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Version 1

## Planet Microbe Semantic Web Application V.1

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**Protocol status:** In development

**We are still developing and optimizing this protocol**

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## Abstract

Placeholder tutorial for the use of the Planet Microbe Semantic Web Application, accompanying the PhD dissertation work of Kai Blumberg.



## Home Page

- 1 This protocol is a temporary place holder for the protocol to use the Planet Microbe Semantic Web API. This protocol is included as part of Kai Blumberg's PhD dissertation work.

This work is contained within this github repository:

<https://github.com/hurwitzlab/planet-microbe-semantic-web-analysis>

Subsequent versions of this protocol will include the following sections:

- 1) A brief introduction and overview of the system
- 2) A description of the command line options (arguments flags) for the `'assemble_query.py'` script. This script is a command line python script which can be used to assemble and submit a SPARQL query to the Planet Microbe RDF database.
- 3) An explanatory page showing how to navigate the relevant OBO ontologies (e.g., GO, NCBITaxon, ENVO) to search for ontology terms which can be used in queries to discover information.
- 4) A "how to" example showing how to use the system to query for all annotations of samples within a specific GO class hierarchy.
- 5) A "how to" example showing how to use the system to query for all annotations of samples within a specific NCBITaxon class hierarchy.
- 6) Documentation of several examples of R code that can be used to process and analyze the query results delivered from the system.

Stay tuned!

-Kai