

# Designing Reusable User-Interfaces for Querying a Collection of Neuroscience Ontologies

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**Abstract.** This paper examines the problem of generating effective, reusable web interfaces for searching and browsing neuroscience data represented in the Web Ontology Language (OWL). We briefly explain our design of a collection of ontologies for the nervous systems of different mollusk. We then motivate our goal to design interfaces that are reusable across these different ontologies. In order to achieve this re-usability, we view the underlying semantic data in the ontology as a graph and are currently exploring the use of different graph properties to infer the structure of the class hierarchy in the ontology. The interface allows a user to query the underlying ontology without the use of a query language like SPARQL.

## 1 Introduction

In this paper we examine techniques for designing reusable user-interfaces for browsing and searching a collection of ontologies representing information on neurons, neural networks and their properties for different mollusks. These ontologies represent the data collected as part of the NeuronBank Project [1, 2]. We have represented this information using the Web Ontology Language (OWL) [3].

In order to make these ontologies accessible to the end users, the information represented in them must be readily available through intuitive web interfaces for browsing and searching this data. However, since these ontologies all differ slightly, it would be much more efficient to design these interfaces in a reusable manner such that the interface is generated dynamically from the underlying data-model.

The remainder of this paper is as follows. In Section 2 we briefly explain the design and structure of our collection of ontologies. In Section 3 we motivate the need for reusable interfaces that can query an ontology and explain our approach to developing these interfaces. Finally, we conclude in Section 4.

## 2 Ontology Design

Across all species, neurons are described by sets of attributes (e.g. neurotransmitter, spike shape etc.) and identified by delineating the subset of attributes

necessary and sufficient to reliably identify that neuron across different specimens. There is variation, however, in the attributes used to describe neurons in different species. We create ontologies for data on two different species of mollusks: *Tritonia diomedea* and *Melibe leonina*. We include information on 45 identified types of neurons and their interconnections for *Tritonia* and 4 different neurons for *Melibe* in our ontologies. The data used for this was taken from NeuronBank [4] and represented in OWL (NeuronBank uses Protege-Frames [5] to represent its data). We reuse a number of classes from other upper ontologies including the Basic Formal Ontology [6] and ontologies includes as part of the Open Biomedical Ontologies Project [7] including the Common Anatomy Reference Ontology (CARO) [8] .

Due to space constraints, we do not explain our ontologies in detail. We create classes derived and organized under the aforementioned upper ontologies for the major components of the nervous system. Hence, some of our classes include Neurite (with Axon and Dendrite as subclasses), Synapse and Neuron. The Neuron class is further subclassed into types of neurons. For example, for *Tritonia*, some subclasses under Neuron include Pleural\_Neuron (for all the neurons below the Pleural Ganglion of *Tritonia*), Cerebral\_Neuron (neuron in the cerebral ganglion), Pedal\_Neuron (neurons in the pedal ganglion) etc. Notice that the classification for this species is based on brain region.

### 3 User-Interface Design

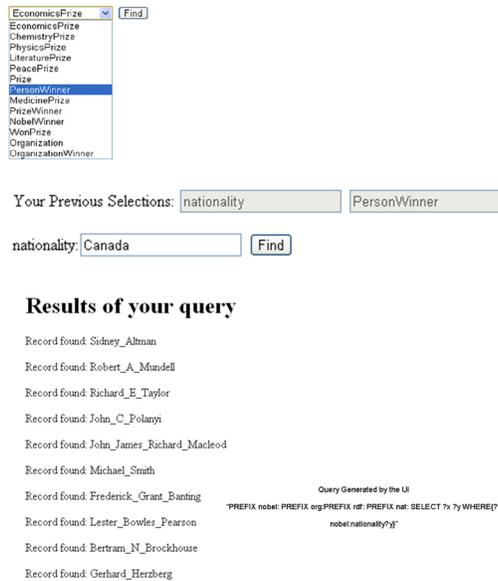
#### 3.1 Motivation

While much research effort has gone into developing standards (like RDF and OWL) for representing information on the Semantic Web and for developing languages to query this information (SPARQL), little has been done to make this information accessible to an end-user not familiar with query languages. For our application, we developed a number of ontologies on closely related mollusk nervous systems. The intended end-users of these ontologies are neuroscientists working on these species and they do not have the training to write queries in SPARQL.

Additionally, despite having a number of concepts in common, each of these ontologies differed in species specific ways. Also, it is envisioned that as new lab techniques to identify this neurons are introduced, the underlying ontologies may evolve over time. This led us to our goal of developing a simple web interface to access the ontology that is capable of generating SPARQL queries for an end-user and presenting the results to these queries. Additionally, the interface should be dynamically generated from the underlying ontology, thereby requiring no changes when the ontology is modified and allowing reuse across different ontologies. The work presented in this paper extends our previous work presented as a poster [9].

### 3.2 Approach

Our approach to generating an interface is based on presenting the user with an upper-level menu that list the most relevant classes. As explained shortly, we infer the most relevant classes based on some properties of the data model graph. Once the user selects a class, the next menu is populated based on retrieving the properties of the class the user selected. As the user interacts with the ontology and makes selections, we build behind the scenes a SPARQL query representing the users choices as filters on the ontology. An example of our method and the generated query is shown for a much simpler ontology - that of all Nobel Prize winners.



**Fig. 1.** The query interface for the Nobel Prize Ontology

Generating an interface from an underlying ontology is a challenging problem because ontologies are viewed as graphs with no explicit hierarchies. However, most users perceive the ontology as a hierarchical data representation containing some upper-level classes that represent a natural entry point for a user searching or browsing this ontology. For example, for the ontologies of the different nervous systems of the mollusks that we are working with, a logical starting point to begin browsing the ontology could be a neuron, a connection, or even a reference. Our goal in this research was to design a means of inferring this hierarchy that underlies most ontologies. This would allow for the design of interfaces that are completely reusable since no class structure information needs to tie the interface to a given ontology.

The basis of our approach consists of examining the graph of all the data triples in the ontology. A triple relates a subject to an object using a predicate. We build from this graph a data-model graph that consists of a node for every class in the ontology. We associate with every class a count of how many instances of that class exist in the ontology. We then join two nodes, representing two different classes by an edge if they are related in the original ontology by a given predicate. For each edge, we compute a weight that denotes the number of times this predicate links the given subject class to the given object class. We are currently examining a variety of heuristics that take into account the degree of the class in the data-model graph to infer if it is an upper-level class.

## 4 Conclusion

In this paper we motivate an application driven need for designing reusable user interfaces that can query a collection of neuroscience ontologies. The interface is capable of generating SPARQL queries based on the users selections and is dynamic in that it adjusts to changes in the class hierarchy of the underlying ontology. The interface also infers relevant entry point classes to the ontology based on properties of the data model for the given ontology. As part of our future work, we are exploring other algorithms to infer the class hierarchy and designing experiments to evaluate the effectiveness of the interface.

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