Standardized classification of prokaryotes is a burgeoning issue resulting from rapid sequencing and identification of species characteristic of modern genomics and metagenomics. Ontological resources are scarce, and resources facilitating access to said ontologies is even more so. MicroO is one such resource - “an ontology of phenotypic and metabolic characters, assays, and culture media found in prokaryotic taxonomic descriptions.” [1] MicroO provides the basic ontological structure and an existing dataset containing over 14,000 classes, but there is no dedicated means to view this structure. While one could easily utilize resources such as WebVOWL[2] or Stanford’s Protégé[3] to view and edit MicroO, a dedicated resource would also facilitate access. I propose to create a dedicated web-based browser for the prokaryotic ontological resources provided by MicroO.

A dedicated browser for MicroO, or any other OWL resource, requires several working elements in order to function. First and foremost, a means to access the content stored in OWL format is required. I propose to use a series of python scripts in order to properly parse the existing OWL content, which will be thereafter stored in a MySQL relational database. A schema will be required to cover all phenotypes of prokaryotic characters and behavior, along with those of their proteins. Tables will exist for other class hierarchies such as those for diagnostic assays, environments, culture media, chemicals (associated with media), drug interactions, and so forth. User interaction with the front-end will necessitate interaction with the SQL backend in the form of SQL queries, and Python scripting will serve to process the user request and format that input into a query such that usable information can be returned.

Next, a visualization system is required to facilitate user interaction. A front-end utilizing HTML5, CSS3, and JavaScript/JQuery will provide a stimulating and interactive UI. Two main modes of interaction are planned - searching and browsing. Searching, as leveraged by a tiered approach using a JavaScript → Python → MySQL hierarchy, will return a list of matching ontological terms, and provide multiple tiers of visualization associated with the terms that users can explore. Autocomplete functionality as provided by JQuery will be included with searching, returning a limited number of potential matches as the user types their query. Browsing will enable users to click through the ontological webs and examine terms visually. WebVOWL[2] is an example of a simple, yet effective means of querying and viewing a web ontological data in a format that facilitates user experience, and will be a helpful example for development. The viewer for data will be dynamic, focusing in on current and immediately-related ontologies while hiding less-relevant ontologies. Each individual term will have their own page separate from the dynamic viewer. This page will include all relevant information to the term, including its parent hierarchy, related sibling terms, source publication(s), as well as a link to NCBI resources for the term (such as a PubMed query).

Finally, should time allow for it, it would be ideal to enable users themselves to add content to the ontological web. They would be required to link new content to existing content - creation of new parent classes would be disallowed. Similar to searching, a JavaScript → Python → MySQL hierarchy would facilitate this access, with the Python intermediary sanitizing all user inputs to prevent SQL injection. Users would be able to immediately view content upon refreshing the page and returning to the viewer.

References:

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