Chapter 11
The Ontological Modelling of Fruit Fly Control and Management Knowledge

Caroline C. Kiptoo, Aurona Gerber, and Alta Van der Merwe

Abstract Fruit fly control and management in Africa has been the topic of several scientific investigations resulting in diverse sources of knowledge on the topic. Despite the existence of this knowledge, frequently it is not readily accessible to all targeted beneficiaries; this can be due to, for example, the remote locations of farms and the complexity of the knowledge. However, recent technological developments such as web technologies and networking allow for the engagement and participation of stakeholder groups in the acquisition and dissemination of knowledge and these technologies can also be applied to fruit fly knowledge. In order to facilitate this stakeholder participation in fruit fly knowledge sharing, the relevant domain knowledge needs to be available in a format that can support stakeholder engagement, preferably through the Web. Fruit fly knowledge has not been modelled in this manner and this paper reports on an investigation to model and capture the relevant domain knowledge using ontologies. The objective of this work is thus the development of the domain ontology and its evaluation using a prototype stakeholder participation system for fruit fly control and management that was capable of utilising the ontology. We describe our findings on the use of ontology technologies for representation of fruit fly knowledge, the fruit fly ontology developed, as well as a prototype Web-based system that uses the ontology as a source of knowledge.

Keywords Ontological modelling • Ontology-driven • Taxonomic key

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C.C. Kiptoo (✉) • A. Van der Merwe
Department of Informatics, University of Pretoria, Pretoria, South Africa
e-mail: cckiptoo@gmail.com

A. Gerber
Department of Informatics, University of Pretoria, Pretoria, South Africa

CAIR, CSIR Meraka Institute, Pretoria, South Africa

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1 Introduction

Fruit flies (Diptera: Tephritidae) are one of the most important pests affecting fruit and vegetable production worldwide (Allwood and Drew 1997; Badii et al. 2015). The spread of fruit flies, particularly exotic invasive species, is as a result of both natural processes and human activities. Natural processes depend on the traits of the species e.g. availability of hosts plants, mating patterns, and survival patterns in different environments amongst others (Malacrida et al. 2007; Vargas et al. 2000). Human activities that encourage spread include transportation of infected fruit by travelers, and trade between countries. Losses due to fruit flies result from direct damage to fruit, reduction in quality and quantity of fruit and loss of markets due either to the quarantine restrictions of the importing countries or because the importer's Maximum Residue Limits (MRL) for pesticides are exceeded (de Bon et al. 2014; Dominiak and Ekman 2013; Ekesi et al. 2005; Manrakhan et al. 2013). Production of high quality fruits and vegetables that meet the required MRL and quarantine measures is therefore a prerequisite for targeting lucrative export markets.

At the request of growers, regional authorities and national authorities, the *icipe*-led African Fruit Fly Programme (AFFP) was established. The broad objective of AFFP is to help stakeholders in the horticulture industry to effectively manage fruit flies and build the capacity of agricultural officers, extension workers, quarantine personnel and growers (Ekesi 2010). The AFFP programme has undertaken different research activities and has developed effective management packages for growers across Africa. Key outcomes of these initiatives include the development of knowledge on the identification of fruit fly species (Billah et al. 2007), on attractants that can be used for monitoring different fruit fly species (Manrakhan 2007; Nagaraja et al. 2014), on the species distribution across Africa (Ekesi and Muchugu 2007) and on the host plant relationships of different fruit fly species (Ekesi and Muchugu 2007; Rwomushana et al. 2008). However, the accessibility of this knowledge to farmers in Africa is still limited due to inadequate resources, complexity of the knowledge, the nature of farming and lack of capacity to engage experts on a continuous basis.

The emergence of Web 2.0 and the social web has created new opportunities for online collaboration in different domains. In ecology and environmental sciences, this type of online collaboration has been used to support citizen science projects such as the eBird project and BioBlitz projects (Bonney et al. 2009; Delaney et al. 2008; Karns et al. 2006; Lewington and West 2008; Lundmark 2003; Silvertown 2009; Sullivan et al. 2009). By harnessing these technologies, we aim to create a platform to support online collaboration between scientists and citizens on the management of fruit flies. Such a platform requires modelling approaches that adequately represent the available expert knowledge to drive the collaboration and we found that the use of ontological modelling was most appropriate. Here we present the development of an ontology that represents the key knowledge necessary for management of fruit flies. We have focused on species with the greatest economic importance in Africa, specifically 30 species from the genera *Ceratitis, Dacus, Bactrocera* and *Trirhithrum*. The scope of knowledge that was modelled included the morphological features of the different taxonomic groups, the attractants used to lure different species and the sets of species supported by different host plants (Billah et al. 2007; Rwomushana et al. 2008; Manrakhan 2007; Ekesi and Muchugu 2007).

2 What are Ontologies and How Are They Developed?

The term ontology has its origin in philosophy (Kunne et al. 1982) and in philosophy, an ontology is defined as “a branch of philosophy that deals with the science of what is, of the kinds and structures of objects, properties, events, processes and relations in every area of reality” (Smith 2003). This concept was adopted by Computer Science where an ontology is used to refer to an information object that contains formally symbolized knowledge. Gruber (1993) defined an ontology as “a body of formally represented knowledge which is based on a conceptualization” and a conceptualization as “an abstract simplified view of the world that we wish to represent for some purpose”. The desired facts on the target set of objects (universe of discourse) is represented in a declarative formalism using computational logic and the relationships between these sets of objects are modelled. In Guarino et al. (2009) an ontology is described as something used to embody the structure of a system. In Horridge et al. (2009) an ontology is seen to be a formalized representation of knowledge consisting of classes, properties and individuals. In this work we adopt the definition of Gruber (1993) where an ontology consists of formally represented knowledge based on a conceptualization.

In Noy and McGuinness (2001), the advantages of using ontologies over other forms of knowledge representation are presented. In our research, the need to bring together stakeholders comprised of experts and non-experts was one of the reasons that motivated the use of ontology to represent knowledge. The gap between experts and novices can be effectively reduced by using ontologies because people and software who adopt a formalism have a common understanding of the represented facts and, therefore, software can be used easily to aid humans in answering questions. In addition, in ontological modelling assumptions are made explicit and, therefore, those who adopt the ontology are aware of all the assumptions.

Building ontologies is arguably still a craft skill. Different methodologies have been proposed, most of them derived from project experiences (Iqbal et al. 2013). Some methodologies are comprehensive while others address specific aspects of ontology development (López 1999). Comprehensive methodologies can be categorized into two types: stage-based models and evolving-prototype models (Jones et al. 1998). Stage-based models, as the name suggests, have step by step processes with clear inputs and outputs at each stage. They are more suitable for building ontologies where the full requirements are clear from the onset. Evolving-prototype methodologies create an initial prototype ontology which is then evolved over time ideally creating improved versions at every iteration. Methodologies of this type are ideal for problems where the requirements are not clear at the initial stages and can emerge and become clearer after some iterative improvements on the initial version.

Noy and McGuinness (2001) argued that there is no correct way to create domain ontologies and approaches depend on the targeted application. A methodology for design and evaluation of ontologies is presented in Grüninger and Fox (1995). The steps include: document motivating scenarios and clearly establishing why existing ontologies cannot meet the needs at hand; developing informal competency questions that the ontology must answer; enumerating first order logic terminology by identifying objects, attributes and relations; creating formal competency questions from the informal questions and the formal terminology; defining first order logic axioms that capture the relationship between the objects and answer the formal competency questions; and developing completeness theorems that guide when the answers to the competency questions are complete. Noy and McGuinness (2001) present a seven step process for building domain ontologies: determine the domain and scope of the ontology, consider reusing existing ontologies, enumerate important terms in the ontology, define the classes and the class hierarchy, define the properties of classes – slots, define the facets of the slots, and create instances. They use terminology from the Web Ontology Language (OWL) to explain their methodology and, although it is slightly different in the steps, the general approach is closely similar to the methodology of Grüninger and Fox (1995).

Construction and maintenance of formal ontologies is done using ontology representation languages. In 2001, a working group called Web Ontology (WebOnt) Working Group was formed by the World Wide Web Consortium (W3C) and their mandate was to make a new ontology markup language for the Semantic Web, called OWL. The second edition, OWL 2, is now recommended as a standard by W3C and to promote interoperability of the web (Corcho et al. 2003). As result of these standardization efforts, tools that ease creation of OWL ontologies have been created (Corcho et al. 2003). An example is Protégé, which is open-source software developed at Stanford University. Protégé allows interactive creation and editing of ontologies in various formats. Protégé comes with core functionalities that can be expanded by the importation of available plugins (Sivakumar and Arivoli 2011). Protégé is available as a stand-alone version that can be installed in individual machines, and as a web version, WebProtege, which can be installed on a web server and allows users to share, create and edit ontologies through a web browser (Gennari et al. 2003; Rubin et al. 2007).

The use of ontologies in representations of biological knowledge is not entirely new. Examples of ontology use within the biological sciences include the highly cited Gene ontology (GO) which represents knowledge on molecular functions, biological processes and cell components (Ashburner et al. 2000; Bard and Rhee 2004); the Plant ontology, which links plant anatomy, morphology, growth and development to plant genomics data; and Mouse gross anatomy ontology representing knowledge on the anatomy of adult mice. More biological ontologies are hosted at the Open Biological Ontologies (OBO) website, hosted by the Berkeley Bioinformatics Open Source Project.

Two ontologies that are closely related to our own study described here are the Hymenoptera Anatomy Ontology (HAO) presented in Yoder et al. (2010) and the Morphology of Afrotropical Bees Ontology (ABO) presented in Gerber et al. (2014). These both model knowledge about organisms from the same class as fruit flies. The HAO represents the anatomy of members of the family Hymenoptera, and its objective was to address the challenge of language discrepancies in anatomical terminology. The ABO uses concepts from the HAO ontology to represent knowledge about the morphological features of different taxonomic groups of bees and a model for modelling morphological features of different taxonomic groups is presented (Gerber et al. 2014).

3 Development of a Fruit Fly Ontology

The construction of the fruit fly ontology was done following the guidelines developed by Grüninger and Fox (1995), Horridge et al. (2009) and Noy and McGuinness (2001).

3.1 Materials and Tools

3.1.1 Materials

The Materials used for this research were:

1. Fruit fly taxonomic key (Billah et al. 2007).
2. Data on the set of host plants used by different fruit fly species (Ekesi and Muchugu 2007).
3. Sets of species attracted by different lures (Manrakhan 2007).

3.2 Tools

The tools used in this research were:

4. Protégé, a graphical editor for building ontologies and knowledge bases (Gennari et al. 2003; Noy et al. 2003).
5. Fact++ reasoner (Tsarkov and Horrocks 2006).
6. Java programming language and JSP (Java Server Pages).

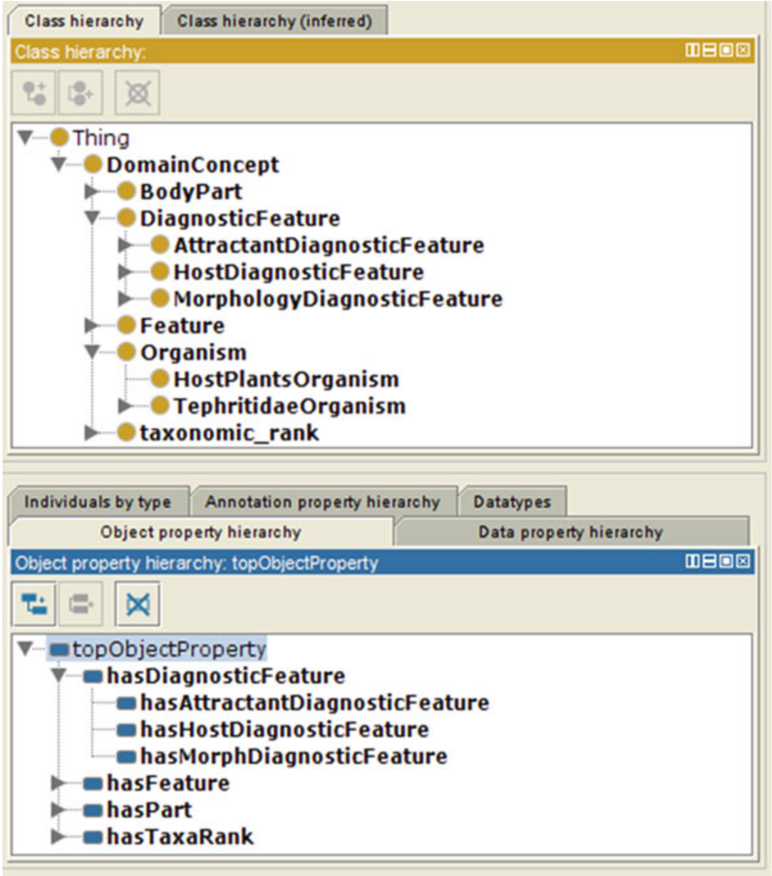
3.3 Construction of the Ontology

In this section, the construction of the ontology is presented. To improve reading, the class names are italicized. The naming convention proposed by Noy and McGuinness (2001) was used to name the concepts in the ontology. The construction of the ontology was done using Protégé and built in Fact++ reasoner. The process began with defining the scope of the ontology. The scope was defined by specifying the competency questions that the ontology must answer and the questions are as listed in Box 11.1.

Box 11.1: Competency Questions

1. Which species have a given set of taxonomic features
   (e.g. which species have patterned wings, dark brown femora and three black spots on the scutellum?)
2. Which set of host plants can a given species attack
   (e.g. which hosts can be attacked by *Bactrocera latifrons* (Hendel)?)
3. Which set of species can a given lure attract
   (e.g. which species are attracted by Trimedlure?).

In the different methodologies, it is recommended that existing ontologies should be used if they can serve the needs of the target project. Modelling of the ontology therefore proceeded with the identification of ontologies that could be re-used. We found that the TAXRANK ontology (http://www.phenoscape.org/wiki/Taxonomic_Rank_Vocabulary) was suitable for the association of our taxonomic groupings with the biological taxon information. Use of the TAXRANK ontology is illustrated later in this section. The other knowledge on identification features, host plants and lures were modelled in the fruit fly ontology presented here and, for easy reading, the names of the concepts are italicized. Class names begin with a capital letter, while properties begin with lower case letters. Top concepts and their sub concepts consisting of classes and properties were identified. The top classes included: *BodyPart* which contained the anatomical parts of the organism; *Feature* which consisted of general characteristics such as colour, shape and texture; *DiagnosticFeature* which described compound features and had three sub-classes (*MorphDiagnosticFeature*, *HostDiagnosticFeature* and *AttractantDiagnosticFeature*); *Organism* which contained the taxonomic groupings of the fruit flies and host plants. The top properties included: *hasDiagnosticFeature* which was used to associate taxonomic groupings with diagnostic features and had three sub properties (*hasHostDiagnosticFeature, hasAttractantDiagnosticFeature, hasMorphDiagnosticFeature*); *hasPart* which was used to describe the parts of a body segment. The *hasTaxaRank* object property was used to associate the taxonomic groupings in the fruit fly key with the biological taxon defined in the TAXRANK ontology. The top concepts and top object properties are as shown in Fig. 11.1.



- Thing
  - DomainConcept
    - BodyPart
    - DiagnosticFeature
      - AttractantDiagnosticFeature
      - HostDiagnosticFeature
      - MorphologyDiagnosticFeature
    - Feature
    - Organism
      - HostPlantsOrganism
      - TephritidaeOrganism
    - taxonomic_rank

- topObjectProperty
  - hasDiagnosticFeature
    - hasAttractantDiagnosticFeature
    - hasHostDiagnosticFeature
    - hasMorphDiagnosticFeature
  - hasFeature
  - hasPart
  - hasTaxaRank

Fig. 11.1 Top concepts in fruit fly ontology

The *BodyPart* class was modelled as sub-classes consisting of the organism body parts and any relationship between parts was inferred using the *hasPart* object property.

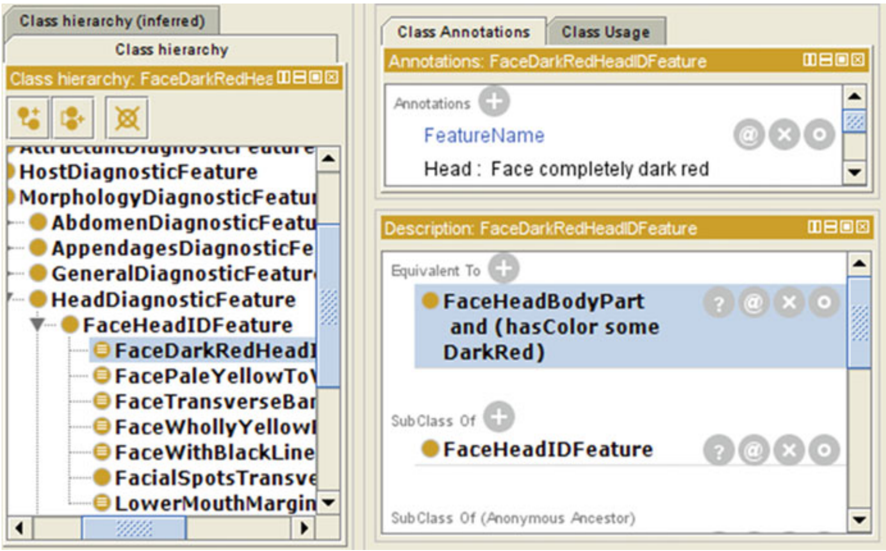
The *Feature* class was modelled as sub classes consisting of features such as colour, shape, size and texture.

The *Morphological Diagnostic feature* was modelled using the Gerber et al. (2014) model, where the concept *MorphDiagnosticFeature* was defined as a *BodyPart* that has a feature *Feature.*

MorphDiagnosticFeature = *BodyPart* and (*hasFeature* some *Feature*)

For instance, to define a feature of a leg that is yellow in colour, the diagnostic feature was represented using the body part class '*LegBodyPart*' and feature class '*YellowColourFeature*' and was modelled as:

(*LegBodyPart* and (*hasColour* some *YellowFeature*))



HostDiagnosticFeature
MorphologyDiagnosticFeatu
AbdomenDiagnosticFeatu
AppendagesDiagnosticFe
GeneralDiagnosticFeatur
HeadDiagnosticFeature
FaceHeadIDFeature
FaceDarkRedHeadI
FacePaleYellowTo
FaceTransverseBar
FaceWhollyYellowI
FaceWithBlackLine
FacialSpotsTransve
LowerMouthMargin

FeatureName
Head : Face completely dark red

FaceHeadBodyPart and (hasColor some DarkRed)

FaceHeadIDFeature

Fig. 11.2 Face dark red diagnostic feature

Note that *hasColour* is a sub property of the property *hasFeature*. As another example the modelling of the diagnostic feature for a dark red face is shown in Fig. 11.2.

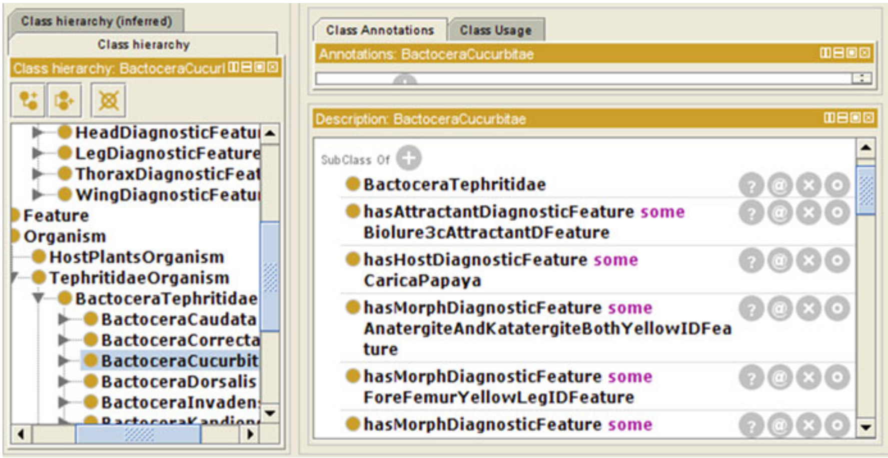
Modelling of attractants and host plants was done by defining them as subclasses of *AttractantDiagnosticFeature* and *HostDiagnosticFeature* respectively.

After the diagnostic features were modelled, the next step was to associate them with the taxonomic grouping of the organism through the *hasDiagnosticFeature* object property using the relevant sub property. The diagnostic features *MorphDiagnosticFeature*, *HostDiagnosticFeature* and *AttractantDiagnosticFeature* were associated with the taxonomic group using *hasMorphDiagnosticFeature*, *hasHostDiagnosticFeature* and *hasAttractantDiagnosticFeature*, respectively. For example, a taxonomic grouping *TG* that has a set of morphological diagnostic features *MDF1*, *MDF2*…. *MDFn* is modelled as:

TG and (*hasMorphDiagnosticFeature* some *MDF1*) and (*hasMorphDiagnosticFeature* some *MDF2*) …and (*hasMorphDiagnosticFeature* some *MDFn*)

To associate attractants and host plants to the taxonomic groupings, the same modelling structure was used. A complete example of modelling all three categories of diagnostic features is described below. The taxonomic group *TG* that has yellow femora, is attracted to protein bait and can be hosted by the custard apple, *Annona muricata* L., was modelled as:

TG and (*hasMorphDiagnosticFeature* some *FemurAllFemoraYellowLegIDFeature*) and (*hasAttractantDiagnosticFeature* some *ProteinBaitAttractantDFeature*) and (*hasHostDiagnosticFeature* some *AnnonaMuricata*)



HeadDiagnosticFeatu
LegDiagnosticFeature
ThoraxDiagnosticFeat
WingDiagnosticFeatu
Feature
Organism
HostPlantsOrganism
TephritidaeOrganism
BactoceraTephritidae
BactoceraCaudata
BactoceraCorrecta
BactoceraCucurbit
BactoceraDorsalis
BactoceraInvaden

BactoceraTephritidae
hasAttractantDiagnosticFeature some Biolure3cAttractantDFeature
hasHostDiagnosticFeature some CaricaPapaya
hasMorphDiagnosticFeature some AnatergiteAndKatatergiteBothYellowIDFeature
hasMorphDiagnosticFeature some ForeFemurYellowLegIDFeature
hasMorphDiagnosticFeature some

Fig. 11.3 Association of taxonomic groupings with morphology, host plant and attractant

A further example showing the association of a morphological feature, a host and an attractant with a taxonomic grouping is presented in Fig. 11.3.

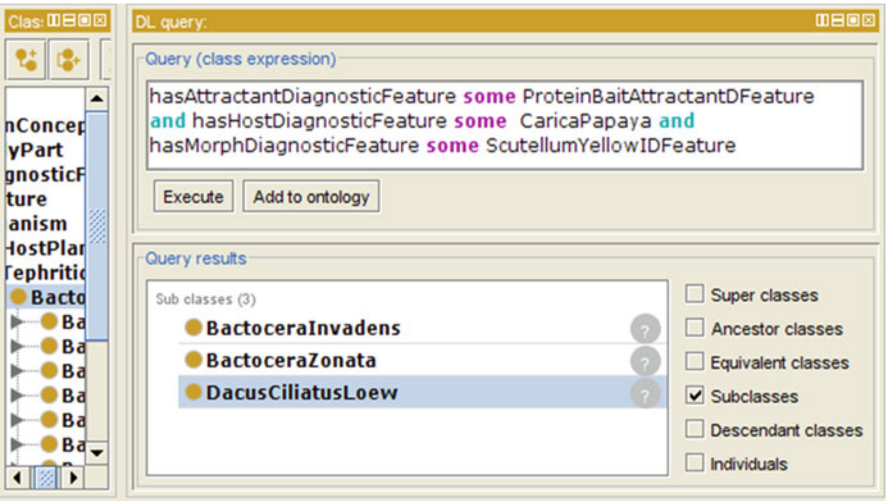
Associating our taxonomic groupings with biological taxa was done by importing the TaxaRank ontology into our ontology and associating our taxonomic groupings with the appropriate taxon in TaxaRank. The association was done using the *hasTaxaRank* object property. This association will enable other applications using the TaxaRank ontology to process our data. For example, associating a taxonomic group *TG* with *subfamily* taxon is as shown below:

TG and (*hasTaxaRank* some *subfamily*)

The development of the ontology was iterative across the presented activities until the ontology was completed. The ontology in its current form has captured knowledge on the simplified taxonomic key and the set of lures for different species. The host plant for the different species have not been captured fully yet, but the basic structure exists. According to Protégé metrics the ontology has 1181 classes and 4600 axioms.

3.4 *Evaluating the Ontology*

Evaluation of the ontology was done based on the competency questions that guided its development (see Box 11.1). The evaluation was done using the DL Query tool within Protégé and through development of a prototype application that used the ontology as a knowledge source.



Query (class expression)

```
hasAttractantDiagnosticFeature some ProteinBaitAttractantDFeature
and hasHostDiagnosticFeature some  CaricaPapaya and
hasMorphDiagnosticFeature some ScutellumYellowIDFeature
```

Query results

Sub classes (3)

- BactoceraInvadens
- BactoceraZonata
- DacusCiliatusLoew

☐ Super classes
☐ Ancestor classes
☐ Equivalent classes
☑ Subclasses
☐ Descendant classes
☐ Individuals

Fig. 11.4 Species that match query criteria

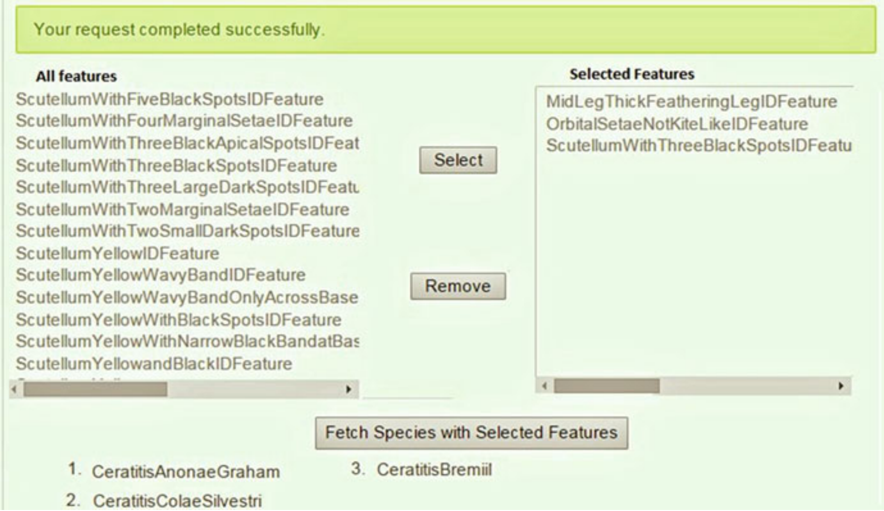
3.4.1 Evaluation Using DL Query

The Protégé DL Query tool was used in conjunction with the integrated Fact++ reasoner to evaluate the ontology. The evaluation was done using the competency questions and was found to give correct answers. For example, the species that have a yellow scutellum, are attracted to protein bait and can be hosted by papaya, *Carica papaya* L., are extracted by the query as shown in Fig. 11.4.

3.4.2 Evaluation Using Application Prototype

An important quality of a domain ontology is to meet the requirements of the application it was intended for (Noy and McGuinness 2001). In this section we present a prototype of an application developed for the purposes of accessing fruit fly knowledge for practical purposes. The fundamental requirements of the application include provision of a taxonomic key for the stakeholders, provision of guidance on baits to use based on the fly species being targeted and the host plants that could be affected by different fly species. The application was developed to evaluate whether the ontology could meet these requirements.

The Prototyping approach (Canning 1981) was adopted in the development of the application and Java, JSP and html were used for programming the application. All the tools were supported by the Fact++ reasoner. The application consisted of a multi-entry key for species identification, tools for querying hosts that a given species could attack, and also species that could be attracted by a selected attractant. The key allowed selection of features from an observation and querying for the


Your request completed successfully.

ScutellumWithFiveBlackSpotsIDFeature
ScutellumWithFourMarginalSetaeIDFeature
ScutellumWithThreeBlackApicalSpotsIDFeat
ScutellumWithThreeBlackSpotsIDFeature
ScutellumWithThreeLargeDarkSpotsIDFeatu
ScutellumWithTwoMarginalSetaeIDFeature
ScutellumWithTwoSmallDarkSpotsIDFeature
ScutellumYellowIDFeature
ScutellumYellowWavyBandIDFeature
ScutellumYellowWavyBandOnlyAcrossBase
ScutellumYellowWithBlackSpotsIDFeature
ScutellumYellowWithNarrowBlackBandatBas
ScutellumYellowandBlackIDFeature

MidLegThickFeatheringLegIDFeature
OrbitalSetaeNotKiteLikeIDFeature
ScutellumWithThreeBlackSpotsIDFeatu

1. CeratitisAnonaeGraham
2. CeratitisColaeSilvestri
3. CeratitisBremiil

Fig. 11.5 Key sample prototype

Your request completed successfully.

Hosted By - Anacardium Occ ▾

Fruit fly Species Hosted by selected plant: AnacardiumOccidentale

1. BactoceraInvadens
2. CeratitisCapitata
3. CeratitisRosaKarsch

Fig. 11.6 Species hosted by selected host plant prototype

species that have all the selected features. The basic interface for the key is as shown in Fig. 11.5.

The tool for querying species that affect a particular host plant consists of an interface where the user can select the host plant name and search for the fly species that the host can support. An example of fruit fly species hosted by cashew, *Anacardium occidentale* L., was queried as shown in Fig. 11.6. Querying for fly species attracted to a given attractant uses a similar interface. By selecting an attractant, it is possible to view the fly species that it can lure. All these tools incorporate the services of a reasoner and therefore use both explicit and implicit facts represented in the ontology to answer questions.

4 Discussion and Further Work

In this chapter, we have presented ontological modeling of knowledge on fruit fly biology and management. The targeted knowledge includes that which can be reasoned upon to provide guidance on management options, including knowledge on identification of species, attractants that lure different species and the host plants that can be attacked by different species. The outcome of this modelling is an ontology containing knowledge on thirty species of fruit flies of economic importance in Africa.

The contributions of this study include, amongst other things, mechanisms to incorporate reasoning into applications that support user access to knowledge on fruit flies. Use of the ontology should reduce the difficulties that non-experts find in understanding these areas of knowledge since the ontological knowledge allows incorporation of reasoning services to provide answers to questions asked over the knowledge base. Another use will be to facilitate tools for collecting user feedback in a structured manner since the ontology exists as a reusable artifact, thus making it possible to collect useful feedback to enhance scientific research. A prototype application that uses the ontology as discussed above is presented and the tools that were developed in the prototype include an ontology-based multi-entry taxonomic key, querying of fruit flies that are attracted to a given attractant and querying of those that are hosted by a given plant species.

It is envisaged that the ontology will be included in the development of an online Web-based platform that supports online collaboration between citizens and scientists in fruit fly biology and management. The platform will use the ontology to enable citizen access to expert knowledge. In future we intend to extend the ontology to capture knowledge on survival environments for the different species of fruit flies. We also intend to develop tools that facilitate creation and editing of this kind of ontology by biologists. This will facilitate knowledge sharing amongst stakeholders without the need to engage specialists in ontological modelling.

References

Allwood AJ, Drew RAI (1997) Management of fruit flies in the Pacific. A regional symposium, Nadi, Fiji 28–31 October 1996. In: Management of fruit flies in the Pacific. A regional symposium, Nadi, Fiji 28–31 October 1996. Australian Centre for International Agricultural Research (Australia)

Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, Davis AP, Dolinski K, Dwight SS, Eppig JT, Harris MA (2000) Gene ontology: tool for the unification of biology. Nat Genet 25:25–29

Badii KB, Billah MK, Afreh-Nuamah K, Obeng-Ofori D, Nyarko G (2015) Review of the pest status, economic impact and management of fruit-infesting flies (Diptera: Tephritidae) in Africa. Afr J Agric Res 10:1488–1498

Bard JB, Rhee SY (2004) Ontologies in biology: design, applications and future challenges. Nat Rev Genet 5:213–222

Billah MK, Mansell MW, De Meyer M, Goergen G (2007) Fruit fly taxonomy and identification. In: Billah MK, Ekesi S (eds) A field guide to the management of economically important tephritid fruit flies in Africa, 2nd edn. icipe Science Press, H1-H32

Bonney R, Cooper CB, Dickinson J, Kelling S, Phillips T, Rosenberg KV, Shirk J (2009) Citizen science: a developing tool for expanding science knowledge and scientific literacy. Bioscience 59:977–984

Canning RG (1981) Developing systems by prototyping. EDP Anal 19:1–14

Corcho O, Fernández-López M, Gómez-Pérez A (2003) Methodologies, tools and languages for building ontologies. Where is their meeting point? Data Knowl Eng 46:41–64

de Bon H, Huat J, Parrot L, Sinzogan A, Martin T, Malézieux E, Vayssières J-F (2014) Pesticide risks from fruit and vegetable pest management by small farmers in sub-Saharan Africa. A review. Agron Sust Devel 34:723–736

Delaney DG, Sperling CD, Adams CS, Leung B (2008) Marine invasive species: validation of citizen science and implications for national monitoring networks. Biol Invasions 10:117–128

Dominiak BC, Ekman JH (2013) The rise and demise of control options for fruit fly in Australia. Crop Prot 51:57–67

Ekesi S (2010) Combating fruit flies in eastern and southern africa (COFESA): elements of a strategy and action plan for a regional cooperation program. International Centre of Insect Physiology and Ecology, Nairobi/Kenya, pp 9–11

Ekesi S, Muchugu E (2007) Tephritid fruit flies in Africa – fact sheet of some economically important species. In: Billah MK, Ekesi S (eds) A field guide to the management of economically important tephritid fruit flies in Africa, 2nd edn. icipe Science Press, B1-B20

Ekesi S, Maniania NK, Mohamed SA, Lux SA (2005) Effect of soil application of different formulations of *Metarhizium anisopliae* on African tephritid fruit flies and their associated endoparasitoids. Biol Contr 35:83–91

Gennari JH, Musen MA, Fergerson RW, Grosso WE, Crubézy M, Eriksson H, Noy NF, Tu SW (2003) The evolution of Protégé: an environment for knowledge-based systems development. Int J Hum Comput Stud 58:89–123

Gerber A, Eardley C, Morar N (2014) An ontology-based taxonomic key for Afrotropical bees. In: Garbacz P, Kutz O (eds) Formal ontology in information systems, vol 267. Ios Press, Amsterdam, pp 277–288

Gruber TR (1993) A translation approach to portable ontology specifications. Knowl Acquisi 5:199–220

Grüninger M, Fox MS (1995) Methodology for the design and evaluation of ontologies. In: Proceedings of the workshop on basic ontological issues in knowledge sharing. IJCAI-95

Guarino N, Oberle D, Staab S (2009) What is an ontology? In: Staab S, Studer R (eds) Handbook on ontologies. Springer, Berlin, pp 1–17

Horridge M, Jupp S, Moulton G, Rector A, Stevens R, Wroe C. (2009) A practical guide to building OWL ontologies using protégé 4 and CO-ODE tools edition1. 2. *The University of Manchester* 107

Iqbal R, Murad MAA, Mustapha A, Sharef NM (2013) An analysis of ontology engineering methodologies: a literature review. Res J Appl Sci Eng Technol 6:2993–3000

Jones D, Bench-Capon T, Visser P (1998) Methodologies for ontology development. In: Proceedings of IT&KNOWS conference, XV IFIP world computer congress

Karns DR, Ruch DD, Brodman RD, Jackson MT, Rothrock PE, Scott PE, Simon TP, Whitaker JO Jr (2006) Results of a short-term BioBlitz of the aquatic and terrestrial habitats of Otter Creek, Vigo County, Indiana. Proc Indiana Acad Sci 115:82–88

Kunne W, Mulligan K, Null G, Simons P, Simons R, Smith B, Willard D (1982) Parts and moments: studies in logic and formal ontology. Retrieved from http://ontology.buffalo.edu/smith/book/P&M/

Lewington RJ, West CJ (2008) Otari Bioblitz: detailing vascular plants, mosses and liverworts. Wellington Bot Soc Bull 51:5–23

López FM (1999) Overview of methodologies for building ontologies. In: Proceedings of IJCAI99's workshop on ontologies and problem solving methods: lessons learned and future trends, Stockholm, Sweden, pp 4.1–4.13

Lundmark C (2003) BioBlitz: getting into backyard biodiversity. Bioscience 53:329

Malacrida AR, Gomulski LM, Bonizzoni M, Bertin S, Gasperi G, Guglielmino CR (2007) Globalization and fruitfly invasion and expansion: the medfly paradigm. Genetica 131:1–9. http://doi.org/10.1007/s10709-006-9117-2

Manrakhan A (2007) Fruit fly monitoring – purpose tools and methodology. In: Billah MK, Ekesi S (eds) A field guide to the management of economically important tephritid fruit flies in Africa, 2nd edn. *icipe* Science Press, C1-C17

Manrakhan A, Kotze C, Daneel J-H, Stephen PR, Beck RR (2013) Investigating a replacement for malathion in bait sprays for fruit fly control in South African citrus orchards. Crop Prot 43:45–53

Nagaraja KS, Gowda VN, Basavarajeshwari SLG, Shabarish PR, Husainnaik M (2014) Effect of protein food baits in attracting fruit flies in mango orchard. Trends Biosci 7:1971–1973

Noy NF, McGuinness DL (2001) Ontology development 101: a guide to creating your first ontology. Stanford knowledge systems laboratory technical report KSL-01-05 and Stanford medical informatics technical report SMI-2001-0880

Noy NF, Crubézy M, Fergerson RW, Knublauch H, Tu SW, Vendetti J, Musen MA (2003) Protégé-2000: an open-source ontology-development and knowledge-acquisition environment. AMIA Annu Symp Proc 953:953

Rubin DL, Noy NF, Musen MA (2007) Protege: a tool for managing and using terminology in radiology applications. J Digit Imag 20:34–46

Rwomushana I, Ekesi S, Gordon I, Ogol CKPO (2008) Host plants and host plant preference studies for *Bactrocera invadens* (Diptera: Tephritidae) in Kenya, a new invasive fruit fly species in Africa. Anns Entomol Soc Amer 101:331–340

Silvertown J (2009) A new dawn for citizen science. TREE 24:467–471

Sivakumar R, Arivoli PV (2011) Ontology visualization protégé tools: a review. Int J Adv Inf Technol 1:1–11. doi:10.5121/ijait.2011.1401

Smith B (2003) Ontology. In: Floridi L (ed) Blackwell companion to philosophy, information and computers. Blackwell, Oxford, pp 155–166

Sullivan BL, Wood CL, Iliff MJ, Bonney RE, Fink D, Kelling S (2009) eBird: A citizen-based bird observation network in the biological sciences. Biol Conserv 142:2282–2292

Tsarkov D, Horrocks I (2006) FaCT++ description logic reasoner: system description. Automated Reasoning. Retrieved from http://link.springer.com/chapter/10.1007/11814771_26

Vargas RI, Walsh WA, Kanehisa D, Stark JD, Nishida T (2000) Comparative demography of three Hawaiian fruit flies (Diptera: Tephritidae) at alternating temperatures. Anns Entomol Soc Amer 93:75–81

Yoder MJ, Miko I, Seltmann KC, Bertone MA, Deans AR (2010) A gross anatomy ontology for Hymenoptera. PLoS One 5:1–8. doi:10.1271/journal.pone.0015991

Caroline Chepkoech Kiptoo is currently a doctoral student at the Department of Informatics, School of Information Technology within the University of Pretoria, South Africa. Her research motivation is in applied computing, particularly the practical application of computing technologies to address challenges in day to day activities. Ms. Kiptoo has experience in information systems development, database systems and development of web based applications. Her research interests are in knowledge technologies, semantic technologies and ontological modelling. She is also interested in crowd computing and more specifically crowdsourcing techniques. Her current practical application areas include biodiversity informatics, knowledge management and knowledge transfer.

Aurona Gerber is an Associate Professor in the Department of Informatics in the Engineering, Build Environment and Information Technology (EBIT) faculty of the University of Pretoria. Her primary interest is research in to the development and use of models and modelling languages (including formal ontologies) within all aspects of Information Systems including Enterprise Architecture and Engineering. She is also interested in IS research methodologies, specifically Design Science Research. She has published more than 50 accredited publications as well as supervised several Masters and Doctoral students to completion. She is current Chapter Chair of the IEEE SMC South African Chapter, as well as Co-chair and founder of the International Technical Committee of the IEEE SMC on Enterprise Architecture and Engineering (EAE TC). She is a member of the AIS and a board member the SA Chapter of the AIS (AISSAC). She is also a board member of SAICSIT (the South African Institute for Computer Scientists and Information Technologists).

Alta Van der Merwe is currently the Head of Department in the Informatics Department within the School of Information Technology, University of Pretoria. She focuses on the design of socio-technical solutions with research activities in Enterprise Architecture, Data Science and different theories supporting the successful use of technology in the organization. Her interest also includes the design of systems using innovative and new approaches such as Crowd Sourcing and Content Awareness. Prof van der Merwe is serving her second term as president of the South African Institute of Computer Scientists and Information Technologists. She is the founder and past chair of the South African IEEE SMCS Chapter, specialist editor of the SAIEE journal (Software Engineering track) and co-founder and past chair of the Enterprise Architecture Research Forum (EARF). On the international level she was involved in the proposal and acceptance of the IEEE SMC Enterprise Engineering and Enterprise Architecture Technical Committee, where she still serves as co-chair.