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JPhyloRef: a tool for testing and resolving phyloreferences

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Software

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Summary

JPhyloRef is a command line tool as well as a web service for reasoning with ontologies containing logical definitions of clades, called phyloreferences, and their accompanying reference phylogenetic trees. It has two main goals. The primary one is to facilitate automated testing that the semantics of the logical definitions imply ("resolve to") the correct nodes in the reference tree as clade ancestors. The secondary goal is to enable integration with external tools that need to obtain the clade ancestor node(s) resulting from a given ontology of phyloreferences and reference tree(s). When run as part of an automated testing workflow, JPhyloRef reports test results in the cross-platform Test Anything Protocol (TAP) format. When used to find clade ancestor nodes implied by logical clade definitions, results are returned as a JSON object. JPhyloRef uses the OWL API reference library for reading Web Ontology Language (OWL) ontologies, and for the actual ontology reasoning step it uses an external and configurable OWL reasoner.

Background

In evolutionary biology, groups of organisms consisting of an ancestor and all of its descendants ("clades") are a fundamental unit for understanding evolution and describing biodiversity (Queiroz, 2007). Clades are defined based on shared ancestry. This provides the theoretical foundation for the semantics of taxon concepts to be defined and reproducibly resolved within a hypothesis of evolutionary relationships, that is, a phylogeny (Queiroz, 1992; Queiroz & Gauthier, 1992, 1990). We have proposed a mechanism, called Phyloreferencing, for representing clade definitions as structured data with fully machine-processable semantics, using the Web Ontology Language (OWL) (W3C OWL Working Group, 2012). We refer to such machine-interpretable clade definitions as "phyloreferences" (Cellinese et al., 2021).

Because phyloreferences have an OWL ontology representation in the form of logically defined classes, combining them with an OWL representation of a phylogenetic tree allows an OWL reasoner to infer, based on their logical definitions, which nodes in the phylogeny, if any, instantiate each phyloreference. We refer to this logical inference as "resolving a phyloreference."

Statement of need

Clade definitions are normally created and published in the form of natural language text, and in the context of a phylogenetic hypothesis, represented by the so-called reference phylogeny.

When digitized to a phyloreference, usually through a process of manual curation, a key question in quality control of the digitization product as well as the involved ontologies and the generated logical expressions arises from one of the founding premises of phyloreferences: given that phyloreferences render the semantics of their represented clades machine-interpretable, can a computational algorithm test whether a phyloreference resolves, and only resolves to the node in the reference phylogeny that the original authors of the published clade definition designate as the expected node? We built JPhyloRef to enable this type of test, and to allow integrating such tests into automated testing frameworks. We also needed other tools to programmatically answer for a given ontology of phyloreferences and an accompanying phylogeny, which phyloreferences resolve to which nodes (as clade ancestors) in the phylogeny.

JPhyloRef feature overview

JPhyloRef is a command-line tool written in Java. When run with the `test` command with an OWL ontology containing phyloreferences as well as reference phylogenies as input, JPhyloRef identifies all the phyloreferences within this ontology, compares for each one the inferred phylogeny node(s) to the expected one, and determines success (inferred node identical to expected) or failure (no inferred node, or inferred node different from expected). To better facilitate use in automated continuous integration testing, JPhyloRef also allows for phyloreferences to be marked as draft (resulting in an "incomplete" test status), or as to be skipped (by no nodes having been annotated as an expected resolution of a particular phyloreference). These test results are reported in the Test Anything Protocol (TAP) format (https://testanything.org/), a cross-platform format for reporting test results. JPhyloRef will also return an exit code indicating success (0), failure (the number of failed phyloreferences as a positive integer) or an ontology containing no phyloreferences (-1, interpreted as 255 by POSIX-compatible operating systems).

Internally, JPhyloRef relies on an external OWL reasoner (which can be configured) to perform the actual OWL inferences, with which it communicates using the OWL API 4.2.7 (Horridge & Bechhofer, 2011). We strongly recommend to use ELK (Kazakov et al., 2014), a reasoner for the OWL-EL profile, which is sufficient for the inferences necessary for phyloreference resolution. In our experience, reasoners for more expressive profiles, such as OWL-DL reasoners, do not perform efficiently enough even for modestly sized ontologies of phyloreferences.

To support integrating Phyloreferencing with other tools, JPhyloRef includes two additional commands: `resolve` and `webserver`. Using the `resolve` command with an input of an OWL ontology in any of the supported formats will result in a JSON object whose keys are the IRIs of all the phyloreferences in the ontology that resolved to any nodes, and whose values are lists of the IRIs of the phylogeny nodes that they resolved to. Using the `webserver` command starts an HTTP server on the hostname and TCP port specified in the command line arguments. This webserver provides a POST endpoint at `/reason` that can be used to submit OWL ontologies in JSON-LD format for reasoning, which returns a JSON object in the same format as produced by the `resolve` command. Neither of these commands return test statuses for phyloreferences.

JPhyloRef is currently in active use for integrating the digitization of clade definitions in the form of phyloreferences into an automated testing framework, as well as for resolving phyloreferences on the command line. For example, we use it in the continuous integration testing infrastructure of the phyx.js JavaScript library (https://github.com/phyloref/phyx.js/actions), where the output from the `test` command is interpreted by a JavaScript-based TAP library to ensure that phyloreferences in example OWL ontology files resolve as expected. We also use the `webserver` command of JPhyloRef as a backend for the Klados phyloreference curation software (https://github.com/phyloref/klados), allowing the curator to submit phyloreferences created from user input or a publication, along with associated phylogenies, to a backend

server running JPhyloRef for resolution. The source code for JPhyloRef has been archived to Zenodo (Vaidya & Lapp, 2021).

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