfaces in which two abnormality groups are created in O_3 . This figure also shows the comparisons of user interfaces between the single observation approach and the multiple observations approach w.r.t. the same observation O_3 .

Regarding the single observation method, it can infer the two possible diseases: **rice brown spot fungal disease** and **rice blast fungal disease**. When more than one possible diseases are identified, the treatments are recommended based on the conjunction of treatments of both diseases. Besides, the specific treatments for each disease are also provided. Hence, RiceMan returns three categories of treatments which are $T(\text{Brown spot}) \cap T(\text{Blast})$, $T(\text{Blast})$, and $T(\text{Brown spot})$. The results of identified diseases and the recommended treatments are shown on the top and bottom parts of the interface, respectively, whereas the specific treatments are shown after clicking on 'See More' button on each disease. This button proceeds to the corresponding 'Rice disease fact sheet' which provides detailed knowledge, treatments, and abnormality groups of each disease.

Consider the multiple observations method. O_2 is a composable observation of O_3 , since it is an existing observation that is nearby, recently happens, and can yield a spreadable disease (cf. Fig. 7). The Composition Service is used to compose the abnormality groups of O_3 and O_2 . Therefore, the composed observation constitutes A2, A3, and A4, and **rice brown spot fungal disease** is the identified disease of the composed observation. Its treatment, returned as the $T(\text{Brown spot})$ is then recommended. Figure 8 shows these results on the right part, in which the identified disease appears on the top part of the interface, followed by its corresponding recommended treatments.

Note that using only the single observation O_3 , two possible diseases are identified (rice brown spot fungal disease, and rice blast fungal disease), while the composed observation of O_3 and O_2 can yield a more specific disease (only one disease: rice brown spot fungal disease), which is determined by combining the abnormalities found in all relevant composable observations, instead of considering each observation separately.

However, since it could be possible that the plants are infected by one or more diseases, where each observation and each abnormality appearing would identify a differing disease, in this case, combining multiple observations would yield only the diseases that have all of the abnormalities occurring, but not ones with some partial abnormalities.

To overcome this limitation in the case of multiple observations approach, the diseases identified by a single observation are alerted as a warning. Thus, rice blast fungal disease is warned for the observation O_3 . In Fig. 8, this warning is also shown at bottom of the interface.

4. *Observation O_4* : O_4 is the fourth observation and consists of two abnormality groups: A5 and A6. Using the single observation approach, rice bacterial blight disease is inferred with the recommended treatment T(Blight).

When considering the multiple observations method, O_2 is a composable observation of O_4 , which is nearby, recently happens, and can yield a spreadable disease. The Composition Service then composed O_4 and O_2 . However, this composed observation with the combined abnormality groups A2, A3, A4, and A5 does not yield any possible diseases related to it. Technically, this means that there are no diseases which can be inferred by A2, A3, A4, and A5 in our ontologies. In other words, the abnormality groups found in O_2 are not related to O_4 . In this situation, the single observation O_4 is considered, and the treatment T(Blight) is suggested. Thus, as shown in Table 2, the identified disease is rice bacterial blight disease. It is worth mentioning that, even though the composed observation infers no disease, RiceMan still considers at the disease identified by O_2 as it is the composable observation of O_4 . Hence, the identified disease, i.e., rice brown spot fungal disease is returned as an early warning.

This section discusses various scenarios of using RiceMan. Observation O_3 and O_4 show that the multiple observations approach can yield more specific results to the user, and can classify the suspect diseases into identified diseases and early warnings. This can support farmers to make a better decision and better manage their farms.

Conclusion

In this paper, we design and develop RiceMan, which is a semantic-based framework in agriculture for rice plant disease management. This framework can help farmers to identify rice diseases, receive early warnings of possible spreadable

diseases, and receive treatments based on multiple observations: a current observation and relevant observations.

To develop RiceMan, we first externalize knowledge from existing reliable sources and propose approaches to manage multiple farmers' observations properly. Our modeled ontologies, namely Rice Diseases Ontology (RiceDO) and Treatment Ontology (TreatO), capture the knowledge related to abnormal characteristics of rice diseases and the recommended treatments, respectively. Second, we represent the abnormal characteristics found in farmer's observation as an ontology expression. Hence, with the usage of a reasoner in RiceMan, possible rice diseases are identified. The same approach is applied to recommend the corresponding treatments. Third, to integrate with relevant observations, we develop a composition service to combine the current observation with relevant observations. RiceMan classifies the results of disease identification into two categories, namely possible diseases and early warning diseases. This helps farmers realizing the importance of the returned results. Finally, we illustrate the usage of RiceMan applications through different scenarios that it can handle.

For future directions, we plan to improve the current UI design to enhance user experience for farmers. Such design involves concepts of text-free user interface such as avoid texts, follow the minimalist designs, use graphics, and use speech feedbacks. For example, symptoms are displayed with their images. Thus, it becomes effortless to use especially, for illiterate farmers. In addition, we intend to further extend RiceDO by including knowledge on season, other insects and animals, weeds, and severity levels of rice diseases. In addition, TreatO can be extended to include more details about treatments and precisely recommend an appropriate treatment for different severity levels. To evaluate the accuracy and effectiveness of our approach, a user study and a usability testing are envisaged, in which farmers use RiceMan to perform observations and manage their plants. Since RiceMan is designed based on multiple observations, our hypothesis is that using more than one observation can yield better responses: possible diseases and early warnings, than using a single observation. The study will involve two types of users, farmers, and agronomists, and the obtained results will be used to evaluate the accuracy and effectiveness of the identified possible diseases, warnings, and recommended treatments as well as to determine the user satisfaction.

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