

Interoperability between phenotype and anatomy ontologies

Robert Hoehndorf^{1,2,*}, Anika Oellrich¹ and Dietrich Rebholz-Schuhmann¹¹European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD and²Department of Genetics, University of Cambridge, Downing Street, Cambridge, UK

Associate Editor: Jonathan Wren

ABSTRACT

Motivation: Phenotypic information is important for the analysis of the molecular mechanisms underlying disease. A formal ontological representation of phenotypic information can help to identify, interpret and infer phenotypic traits based on experimental findings. The methods that are currently used to represent data and information about phenotypes fail to make the semantics of the phenotypic trait explicit and do not interoperate with ontologies of anatomy and other domains. Therefore, valuable resources for the analysis of phenotype studies remain unconnected and inaccessible to automated analysis and reasoning.

Results: We provide a framework to formalize phenotypic descriptions and make their semantics explicit. Based on this formalization, we provide the means to integrate phenotypic descriptions with ontologies of other domains, in particular anatomy and physiology. We demonstrate how our framework leads to the capability to represent disease phenotypes, perform powerful queries that were not possible before and infer additional knowledge.

Availability: <http://bioonto.de/pmwiki.php/Main/PheneOntology>

Contact: rh497@cam.ac.uk

Received on July 23, 2010; revised on September 13, 2010; accepted on October 9, 2010

1 INTRODUCTION

Large-scale genomics research increasingly includes the collection of phenotypic information to infer disease states from genetic conditions. Similarly, evolutionary studies heavily rely on phenotypic descriptions across species. Several biomedical databases collect and organize phenotypic information (Bult *et al.*, 2008; Firth *et al.*, 2009; The Flybase consortium, 1999). To integrate this information across different domains and databases and to communicate the data to the research community, phenotype ontologies were developed which formalize the meaning of terms used to characterize phenotypes (Gkoutos *et al.*, 2004b; Robinson *et al.*, 2008; Smith *et al.*, 2004).

Ontologies are specifications of a conceptualization of a domain (Gruber, 1993) and are used to make the meaning of terms in a vocabulary explicit (Guarino, 1998) such that they can be used for consistency verification, information retrieval and knowledge discovery. At least two kinds of phenotype ontologies can be distinguished: ontologies in which each term contains one specific phenotypic trait (Robinson *et al.*, 2008; Smith *et al.*, 2004), and ontologies and methods that permit the composition of a term

through the combination of an entity and a quality (Gkoutos *et al.*, 2004a, b; Mungall *et al.*, 2010). Each of these approaches describes a phenotype through *qualities* that are attributes of an *entity*. For example, a size of an arm would be described as a quality *Size* which is the quality of *Arm*.

In addition to these qualities, phenotype ontologies contain classes describing absence and presence of parts, functions, dispositions and processes, as well as *abnormality*. Currently, these features are also represented as qualities and rarely further analyzed. In particular, the attribution of qualities like *Absent* or *Dysfunctional* does not yet enable inferences about the parts or functions of an entity. Consequently, these approaches fail to interoperate with anatomy or physiology ontologies. If, however, the meaning of these qualities would be made explicit and classes like *Absent* or *Dysfunctional* characterized in terms of the **has-part** and **has-function** relations, information flow between phenotype and anatomy or physiology ontologies would be possible, thereby leading to a semantic integration of these ontologies and the capability for expressive queries.

As anatomy ontologies often represent *canonical*, prototypical organisms, inconsistencies may arise when they are combined with phenotype ontologies (Hoehndorf *et al.*, 2007). For example, an anatomy ontology may contain a statement that asserts that every human has an appendix as part, while a phenotypic description of a human may assert that this human has no appendix as part. Because inconsistencies prevent query answering and semantic interoperability, a framework for phenotypic descriptions must accommodate statements about deviations from reference models without leading to inconsistencies.

We provide a method to make the intended meaning of phenotypic descriptions explicit and interoperable with anatomy and physiology ontologies. For this purpose, we first provide the means to formalize phenotypic traits while reusing classes and relations from other ontologies. Based on this formalization, we describe how to consistently integrate phenotypic descriptions with canonical ontologies and demonstrate how our method leads to expressive and flexible descriptions of disease phenotypes as well as the possibility for automated inference and knowledge discovery. We applied our method to examples taken from phenotype ontologies and provide an example ontology which is available from our project web site.

Our framework for formalizing phenotypic descriptions is based on the Web Ontology Language (OWL; Motik *et al.*, 2009). OWL is based on an expressive, decidable fragment of first-order logic and provides the foundation for the Semantic Web. To maintain compatibility with currently established methods for representing phenotypes and reuse the data that has been annotated with it, we also demonstrate an implementation in the OBO Flatfile Format.

*To whom correspondence should be addressed.

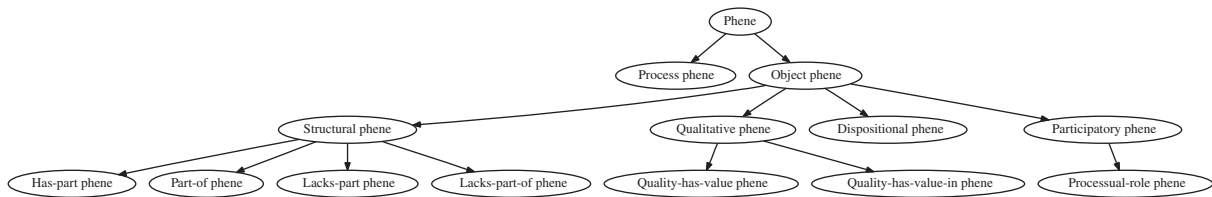


Fig. 1. The first distinction is drawn between phenes of objects and phenes of processes. We primarily classify phenes of objects into four main categories: structural, functional, qualitative and participatory phenes. Under the structural phenes, we show possible further classifications based on the relations we use in our method. Qualitative phenes can be further distinguished into those where only the quality is relevant and those where the quality's value is considered.

2 SYSTEMS AND METHODS

2.1 Overview

An organism is composed of organs, cells and other structural components. The variability of the structural components can be observed and described with the Entity–Quality (EQ) representation based on the Phenotypic Attribute and Trait Ontology (PATO; Gkoutos *et al.*, 2004a; Mungall *et al.*, 2010). Beyond the structure of organisms and its variability, we can observe processes in which the organism and its anatomical parts may participate. These processes may lead to changes in the structure or its variability in response to the organism's requirements. Developmental processes and functions such as growth and synaptic plasticity serve to change the organisms' structure and consequently lead to new dispositions. Furthermore, all living beings have to adapt to their environment and therefore expose responses in terms of changes to their structure and functioning. Structure and function form dual components (Hoehndorf *et al.*, 2010a; Wright, 1973) in a system that describes the complexity of the phenotypes.

Many aspects of this complex network of interdependencies can currently be captured using biomedical ontologies. For example, the components and parts of organisms are described in anatomy ontologies such as the Foundational Model of Anatomy (FMA; Rosse and Mejino, 2003) or the cellular component branch of the Gene Ontology (GO; Ashburner *et al.*, 2000). Organismal, cellular and molecular processes are described in the biological process branch of the GO, developmental anatomy ontologies are available for various species (Bult *et al.*, 2008; Tweedie *et al.*, 2009) and environmental features can be characterized with the Environment Ontology (Environment Ontology Consortium, 2008).

An ontological framework for phenotypes should enable the description of this variability and complexity, and interoperate with the existing ontologies and resources that were developed for it. In particular, a framework for representing phenotypes should enable the inference of consistent dependencies between different aspects in this network of dependencies, and provide for the detection of inconsistencies in the phenotypic description of an organism.

We first define a uniform framework for characterizing phenotypic properties of entities. For this purpose, we introduce the concept of *phene* that allows to make the semantics of an entity's features explicit and accessible to automated reasoning. As phenotypic characterizations are usually done comparatively with respect to the features of another reference entity, we show how to use the phene concept to facilitate interoperability of phenotypic descriptions with reference ontologies in biomedicine. In particular, we demonstrate how to formally represent and infer normality and abnormality. Based on the development of our formal framework for representing phenotypic information, we demonstrate how to apply it to knowledge discovery and querying across the diversity of knowledge resources containing phenotypic information.

2.2 Formalizing phenotypic traits

We define *phene* as a basic characteristics possessed by an organism. Phenens are attributive entities which are existentially dependent on a bearer, and phenens characterize the properties of their bearer. Therefore, we formally

define phenens as the properties that are possessed by 'entities which are *Y*', and express *Y* as class-membership in description logic, or as a unary predicates in first-order logic. We call *Y* the *defining property* of a phene.

The defining property of a phene characterizes the phene's bearer, and therefore we can distinguish different kinds of phenens based on the relations that are necessary to formulate this characteristic. For example, a class of phenens, such as *producing endorphines*, refer to participation in processes of a certain kind. A large portion of phenens refer to ontological qualities: *being cyanotic*, *being 7.5µm* in size. Further phenens are structural, such as having or not having certain parts, refer to topology (being connected in a certain way) or to dispositions (being able to hear). To analyze and distinguish these differences, we derive a top-level classification of phenens based on the relations that are necessary to formulate their defining properties. Figure 1 gives an overview of this top-level classification.

2.2.1 Structural phenens *Structural phenens* are based on the mereological relation **part-of**. The defining property of structural phenens is expressed using the **part-of** or **has-part** relation. Examples of structural phenens are *present spleen* and *absent spleen* which are defined as phenens of things which have (or do not have) a spleen as part:

```

Present_spleen equivalentTo:
    phene-of some (has-part some Spleen)
Absent_spleen equivalentTo:
    phene-of some (not has-part some Spleen)
  
```

The defining property is `has-part some Spleen` and `not has-part some Spleen`, and the instances of the defining property are entities that either have or do not have a spleen as part. Because our definition of these phenens uses the **has-part** relation, we can combine phenotypic information with anatomical information, thereby establishing an informative link between both.

2.2.2 Qualitative phenens Another group of phenens represents ontological qualities and we call them *qualitative phenens*. Qualities are related to their bearer by the **inheres-in** relation and its inverse **has-quality**. We can express qualitative phenens using our definition pattern in a similar way as structural phenens: as phenens of things in which a certain quality inheres. For example, the phene *being cyanotic* is represented as a phene of things which have the quality (**has-quality**) *cyanotic*. We can further refine this by distinguishing qualities from their values and relate both used the **value-of** and **has-value** relations. Then, *being cyanotic* is represented as a phene of things that have a color within a certain value range.

2.2.3 Function and disposition phenens Another group of phenens is related to functions and disposition of entities, and can be expressed using the **has-function**, **function-of**, **has-disposition** and **disposition-of** relations. We call these *dispositional phenens*. Intuitively, functions of biological entities establish the *reason* (or cause) that an entity exists (Wright, 1973) while their dispositions determine their capabilities and potentials (Lewis, 1997). For example, the endocrine pancreatic cells have a function to produce insulin, and normally have a disposition to produce insulin.

In many cases, neither functions nor dispositions are explicitly included in ontologies, but rather the processes that **realize** these functions or dispositions. Therefore, dispositional phenes will often be represented using the **has-function-realized-by** or **has-disposition-realized-by** design patterns (Hoehndorf et al., 2010a). Using these, a relation between a class C and a class of processes P is established such that every instance of C has a function (or disposition) that is only realized by processes of the kind P . For example, the endocrine pancreatic cells have a function to produce insulin which is realized through *insulin production* processes. The processes that result from the realizations of functions are called *functionings* (Johansson, 2004).

2.2.4 Functionings and processes An organism or anatomical structure may participate in certain processes, for example in physiological, metabolic or developmental processes, or in the organism's activities. To participate in these processes is a *participatory phene*. Participatory phenes are represented with the **participates-in** and **has-participant** relations. Furthermore, we can distinguish different modes of participation for a phene of a process participant and thus determine *how* an entity participates in a process. We represent these phenes with the relation **plays-processual-role** (Loebe, 2005). For example, the sinoatrial nodes participate in blood pumping processes and play the processual role of an initiator of the rhythmic excitation of the heart muscle.

Apart from the phenes of process participants, we can distinguish a second kind of phene which represents characteristics of the processes themselves. We call this kind the *process phenes*, and they include characteristics of physiological processes, metabolic processes, biological pathways, chemical reactions and their parts. These processes can have attributes such as duration or a heart beat rate, they can have parts or participants. Although some aspects of our classification of phenes can also be applied to process phenes, we leave a detailed classification of process phenes as subject to future work.

2.2.5 The logic of phenes

Axioms for classes and relations: phenes are related to their bearers using the **phene-of** and **has-phene** relations. Because phenes are existentially dependent on their bearer, phenes are always the **phene-of** some entity. Furthermore, **phene-of** is functional, i.e. a phene belongs to at most one entity. Therefore, the following restriction holds for the class *Phene*:

```
Phene subclassOf: phene-of exactly 1 Thing
```

The domain of the **phene-of** relation is the class *Phene*, while the range is `owl:Thing`, i.e. the class of all things. The relation **has-phene** is the inverse of the **phene-of** relation, i.e. whenever an individual x is the **phene-of** an individual y , then y stands in the **has-phene** relation to x . Because **phene-of** is functional, and **has-phene** is inverse functional.

Applying phenes to entities. a particular class of phenes P is defined with respect to a defining property Y of its bearers. Therefore, the definition pattern for phenes is

```
P subclassOf: phene-of some Y
```

or

```
P equivalentTo: phene-of some Y
```

Because the **phene-of** relation is functional and the **has-phene** relation inverse functional, the following is true: if an individual i is the bearer of a phene of the kind P , i is an instance of Y .

For example, we have defined the phene *Absent spleen* as the phene of things that have no *Spleen* as part. Based on this phene, we can define a class of *Human without spleen* as:

```
Human_without_spleen equivalentTo:
  Human and has-phene some Absent_spleen
```

Based on the inference rules for OWL, we can show that this definition is equivalent to

```
Human_without_spleen equivalentTo:
  Human and has-phene some (phene-of some
    (not has-part some Spleen))
```

and due to the functionality of **phene-of** and the inverse functionality of **has-phene**, this is equivalent to

```
Human_without_spleen equivalentTo:
  Human and (not has-part some Spleen)
```

Composing complex phenes: besides applying phenes to entities, we can introduce intersections and unions of phenes to form *complex phenes*. Due to the axioms for the **phene-of** and **has-phene** relations, intersections and unions of phenes correspond to intersections and unions of the defining properties of these phenes: when the class of phenes P_1 is based on the defining property Y_1 , and P_2 based on Y_2 , then the complex phene P_1 and P_2 is based on the defining property Y_1 and Y_2 .

For example, in addition to the *Absent spleen* phene we define *Absent kidney* similar to *Absent spleen*. Then, we can define a complex phene *Absent spleen and absent kidney* (ASAK):

```
ASAK equivalentTo: Absent_spleen and Absent_kidney
```

Through inference, we can show that this definition is equivalent to

```
ASAK equivalentTo:
  phene-of some (not has-part some Spleen)
  and
  phene-of some (not has-part some Kidney)
```

and due to the functionality of the **phene-of** relation, this is equivalent to

```
ASAK equivalentTo: phene-of some
  ((not has-part some Spleen)
  and
  (not has-part some Kidney))
```

The defining property of ASAK is not defined based on either of the relations in our ontology of phenes, and therefore it is not a primitive phene. However, through inference we can show that ASAK becomes a subclass both of *Absent spleen* and *Absent kidney*.

Reasoning with phenes: phenes can be used to infer additional knowledge and verify consistency. The simplest case is a contradictory application of phenes, e.g. an individual organism with both the *Absent spleen* and *Present spleen* phene. Due to the definition of both phenes, such an assertion would be inconsistent and can be automatically detected using automated inference.

More importantly, phenes can make use of the information in ontologies to infer that other phenes must hold as well. For example, when integrated with an anatomy ontology like the FMA, the phene *Absent spleen* entails the *Absent serosa of spleen* phene, because *Serosa of spleen* (FMA:15848) must be a **part-of** some *Spleen* according to the FMA. Similar entailments hold for relations between anatomical entities and their functions. For example, if endocrine pancreatic cells are the only cells with a function to secrete insulin, their absence can entail the absence of insulin secretion.

2.3 Phenens and comparative descriptions

Phenes are properties of entities and phenes whose defining property involves negation can be attributes of a large number of entities. Therefore, phenes alone should rarely be used to describe the set of phenotypic characteristics of an organism.

As phenotypic descriptions are often comparative statements with respect to a reference model, either a model of normality, a control group, another organism or similar, we can exploit these descriptions to record phenes that characterize deviations from such a reference model. In particular, we show how to integrate phenes with *canonical ontologies*, although other artifacts can serve as reference models as well.

2.3.1 Interoperability with canonical ontologies Canonical ontologies are those that serve as reference models within their domain and characterize prototypical, idealized entities (Smith and Rosse, 2004). Phenotypic descriptions and representations should interoperate with such resources and use them to infer knowledge and verify consistency.

When phenes are combined with canonical ontologies, inconsistencies and unsatisfiable classes may arise (Hoehndorf *et al.*, 2007). For example, the FMA states that every *Human* has a *Spleen* as part. Characterizing an instance of *Human* *h* with the *Absent spleen* phene will lead to an inconsistency: as an instance of *Human*, *h* must stand in the **has-part** relation to some instance of *Spleen*; because *h* has a phene of the *Absent spleen* type, *h* must not have an instance of *Spleen* as part.

For the purpose of integrating canonical ontologies and the phene method, we restructure canonical ontologies to explicitly state that they describe only canonical entities. For example, instead of stating that every human has a spleen as part, we restructure the corresponding anatomy ontology to state that every *canonical* human has some *canonical* spleen as part.

For phenotypic descriptions, we need to describe *non-canonicity* in a flexible way, and we have at least two choices: the *non-canonicity of the spleen* could either be the absence of a canonical spleen or the presence of a non-canonical spleen. The first choice is more general, as it allows both for the presence of a non-canonical spleen as well as for the absence of the spleen. Therefore, we adopt this option and define a non-canonicity of the spleen as a phene of things that have no canonical spleen as part. A non-canonicity is different from an *absence* of the spleen, which is a phene of things which have *no* spleen as part, whether canonical or not. An absence of the spleen automatically becomes a subcategory of a non-canonicity of the spleen according to this definition.

Formally, we introduce two new unary predicates called *C* and *NC* (for canonical and non-canonical, respectively). In description logics, both *C* and *NC* are classes. *C* and *NC* are disjoint and exhaustive, i.e. everything is either *C* or *NC* but not both. Based on these classes, we restructure canonical ontologies such that all occurrences of class symbols *X* are replaced with *X* and *C*. Biomedical ontologies consist to a large portion of statements of the kind *X* `subClassOf: R some Y` (Horrocks, 2007). Assertions of this kind are consequently replaced with *X* and *C* `subClassOf: R some (Y and C)`. For example, the FMA statement that all *Humans* have a *Spleen* as part (`Human subClassOf: has-part some Spleen`) is replaced by 'all canonical humans have a canonical spleen as part' (`Human and C subClassOf: has-part some (C and Spleen)`). This replacement can be performed automatically using the OWLDEF method (Hoehndorf *et al.*, 2010b).

Based on these definitions, we can formally define a non-canonicity of the spleen (NCOS):

```
NCOS EquivalentTo: phene-of some (not has-part some
    (Spleen and C))
```

Following our pattern, we can define a human with an *NCOS* as

```
NCOS-Human EquivalentTo: Human and hasPhene
    some NCOS
```

from which we derive, using deductive reasoning in OWL, that an *NCOSHuman* has no canonical spleen as part. We can also prove that a *NCOSHuman* is a subclass of a non-canonical human, i.e. of *Human* and *NC*, because canonical humans must have a canonical spleen as part.

We demonstrate these features in an OWL ontology that formalizes abnormality and absence of the appendix, liver and β -cells. The demonstration ontology is available from our project website.

3 IMPLEMENTATION

A large portion of our method is based on description logic and the Web Ontology Language (OWL) (W3C OWL Working Group,

2009). Using OWL has the advantage that the myriad of software tools, methods and libraries that have been developed for the Semantic Web can be reused with the method. In particular, OWL has an explicit semantics that makes it amenable for automated reasoning. However, many biomedical ontologies are developed using the OBO Flatfile Format (Horrocks, 2007). For our method to be successful, we provide an implementation in the OBO Flatfile Format that is compatible with the description logic treatment of phenes and phenotypes put forward in this manuscript. For this purpose, we use the OWLDEF method (Hoehndorf *et al.*, 2010b) to provide OWL definitions for relations in the OBO Flatfile Format. These relations follow our top-level ontology of phenes and are listed in Table 1.

4 DISCUSSION

4.1 Towards canonical disease phenotypes

We envision one application of our method to provide a means for representing canonical disease states. For this purpose, we introduce the notion of *canonical disease phenotype*: a complex phene which is the combination of those phenes that constitute the idealized or *canonical* form of a disease. Some of the phenes in a disease phenotype are dispositional, while others relate to qualities, absence or presence of body parts and participation in physiological processes.

To characterize disease phenotypes further and utilize the existing ontologies for automated inferences and knowledge discovery, several domains have yet to be covered by canonical ontologies so that they can serve as a bridge that links existing resources. Table 2 provides an overview of available and missing resources and their relation to our method.

To infer and reason over developmental abnormalities, a developmental anatomy must be available. There are developmental anatomies for several model organisms (Segerdell *et al.*, 2008; Tweedie *et al.*, 2009). To describe human developmental defects, a human developmental anatomy ontology integrated with the FMA would be beneficial as reference model on which deviations can be based. Similarly, to describe missing, abnormal or additional dispositions and functions, a functional anatomy ontology should be developed. Although there are approaches to construct such a resource (Hoehndorf *et al.*, 2010a; Johansson *et al.*, 2005), no comprehensive ontological resource for anatomical functions has been developed so far. Similarly, almost no ontologies for canonical physiology are currently available.

To describe qualitative phenes such as those relating to color or size, qualitative descriptions can be added to anatomy ontologies. For this purpose, it is important to use ranges of values for qualities, because values for qualities are often highly variable. Using the phene method, it would further be beneficial to describe the qualities of the wild type or control group in genetic experiments. This has the additional benefit of providing additional documentation to an experiment. Such a documentation can increase the interoperability with ontologies of investigations such as the Ontology of Biomedical Investigations (OBI; Courtot *et al.*, 2008).

The method we propose can be used to represent and infer dependencies between phenotypic traits and verify the consistency of descriptions of phenotypes. For example, the absence of liver cells entails that they cannot have qualities or functions, because both

Table 1. List of relations defined using the OWLDEF method

Relation	OWLDEF	Example
CC-pheneOf-has-part	?X subclassOf: Phene and pheneOf some (has-part some ?Y)	Having an appendix as part
CC-pheneOf-lacks-part	?X subclassOf: Phene and pheneOf some not (has-part some ?Y)	Not having an appendix as part
CC-pheneOf-part-of	?X subclassOf: Phene and pheneOf some (part-of some ?Y)	Being part of an appendix
CC-pheneOf-not-part-of	?X subclassOf: Phene and pheneOf some not (part-of some ?Y)	Not being part of an appendix
CC-pheneOf-has-quality	?X subclassOf: Phene and pheneOf some (has-quality some ?Y)	Having a color
CC-pheneOf-lacks-quality	?X subclassOf: Phene and pheneOf some not (has-quality some ?Y)	Not having a size
CC-pheneOf-has-quality-value-of	?X subclassOf: Phene and pheneOf some (has-quality some (?Y and has-value some ?Z))	Having color #4F1A33 (in RGB color space)
CC-pheneOf-lacks-quality-value-of	?X subclassOf: Phene and pheneOf some (has-quality some (?Y and not (has-value some ?Z)))	Not having a mass of 0.12g
CC-pheneOf-has-quality-value-in	?X subclassOf: Phene and pheneOf some (has-quality some (?Y and has-value-in some ?Z))	Being between 1.2 and 1.7 m in height
CC-pheneOf-lacks-quality-value-in	?X subclassOf: Phene and pheneOf some (has-quality some (?Y and not (has-value-in some ?Z)))	Not having between 13 and 18 gm/dl hemoglobin concentration
CC-pheneOf-has-disposition	?X subclassOf: Phene and pheneOf some (has-disposition some ?Y)	Being able to hear
CC-pheneOf-lacks-disposition	?X subclassOf: Phene and pheneOf some not (has-disposition some ?Y)	Not being able to hear
CC-pheneOf-has-disposition-realized-by	?X subclassOf: Phene and pheneOf some (has-disposition some (realized-by only ?Y))	Being able to hear
CC-pheneOf-lacks-disposition-realized-by	?X subclassOf: Phene and pheneOf some not (has-disposition some (realized-by only ?Y))	Not being able to hear
CC-pheneOf-plays-p-role	?X subclassOf: Phene and pheneOf some (plays-p-role some ?Y)	Playing the role of catalyst within some process

Table 2. The table lists dependencies between different kinds of phenes, and resources which are necessary to formally represent them

Type	Provides	Dependencies	Relevant resources	Missing resources	Example 1: Diabetes	Example 2: Coagulation
Structural	Components composing the organism, both macroscopic and microscopic. Topology of structures.	Structures can be part of larger structures and are the result of developmental processes	FMA, GO-CC	Developmental anatomy (human)	β -cells in the pancreas	Liver cells
Quality	Attributes of the structures, observables pertaining to the variability of the structures	Qualities are existentially dependent on their bearers.	PATO, HPO, MPO	Qualities of anatomical entities	Reduced amount of β -cells in the pancreas	Liver cells are reduced and increased in size, increased fatty acid vacuoles
Functional and dispositional	Capabilities of the structures	Functions and dispositions are existentially dependent on a bearer	GO-MF	Anatomical functions	Function of β -cells to produce insulin	Function to produce coagulation factors
Process	Functionings of the structures, changes in the structures and the organism caused through functionings; physiology	Processes require structures as participants, and result from functionings of anatomical structures	GO-BP, FMA, functional systems	Physiology, metabolism	Import of glucose into muscle cells, reduction of lipid catabolism	Coagulation

qualities and functions are dependent on a bearer. Consequently, physiological processes that rely on liver cells' functionings will be impaired. Similarly, the absence of insulin producing β cells will prevent them from exerting their function, leading to a disruption in glucose metabolism and consequently an increased concentration of glucose in the blood. Because phenes make the semantics behind

phenotypic traits explicit, these interrelations can be asserted or inferred, depending on the information present in the corresponding canonical ontologies. In addition, if β cells are absent, they may not be increased in size or have dispositions, and making such an assertion would lead to an inconsistency that can be automatically detected.

Although the phene method intends to provide a semantic framework for representing phenotypic information, it can also be applied to other domains such as representing clinical information. In particular, canonical disease phenotypes are similar to *canonical conceptual graphs* which are used in the Canon Group's model to represent prototypical clinical findings (Friedman *et al.*, 1995). Consequently, the phene method is currently being applied to represent the canonical disease phenotypes of primary immunodeficiency diseases in the PID Ontology (Adams *et al.*, 2010).

4.2 Phenes and the EQ formalism

The phene method can provide a semantics for the Entity-Quality (EQ) formalism and make it amenable to automated reasoning. EQ is currently widely used to annotate and formalize phenotypes and phenotypic descriptions (Mungall *et al.*, 2010), and its formalization states that an EQ statement is equivalent to a *Quality* (Q) that **inheres-in** an *Entity* (E) (Mungall, 2007). This approach is strictly weaker than our method and corresponds to the use of the relation **CC-pheneOf-has-quality** (Table 1) in our method.

The currently employed semantics for EQ has several shortcomings. First, it is based on the assumption that phenotypic characters are qualities. Qualities do not allow to infer further information about other kinds of entities such as parts, functions and processes, and therefore the EQ semantics limits interoperability with other ontologies. For example, having a quality *Lacks all parts of type* (PATO:0002000) or *Lacks function of type* (PATO:0001641) formally conveys no information about the parts or functions of an entity. Even more problematic is the use of the **towards** relation to specify the kind of entity that is absent: in its currently used semantics (Horrocks, 2007), *Absent spleen* is interpreted as a *Lacks all parts of type* quality that is directed **towards** some *Spleen*. In this statement, **towards** is used in an existential restriction over *Spleen*, thereby leading to the inference that an instance of *Spleen* must exist in order to be absent.

The second shortcoming of EQ relates to the combination of qualities, which is important to describe complex phenotypic characteristics or disease phenotypes. In EQ, qualities from PATO are characteristics such as *color* or *length*, and intersections of *color* and *length* would be qualities which are *both* a color and a length at the same time. Such qualities do not exist in the domain of phenotypes. However, combined qualities such as *Absent spleen and absent kidney* are intended to be the qualities of organisms that have both an absent spleen and an absent kidney.

The method we propose overcomes these shortcomings by explicitly defining phenotypic characteristics using relations and classes from other ontologies. In addition, we demonstrated how phenes can be combined through intersections to form complex phenes.

4.3 Normality and abnormality

Being *normal* and being *canonical* are sometimes used synonymously, but we make a distinction between both because canonicity does not always coincide with normality. For example, although the canonical human body represented by the FMA is both male and female (in virtue of having both ovaries and testes as part), *normal* humans are either male or female, but not both. Being both male and female would instead be considered to be *abnormal*.

Additionally, in experiments, *normal* is defined with respect to a control group of organisms, and not directly based on a canonical ontologies. Also, *normal* affects *all* phenes, while canonicity is often restricted to structure, function and physiology. Consequently, a tail size of a mouse may be within a certain *normal* range within a population of mice, *abnormal* within another population, and not considered in a canonical ontology at all. The reason is that *normal* and *abnormal* are statistical, empirical measures, while *canonical* and *non-canonical* are based on prototypical idealizations constructed by humans.

Our method is neutral with respect to these distinctions. We could introduce another set of predicates, *Normal* and *Abnormal*, both of which are neither a sub- nor a super-class of *C* and *NC*. Being *Normal* would, for example, entail being either male or female, but not both. In an ontology of *Normal* humans, sex would either not be considered (when the ontology is open or incomplete in this aspect), or two kinds of humans would be distinguished based on their sex.

An important application is the specification of *Normal* phenes of organisms within the context of an experiment. These phenes can include qualities such as fur color, tail size or similar, i.e. the phenes that are measured within an experiment protocol. Then, an organism or anatomical part of the organism is *Abnormal* if it lies outside the range of values that is considered normal. As for canonical and non-canonical entities, a phene *P* is an abnormality with respect to the *Normal* phene *Q* if having the phene *P* implies not having *Q*.

4.4 Future research

To integrate phenotype and canonical ontologies, we rely on introducing explicit classes for canonicity and non-canonicity. This permits a consistent integration of these ontologies, but has some drawbacks. In particular, when an organism has a single deviation from its canonical form, the organism is non-canonical and inferences from assertions in canonical ontologies cannot be drawn anymore. To prevent this issue, more distinctions than canonical versus non-canonical can be introduced (Rector, 2004). In the future, we plan to integrate our method of representing phenotypes in a framework that supports default reasoning (Hoehndorf *et al.*, 2007).

4.5 Conclusions

We developed a method to represent phenotypic information in ontologies such that the semantics is made explicit. For this purpose, we introduce a category of *phenes*. Phenes are basic observable features of organisms which are defined with respect to a defining property. Defining properties can include absence or presence of parts or functions. This defining property is the feature of phenes that allows to make their semantics explicit and facilitate information flow with other ontologies based on the use of common relations.

Using our method to represent phenotypic information, we suggest a new top-level classification of phenotypic characteristics, based on the relations used in the defining properties of the phenes. The main distinction is between phenes of processes and phenes of objects. Those of objects are further distinguished into structural, qualitative, functional and participatory phenes. The first kind pertain to presence or absence of parts, the second to having qualities or values of qualities within certain ranges. Functional phenes characterize the functionality or dysfunctionality of organisms or their parts. Participatory phenes characterize the participation and the mode of participation of organisms and their parts in processes.

The formal representation of phenotypic information permits the integration of canonical ontologies with phenotype ontologies. For this purpose, canonical ontologies must be re-interpreted as explicitly referring to canonical entities, while phenotype ontologies can refer to either the canonical, the non-canonical or both kinds of entities. This simple restructuring, which can be hidden from ontology users, together with our proposed method enables the representation of canonical disease phenotypes as a means for characterizing disease states.

Altogether, we provide an explicit and formal framework for representing phenotypes that is applicable within biomedical ontologies for reasoning, answering queries and integrating knowledge about domains ranging from molecular biology to medicine. This enables the use of knowledge-based methods to infer, structure, classify and query information about disease and phenotype, thereby facilitating translational research and medicine.

ACKNOWLEDGEMENTS

We thank Nico Adams and George Gkoutos for valuable discussions about phenotypes and their representations.

Funding: This research was funded by the European Bioinformatics Institute.

Conflict of Interest: none declared.

REFERENCES

- Adams,N. et al. (2010) The ontology of primary immunodeficiency diseases (PIDs): using PIDs to rethink the ontology of phenotypes. In Herre,H. et al. (eds) *Proceedings of "Ontologies in Biomedicine and Life Sciences"*, Institute for Medical Informatics, Statistics and Epidemiology (IMISE), University of Leipzig.
- Ashburner,M. et al. (2000) Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nat. Genet.*, **25**, 25–29.
- Bult,C.J. et al. (2008) The mouse genome database (MGD): mouse biology and model systems. *Nucleic Acids Res.*, **36**, D724–D728.
- Courtot,M. et al. (2008) The OWL of biomedical investigations. In Dolbear,C. et al., (eds) *Proceedings of the Fifth OWLED Workshop on OWL: Experiences and Directions*, Vol. 432 of *CEUR Workshop Proceedings*. Available at <http://sunsite.informatik.rwth-aachen.de/Publications/CEUR-WS/Vol-432/> (last accessed date October 29, 2010).
- Environment Ontology Consortium (2008) Environment Ontology (EnvO). Available at: <http://www.obofoundry.org/cgi-bin/detail.cgi?id=envo> (last accessed date October 29, 2010).
- Firth,H.V. et al. (2009) Decipher: database of chromosomal imbalance and phenotype in humans using ensembl resources. *Am. J. Hum. Genet.*, **84**, 524–533.
- The Flybase consortium (1999) The FlyBase database of the Drosophila genome projects and community literature. The FlyBase Consortium. *Nucleic Acids Res.*, **27**, 85–88.
- Friedman,C. et al. (1995) The canon group's effort: working toward a merged model. *J. Am. Med. Inform. Assoc.*, **2**, 4–18.
- Gkoutos,G.V. et al. (2004a) Building mouse phenotype ontologies. *Pac. Symp. Biocomput.*, 178–189.
- Gkoutos,G.V. et al. (2004b) Using ontologies to describe mouse phenotypes. *Genome Biol.*
- Gruber,T.R. (1993) Towards principles for the design of ontologies used for knowledge sharing. In Guarino,N. and Poli,R. (eds) *Formal Ontology in Conceptual Analysis and Knowledge Representation*, Kluwer Academic Publishers, Deventer, The Netherlands.
- Guarino,N. (1998) Formal ontology and information systems. In Guarino,N. (ed.) *Proceedings of the 1st International Conference on Formal Ontologies in Information Systems*. IOS Press, pp. 3–15.
- Hoehndorf,R. et al. (2007) Representing default knowledge in biomedical ontologies: application to the integration of anatomy and phenotype ontologies. *BMC Bioinformatics*, **8**, 377.
- Hoehndorf,R. et al. (2010a) Applying the functional abnormality ontology pattern to anatomical functions. *J. Biomed. Semantics*, **1**, 4.
- Hoehndorf,R. et al. (2010b) Relations as patterns: Bridging the gap between OBO and OWL. *BMC Bioinformatics*, **11**, 441+.
- Horrocks,I. (2007) OBO flat file format syntax and semantics and mapping to OWL Web Ontology Language. Technical report, University of Manchester. Available at: <http://www.cs.man.ac.uk/~horrocks/obo/> (last accessed date October 29, 2010).
- Johansson,I. (2004) Functions, function concepts, and scales. *Monist*, **87**, 96–114.
- Johansson,I. et al. (2005) Functional anatomy: a taxonomic proposal. *Acta Biotheor.*, **53**, 153–166.
- Lewis,D. (1997) Finkish dispositions. *Philos. Q.*, **47**, 143–158.
- Loebe,F. (2005) Abstract vs. social roles: A refined top-level ontological analysis. In Boella,G. et al. (eds) *Proceedings of the 2005 AAAI Fall Symposium 'Roles, an Interdisciplinary Perspective: Ontologies, Languages, and Multiagent Systems'*. AAAI Press, Menlo Park, CA, USA.
- Motik,B. et al. (2009) OWL 2 web ontology language structural specification and functional-style syntax. *Technical report*, W3C.
- Mungall,C. (2007) Representing phenotypes in OWL. In Golbreich,C. et al. (eds) *Proceedings of the OWLED 2007 Workshop on OWL: Experiences and Directions*. Available at <http://sunsite.informatik.rwth-aachen.de/Publications/CEUR-WS/Vol-258/> (last accessed date October 29, 2010).
- Mungall,C. et al. (2010) Integrating phenotype ontologies across multiple species. *Genome Biol.*, **11**, R2+.
- Rector,A.L. (2004) Defaults, context, and knowledge: Alternatives for OWL-indexed knowledge bases. In Altman,R.B. et al. (eds) *Proceedings of the 9th Pacific Symposium on Biocomputing (PSB 2004)*, Hawaii, USA, Jan 6-10, World Scientific, London.
- Robinson,P.N. et al. (2008) The human phenotype ontology: a tool for annotating and analyzing human hereditary disease. *Am. J. Hum. Genet.*, **83**, 610–615.
- Rosse,C. and Mejino,J.L.V. (2003) A reference ontology for biomedical informatics: the Foundational Model of Anatomy. *J. Biomed. Inform.*, **36**, 478–500.
- Segerdell,E. et al. (2008) An ontology for xenopus anatomy and development. *BMC Dev. Biol.*, **8**, 92.
- Smith,B. and Rosse,C. (2004) The role of foundational relations in the alignment of biomedical ontologies. *Medinfo*, **11**, 444–448.
- Smith,C.L. et al. (2004) The mammalian phenotype ontology as a tool for annotating, analyzing and comparing phenotypic information. *Genome Biol.*, **6**, R7.
- Tweedie,S. et al. (2009). Flybase: enhancing drosophila gene ontology annotations. *Nucleic Acids Res.*, **37** (Suppl. 1), D555–D559.
- W3C OWL Working Group (2009) OWL 2 Web Ontology Language: Document overview. *Technical report*, W3C, Cambridge, MA, USA. Available at: <http://www.w3.org/TR/owl2-overview/> (last accessed date October 29, 2010).
- Wright,L. (1973) Functions. *Philos. Rev.*, **82**, 139–168.