

COMPUTING SCIENCE

Scaffolding the Mitochondrial Disease Ontology from extant
knowledge sources

Jennifer D. Warrender and Phillip Lord

TECHNICAL REPORT SERIES

No. CS-TR-1465

May 2015

No. CS-TR-1465

May, 2015

Scaffolding the Mitochondrial Disease Ontology from extant knowledge sources

J. D. Warrender and P. Lord

Abstract

Bio-medical ontologies can contain a large number of concepts. Often many of these concepts are very similar to each other, and similar or identical to concepts found in other bio-medical databases. This presents both a challenge and opportunity: maintaining many similar concepts is tedious and fastidious work, which could be substantially reduced if the data could be derived from pre-existing knowledge sources. In this paper, we describe how we have achieved this for an ontology of the mitochondria using our novel ontology development environment, the Tawny-OWL library.

Bibliographical details

WARRENDER, J. D; LORD, P;
Scaffolding the Mitochondrial Disease Ontology from extant knowledge sources
[By] J. D. Warrender and P. Lord
Newcastle upon Tyne: Newcastle University: Computing Science, 2015.
(Newcastle University, Computing Science, Technical Report Series, No. CS-TR-1465)

Added entries

NEWCASTLE UNIVERSITY
Computing Science. Technical Report Series. CS-TR-1465

Abstract

Bio-medical ontologies can contain a large number of concepts. Often many of these concepts are very similar to each other, and similar or identical to concepts found in other bio-medical databases. This presents both a challenge and opportunity: maintaining many similar concepts is tedious and fastidious work, which could be substantially reduced if the data could be derived from pre-existing knowledge sources. In this paper, we describe how we have achieved this for an ontology of the mitochondria using our novel ontology development environment, the Tawny-OWL library.

About the authors

Jennifer D. Warrender is a PHD student in the School of Computing Science at Newcastle University. Her research is focused on ways in which to consistently represent knowledge in ontologies.

Phillip Lord is a lecturer at the School of Computing Science, Newcastle University. His research covers a variety of different areas; mostly it focuses on the use of ontological technology in biology, or more generally mechanisms for presenting and publishing scientific information.

Suggested keywords

TAWNY-OWL
MITOCHONDRIAL DISEASE ONTOLOGY
ONTOLOGY DEVELOPMENT
EXTANT KNOWLEDGE SOURCE

Scaffolding the Mitochondrial Disease Ontology from extant knowledge sources

Jennifer D. Warrender and Phillip Lord*

School of Computing Science, Newcastle University, Newcastle-upon-Tyne, UK

ABSTRACT

Bio-medical ontologies can contain a large number of concepts. Often many of these concepts are very similar to each other, and similar or identical to concepts found in other bio-medical databases. This presents both a challenge and opportunity: maintaining many similar concepts is tedious and fastidious work, which could be substantially reduced if the data could be derived from pre-existing knowledge sources. In this paper, we describe how we have achieved this for an ontology of the mitochondria using our novel ontology development environment, the Tawny-OWL library.

1 INTRODUCTION

Bio-medical ontologies vary in size, with largest containing millions of concepts. Building ontologies of this size is complex, time-consuming and expensive and just as challenging to maintain and update.

Ontologies are only one of many mechanisms for the computational representation of knowledge. In some cases, ontologies are created where many of the needed concepts will be available elsewhere as terms in different structured representations. Being able to reuse these representations as a *scaffold* for the rest of an ontology might be able to reduce the cost and work-load of producing ontologies.

This is evidenced by, for instance, SIO (Dumontier *et al.*, 2014) which contains a list of all the chemical elements. Or the Gene Ontology (GO) (Ashburner *et al.*, 2000), which contains many terms related to chemical homeostasis, each of which need to relate to a specific chemical described in ChEBI (Hastings *et al.*, 2013). In addition to being described elsewhere, these concepts are often highly similar to each other. In extreme cases such as the amino acid ontology (Stevens and Lord, 2012), ontologies can consist of only related concepts, and “support” concepts that are used to describe them.

One solution to this is the use of patterns. A pattern is an abstract specification of an ontology axiomatisation with a number of “variables”. The pattern is instantiated by providing values for these variables, which are then expanded into the full axiomatisation providing one or more concepts.

Patterns have been implemented by a number of different tools, which differ in how the patterns are specified, and how and when the values are provided for the variables. For example, *termgenie* is a website which allows submission to GO (and others) (Dietze *et al.*, 2014). Variable values are entered through a form which then generates axioms, definitions and cross-references. For instance, this is the axiomatisation from *termgenie* when defining the term “cytosine homeostasis”

```
is_a: GO:0048878 {is_inferred="true"}
    ! chemical homeostasis
intersection_of: GO:0048878
    ! chemical homeostasis
intersection_of:
    regulates_levels_of CHEBI:16040 ! cytosine
relationship:
    regulates_levels_of CHEBI:16040
    {is_inferred="true"} ! cytosine
```

As well as the axiomatisation, *termgenie* also generates a number of different annotations including a definition, submitter information, and status. With *termgenie*, patterns are specified through the use of JavaScript functions.

In addition to *termgenie*, other systems also allow patterns. For example, both the desktop and web version of Protégé contain forms, which grant users the ability to customise the GUI and specify several axioms at once. In this case, patterns are declaratively defined (implicitly, with a GUI design) in XML (Tudorache *et al.*, 2013). Applications like Populous (Jupp *et al.*, 2011) and Rightfield (Wolstencroft *et al.*, 2011) use spreadsheets or spreadsheet-like interfaces to enter data, which is then transformed into a set of OWL axioms based on a pattern. In the case of these two, the patterns are specified in OPPL, a pattern language for OWL which can also be used independently (Egana Aranguren *et al.*, 2009). Finally, the Brain API allows programmatic construction of ontologies in an easy to use manner using Java (Croset *et al.*, 2013).

While these systems are all aimed at somewhat different use-cases, they all address the same problem; how to produce a large number of concepts all of which are similar, and to do so with a high-degree of repeatability. However, the use of this form of patternised ontology tool presents a number of problems. These tools provide a mechanism for adding many axioms at once, but not removing them again¹. If the knowledge changes, then this is a problem as the axioms added from a given pattern need to be removed or updated. Furthermore, if the knowledge engineering changes i.e. the pattern is updated, then all axioms added from any use of the pattern must also be updated.

In this paper, we describe how we have addressed these problems with the Mitochondrial Disease Ontology (MDO), through the use of the Tawny-OWL environment, which is a fully programmatic environment for ontology development. With Tawny-OWL, we can use a *pattern-first* ontology development process, building with patterns and data from extant knowledge sources from the start. This has allowed us to generate a *scaffold* which we can then populate further with hand-crafted links between parts of this scaffold where the knowledge exists. As a result, it is possible to

*To whom correspondence should be addressed:
phillip.lord@newcastle.ac.uk

¹ OPPL can remove axioms as well as add them but this is not automatic.

update both the knowledge and the patterns by simply regenerating the ontology. This process promises to aid in both the construction and maintenance of ontologies.

The MDO is available from <https://github.com/jaydchan/tawny-mitochondria>. Tawny-OWL is available from <https://github.com/phillord/tawny-owl>.

2 THE MITOCHONDRIA DISEASE ONTOLOGY (MDO)

Mitochondria are complex organelles found in most eukaryotic cells. Their key function is to enable the production of ATP through oxidative phosphorylation, providing usable energy for the rest of the cell. The mitochondria carry their own small genome containing 37 genes in human. Many other genes are involved in producing proteins involved in mitochondrial function, but these are encoded in the nuclear genome. A number of mitochondrial genes are associated with diseases; the first identified of these is the MELAS (Pavlakis *et al.*, 1984), which is most commonly caused by a point mutation in a tRNA found in the mitochondrial genome.

As with many areas of biology, mitochondrial research is a large, knowledge-rich discipline. Our purpose with the MDO is to attempt to formalise this knowledge, using an incremental or “pay-as-you-go” data integration approach. The ontology here serves as a tool for reasoning and knowledge exploration, rather than to form as a reference ontology (Stevens and Lord, 2008). This is an approach we have previously found useful in classifying phosphatases (Wolstencroft *et al.*, 2006). The hope is that we can incorporate new knowledge as it is released, checking it for consistency and cross-linking it with existing knowledge.

3 TAWNY-OWL

In this section, we give a brief description of Tawny-OWL (Lord, 2013) and how it supports pattern-first development. Tawny-OWL is a library written in Clojure, a dialect of lisp. It wraps the OWL API (Horridge and Bechhofer, 2011) and allows the fully programmatic constructions of ontologies. It has a simple syntax which was modelled on the Manchester Syntax (Horridge and Patel-Schneider, 2012), modified to integrate well with Clojure. It can be used to make simple statements in OWL:

```
(defclass A :super (some r B))
```

which makes defines a new class A such that $A \sqsubseteq \exists r B$. Although this is similar to the equivalent Manchester Syntax statements, Tawny-OWL provides a feature called “broadcasting” which is, essentially a form of pattern. So this following statement:

```
(some r B C)
```

is equivalent to the two statements $\exists r B$ and $\exists r C$. We apply the first two arguments (`some` and `r`) to the remaining ones consecutively. It also provides simple patterns, such as the covering axiom, so:

```
(some-only r B C)
```

is equivalent to three statements $\exists r B$, $\exists r C$ and $\forall r (B \sqcup C)$. While the patterns shown here are provided by Tawny-OWL, end ontology developers are using the same programmatic environment.

Patterns are encoded as functions and instantiated with function calls. For instance, we could define `some-only` as follows:

```
(defn some-only [property & classes]
  (list (some property classes)
        (only property
            (or classes))))
```

Here `defn` introduces a new function, `property & classes` are the arguments, and `list` packages the return values as a list. `some`, `only` and `or` are defined by Tawny-OWL as the appropriate OWL class constructors.

It is, therefore, possible to build *localised patterns* — custom patterns for use predominately with the current ontology (Warrender, 2015). Patterns can call each other and can be of arbitrary complexity. The use of Tawny-OWL, therefore, inverts the usual style of ontology development. Non-patternised classes are just trivial instantiations of patterns.

4 BUILDING A MITOCHONDRIAL SCAFFOLD

Following a requirements gathering phase for MDO, it was clear from our competency questions (for example “What are all the genes/proteins that are associated with a specific syndrome?”) that we needed many concepts which were heavily repetitive, and further which have comprehensive and curated lists available. We describe these parts of the domain knowledge as the *scaffold*. For example, there are around 761 genes whose products are involved in mitochondrial function. Classes representing these genes do not, in the first instance, require complex descriptions, and are defined within MDO as follows:

```
(defclass Gene)

(defn gene-class [name]
  (owl-class name :label name :super Gene))
```

This pattern is then populated using a simple text file, with the 761 gene names present. The gene pattern is an extremely simple pattern, as these concepts are self-standing. Other parts of the ontology are even simpler; for instance, for describing mitochondrial anatomy, the classes have similar complexity to the genes, but there are only 15. In this case, classes are defined with a pattern and a list “hard-coded” into the MDO source code, rather than using an external text file. Other patterns are more complex. For instance, the subclasses of `Disease` are defined as follows:

```
(defn disease-class [name omim lname]
  (let [disease
        (owl-class name
                    :label name
                    :super Disease)]
    (if-not (nil? omim)
      (refine disease
               :annotation
               (see-also
                (str "OMIMID:" omim))))
    (if-not (nil? lname)
      (refine disease
               :label
               (str "Long name:" lname))))))
```

This function adds two annotations to each disease class, if they are available. This function also demonstrates the use of conditionals (`if`), predicates (`nil?`) and string concatenation (`str`); these are not provided by Tawny-OWL, but by Clojure and demonstrate the value of building Tawny-OWL inside a fully programmatic environment.

5 FITTING OUT THE SCAFFOLD

The top-level of the MDO is shown in Figure 1. Of these classes, “Paper” and “Term” are described later.

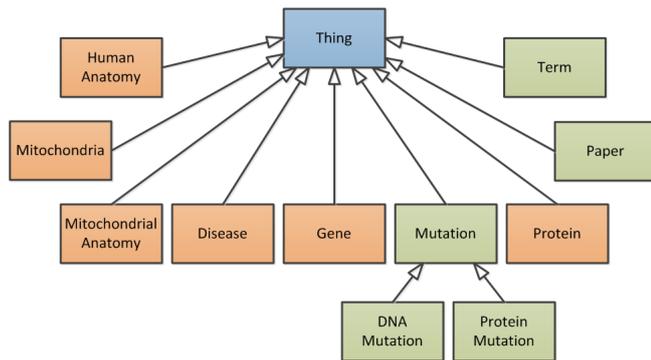


Fig. 1. The top-level structure of Mitochondrial Disease Ontology. Classes that are a part of the scaffold are coloured in orange, while classes that are built on top of the scaffold are coloured in green.

The remaining classes define the scaffold, which now has a total of 1357 classes; a break-down of these classes and their sources is shown in Table 1.

Class type	Count	Data source
Disease	41	UMDF website
Gene	761	The NCBI Gene portal
Human Anatomy	61	The Terminologia Anatomica.
Mitochondrial Anatomy	15	Mitochondrial Research Group
Protein	479	UniProt

Table 1. Table showing the type, number of and data source for each generic mitochondrial ontology class

For the next stage of the process, we are now building on top of this scaffold, using hand-crafted and bespoke knowledge. This is being achieved by manual extraction of knowledge from papers about mitochondria. Our initial process is to find references in papers to the terms that are represented by classes we have built in the scaffold, and draw explicit relationships between these papers and the scaffolded knowledge that they describe. Currently, these classes also use a patternised approach; the raw data is held in a bespoke (but human readable) syntax², which is then parsed and used to instantiate patterns. In total, there are now 2174 classes

² In this case *EDN* which is a text representation of Clojure data structures; it looks rather like JSON.

created from this approach from around 30 papers. These terms currently are not defined beyond their name and the source paper from which they were identified. We do not consider them directly as part of the scaffold, as they are not from an extant knowledge source, but one that we have created; they are the first layer build on top of our scaffold. We expect future layers to use the Tawny-OWL syntax directly, as the knowledge increases in complexity and decreases in regularity.

6 RESILIENCE TO CHANGE

One key feature of our development process is that the OWL which defines the MDO is no longer *source code* but generated. Rather it is generated from patterns defined in Tawny-OWL and text files which are used to instantiate these patterns. The in-memory OWL classes and associated OWL files are generated on-demand, by *evaluating* the patterns. Effectively, we regenerate the ontology every time we restart the environment. In this section, we consider the types of changes that can happen, and how these changes impact on MDO.

The scaffold of MDO is sensitive to changes in its dependency knowledge sources. First, new terms can be entered into extant sources, which will necessitate the addition of new classes. For the MDO, this simply necessitates re-importing the knowledge. The addition of equivalent new classes will then happen automatically according to the patterns already defined; no other changes should be necessary for the MDO, although we may wish to refer to the new classes in other parts of the ontology.

Second, terms may be removed from dependencies; so, for example, a disease may be redefined by the UMDF. In many cases, for the MDO, this is not problematic – the equivalent classes will simply disappear from the ontology. Tawny-OWL provides two features to help with changes to terms in the scaffold when these terms are also referred to outside of the scaffold. Tawny-OWL uses a “declare-before-use” semantics, so removal of classes from the scaffold will cause fail-fast behaviour when they are used elsewhere. The Brain environment uses the same semantics for similar reasons (Croset *et al.*, 2013). In addition, Tawny-OWL provides a “deprecation” facility which allows the developer to continue refer to terms from the scaffold which have been removed, but to receive warnings about this use; this is rather like obsolescence, but happens automatically³.

Third, the MDO scaffold can also cope straight-forwardly with changes to patterns. As with the addition or removal of terms from dependencies, pattern changes will simply take place by re-evaluating the ontology.

Finally, the MDO is resilient to changes in ontology engineering conventions. For example, MDO does not use OBO style numeric identifiers, nor provide stable IRIs for integration with linked data sources since these are not critical at the current time⁴. They, however, could be added easily to all existing (and future) terms in a few lines of code, using an existing facility within Tawny-OWL for minting and persisting numeric identifiers in an automatic, yet managed, way. This change would just alter IRIs and would have

³ Tawny-OWL is implemented in a Lisp and so is homoiconic; this makes it particularly straight-forward to automate code updates if we choose.

⁴ Our initial intention was to use PURLs from www.purl.org but have found practical problems with generating these.

no impact on references between concepts inside or outside of the scaffold.

In conclusion, as well as enabling rapid construction of the MDO, we believe that the pattern-first scaffolding approach should also allow easy maintenance of the ontology.

7 DISCUSSION

In this paper, we have described how we have used a number of extant knowledge sources, combined with patterns defined using the Tawny-OWL library to rapidly, reliably and repeatedly construct a scaffold for MDO.

We have previously used a related patternised methodology to construct a complex ontology describing human chromosome rearrangements (i.e. The Karyotype Ontology (KO) (Warrender and Lord, 2013b)). However, unlike KO, the mitochondrial knowledge we want to encapsulate is found in numerous independent sources (e.g. published papers and online databases) and in a variety of formats (e.g. “free text” and CSV); the use of several patterns to form a scaffold is unique to MDO. Conversely, the axiomatisation of MDO from these sources is simple; this cannot be said for KO, most of which is generated from a single large pattern (Warrender and Lord, 2013a). In addition, while our knowledge of the karyotype is constrained and is essentially finished, the community’s understanding of mitochondria and mitochondrial disease is incomplete and will grow in response to the demands of changing knowledge.

This methodology is extremely attractive for a number of reasons. First of all, it allows a very rapid way of scaffolding an ontology for a complex area of knowledge. At this stage, most of the classes created are simple and self-standing, although in some cases do have relationships to other entities in the scaffold. At this point, we have built the ontological equivalent of a data warehouse: terms have been taken from elsewhere and have undergone a form of schema reconciliation into ontological classes.

One key feature of the MDO is that it has been built using tools designed for software development; these tools are relatively advanced and well-maintained⁵ (Lord, 2013). Moreover, recreating the MDO ontology from our original Tawny-OWL source code is an intrinsic part of the development process; there is no complex release process and any ontology developer can recreate the OWL file with a single command. While, the system as it stands has a high-degree of replicability, the design decisions implicit in the source code are not necessarily apparent. For the basic scaffold this is, perhaps, not a major issue, however as MDO is developed outside of its scaffold, we expect to integrate more documentation into the source code itself, using *lentic*, a recently developed tool for literate programming (Lord, 2015).

We believe that the engineering process that we have used to build the scaffold is resilient to change, as described in Section 6. Despite this resilience, our use of external sources of knowledge does bring with it new dependencies, with all the issues that this entails for change management. We believe that we can manage this by borrowing best practice from software engineering. Importing knowledge into the scaffold can, in many cases, happen entirely automatically from our extant knowledge sources. Considering just

the gene lists, we can either import from a local, fixed copy of this list, or take the current version live from the NCBI portal. In software engineering terms, the former is a *release dependency* and provides stability, while the latter is a *snapshot dependency* which will fail-fast, allowing rapid incorporation of new knowledge. The latter is particularly useful within a continuous integration environment which are used with other ontologies (Mungall *et al.*, 2012), and are also fully supported by Tawny-OWL (Lord, 2013).

Although we have not described its usage here, with the MDO we are not forced to use Tawny-OWL for all development. It would be possible to combine predominately hand-crafted development using Protégé, for instance, with some patternised classes; for example, the OBI uses this approach (Brinkman *et al.*, 2010). For, the MDO, in fact almost all terms other than the top-level has been created from other syntaxes, generally a flat-file. For larger projects, we envisage that most ontology developers would not need to use the programmatic nature of Tawny-OWL. While we appreciate the value of a single environment, a tool should not force all users into it.

In this paper, we have described our approach to building the MDO using a patternised scaffold based around existing knowledge sources. While the work described in this paper allows us to integrate structured data into an ontology, we are now investigating new ways of integrating unstructured literate-based knowledge into our ontology; while we have started the process of formalising, this new knowledge is far from finished. As described in this paper, though, a pattern-first, scaffolded approach to ontology development has enabled us to make significant advances with the MDO. We believe that this approach is likely to be applicable to many other domains also.

REFERENCES

- Ashburner, M., Ball, C. A., Blake, J. A., Botstein, D., Butler, H., Cherry, J. M., Davis, A. P., Dolinski, K., Dwight, S. S., Eppig, J. T., Harris, M. A., Hill, D. P., Issel-Tarver, L., Kasarskis, A., Lewis, S., Matese, J. C., Richardson, J. E., Ringwald, M., Rubin, G. M., and Sherlock, G. (2000). Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nature Genetics*, **25**(1), 25–29.
- Brinkman, R., Courtot, M., Derom, D., Fostel, J., He, Y., Lord, P., Malone, J., Parkinson, H., Peters, B., Rocca-Serra, P., Ruttenberg, A., Sansone, S.-A., Soldatova, L., Stoeckert, C., Turner, J., Zheng, J., and the OBI consortium (2010). Modeling biomedical experimental processes with obi. *Journal of Biomedical Semantics*, **1**(Suppl 1), S7.
- Croset, S., Overington, J. P., and Rebholz-Schuhmann, D. (2013). Brain: biomedical knowledge manipulation. *Bioinformatics*, **29**(9), 1238–1239.
- Dietze, H., Berardini, T. Z., Foulger, R. E., Hill, D. P., Lomax, J., Osumi-Sutherland, D., Roncaglia, P., and Mungall, C. J. (2014). Termgenie - a web application for pattern-based ontology class generation. *Journal of Biomedical Semantics*, **5**(1), 48.
- Dumontier, M., Baker, C., Baran, J., Callahan, A., Chepelev, L., Toledo, J. C., Del Rio, N., Duck, G., Furlong, L., Keath, N., Klassen, D., McCusker, J., Rosinach, N. Q., Samwald, M., Rosales, N. V., Wilkinson, M., and Hoehndorf, R. (2014). The Semanticscience Integrated Ontology (SIO) for biomedical research and knowledge discovery. *Journal of Biomedical Semantics*, **5**(1), 14+.
- Egana Aranguren, M., Stevens, R., and Antezana, E. (2009). Transforming the axiomisation of ontologies: The ontology pre-processor language. *Nature Precedings*.
- Hastings, J., de Matos, P., Dekker, A., Ennis, M., Harsha, B., Kale, N., Muthukrishnan, V., Owen, G., Turner, S., Williams, M., and Steinbeck, C. (2013). The ChEBI reference database and ontology for biologically relevant chemistry: enhancements for 2013. *Nucleic Acids Research*, **41**(D1), D456–D463.
- Horridge, M. and Bechhofer, S. (2011). The OWL API: A Java API for OWL ontologies. *Semant. web*, **2**(1), 11–21.
- Horridge, M. and Patel-Schneider, P. F. (2012). Owl 2 web ontology language manchester syntax (second edition). Technical report.

⁵ And, usefully, not dependent on academic developers for future maintenance.

- Jupp, S., Horridge, M., Iannone, L., Klein, J., Owen, S., Schanstra, J., Wolstencroft, K., and Stevens, R. (2011). Populous: a tool for building owl ontologies from templates. *BMC Bioinformatics*, **13**(Suppl 1), S5.
- Lord, P. (2013). The Semantic Web takes Wing: Programming Ontologies with Tawny-OWL. <http://arxiv.org/abs/1303.0213>.
- Lord, P. (2015). Lenticular text: Looking at code from different angles. <http://www.russet.org.uk/blog/3035>.
- Mungall, C., Dietze, H., Carbon, S., Ireland, A., Bauer, S., and Lewis, S. (2012). Continuous integration of open biological ontology libraries. <http://bio-ontologies.knowledgeblog.org/405>.
- Pavlakīs, S. G., Phillips, P. C., DiMauro, S., De Vivo, D. C., and Rowland, L. P. (1984). Mitochondrial myopathy, encephalopathy, lactic acidosis, and stroke-like episodes: a distinctive clinical syndrome. *Ann. Neurol.*, **16**(4), 481–488.
- Stevens, R. and Lord, P. (2008). Application of ontologies in bioinformatics. In S. Staab and R. Studer, editors, *Handbook on Ontologies in Information Systems*. Springer, second edition.
- Stevens, R. and Lord, P. (2012). Semantic publishing of knowledge about amino acids. <http://ceur-ws.org/Vol-903/paper-06.pdf>.
- Tudorache, T., Nyulas, C., Noy, N., and Musen, M. (2013). Using semantic web in icd-11: Three years down the road. In H. Alani, L. Kagal, A. Fokoue, P. Groth, C. Biemann, J. Parreira, L. Aroyo, N. Noy, C. Welty, and K. Janowicz, editors, *The Semantic Web ISWC 2013*, volume 8219 of *Lecture Notes in Computer Science*, pages 195–211. Springer Berlin Heidelberg.
- Warrender, J. D. (2015). *The Consistent Representation of Scientific Knowledge: Investigations into the Ontology of Karyotypes and Mitochondria*. Ph.D. thesis, School of Computing Science, Newcastle University.
- Warrender, J. D. and Lord, P. (2013a). A pattern-driven approach to biomedical ontology engineering. *SWAT4LS 2013*.
- Warrender, J. D. and Lord, P. (2013b). The Karyotype Ontology: a computational representation for human cytogenetic patterns. *Bio-Ontologies SIG 2013*.
- Wolstencroft, K., Lord, P., Taberero, L., Brass, A., and Stevens, R. (2006). Protein classification using ontology classification. *Bioinformatics*, **22**(14), e530–538.
- Wolstencroft, K., Owen, S., Horridge, M., Krebs, O., Mueller, W., Snoep, J. L., du Preez, F., and Goble, C. (2011). RightField: embedding ontology annotation in spreadsheets. *Bioinformatics*, **27**(14), 2021–2022.