

The ROBOT Tool as implemented in DO



Introduction

[ROBOT](#) is a tool for working with Open Biomedical Ontologies (OBO), developed by James Overton and Rebecca Jackson. It can be used as a command-line tool or as a library for any language on the Java Virtual Machine.

ROBOT is:

- Open source on GitHub
- Used in other OBO foundry ontologies such as the Ontology for Biomedical Investigations and the Gene Ontology
- Developed in Java

The Disease Ontology (DO) project has been able to automate its workflow using the ROBOT command line tool. ROBOT allows developers to quickly integrate logical definitions and class annotations using the 'template' command, which transforms a spreadsheet into OWL axioms.

1) Installing ROBOT

Follow Step 1 at <http://robot.obolibrary.org/>

2) Cloning DO Github Repository

Clone <https://github.com/DiseaseOntology/HumanDiseaseOntology> onto local machine

- 1) In command-line/terminal of choice, cd into Github/HumanDiseaseOntology/build directory
- 2) Run command: `robot query --input ../src/ontology/doid-edit.owl --query ../src/sparql/def-report.rq def-report.tsv`

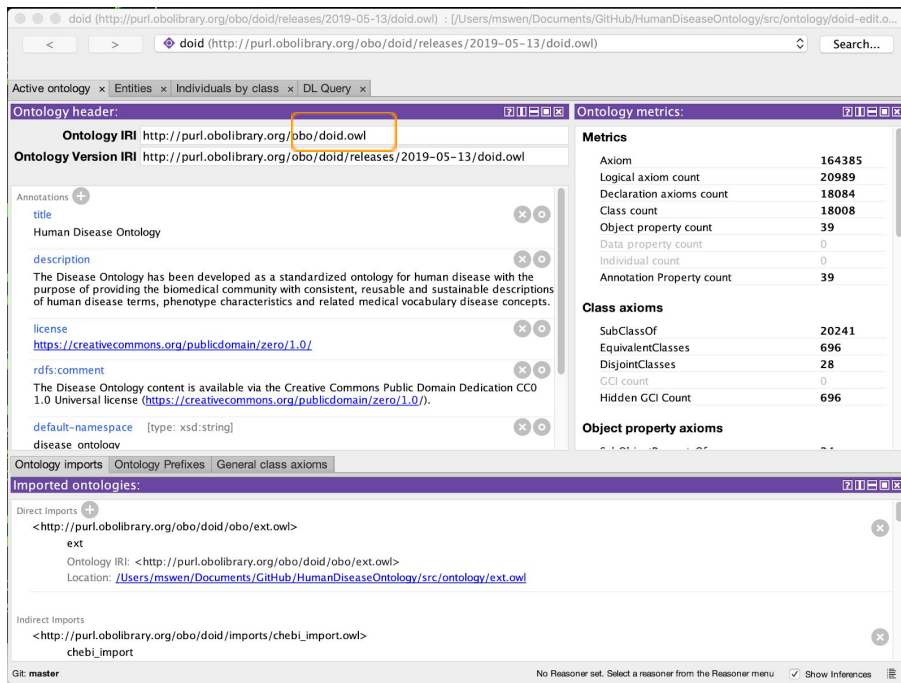
3) Integrate with Protégé

Download Protégé at <https://protege.stanford.edu/products.php>

- 1) In your local machine, navigate to the GitHub folder containing the HumanDiseaseOntology files.
 - 2) Double-click "doid-edit.owl" located in the src folder. The doid-edit.owl file is the most recent .owl file between builds
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3) doid.owl will be loaded into Protégé



Toggle back to ROBOT in your command-line window/terminal

1) ROBOT template command

```
robot template --input edit.owl --merge-before --template
basic-template.csv --output template.owl
```

2) Add in new DO terms

→ Output is directed to the build directory, confirm the updates in Protege, then copy the new doid-edit.owl file to the src/ontology directory and git commit

```
robot template --input ../src/ontology/doid-edit.owl --merge-before --template  
OMIM_splits_loaded_ROBOT_Feb_2019.tsv --output doid-edit.owl
```

To Query DO via customized SPARQL queries

DO SPARQL queries enable semantic queries of the Disease Ontology database and data retrieval of customized datasets (upon request of DO Users) and reports utilized for Quality Control assessment, identification of targeted curation datasets and reporting of DO release statistics. SPARQL queries utilized in the Human Disease Ontology or requested by the DO's community are provided for reuse on the DO's GitHub repository.

To query DO via SPARQL:

```
robot query --input ../src/ontology/doid-edit.owl --query [sparql dir file].rq  
[output of query file].tsv
```