

Plant Pathogen Interactions Ontology (PPIO)

Alejandro Rodríguez Iglesias ^{a,*}, Mikel Egaña Aranguren ^a Alejandro Rodríguez González ^a
Mark D. Wilkinson ^a

^a *Biological Informatics Group, Centre for Plant Biotechnology and Genomics (CBGP), Technical University of Madrid (UPM), Spain*

Abstract. Plant-pathogen interactions are an important knowledge domain within plant biology and biotechnology, both scientifically and in economic terms. Unlike other knowledge domains within life sciences, however, semantic technologies have not been used extensively to codify it; therefore, there is a lack of axiomatic models amenable to automated integration and inference. We present the Plant-Pathogen Interactions Ontology (PPIO), a first step towards the axiomatization of plant-pathogen interactions knowledge. PPIO encourages consistent annotation and supports both query and inference.

Keywords: Plant pathogenic bacteria, Ontologies, Semantic Web

1. Introduction

2. Modelling

2.1. Design principles

3. Creation methodology

Numerical IDs + label.

The development of PPIO is automated as much as possible. Once the basic structure is set, some parts of the ontology are produced programmatically by introducing the ontology in a tailored Galaxy [2] workflow (picture of workflow).

OWL Punning¹ is used in the X hierarchy of PPIO to represent X classes both as OWL classes and individuals, in order to link pathogens, which are individuals, with symptoms?. This is achieved by defining an Ontology Pre Processor Language (OPPL)² script (picture) and executing it via OPPL-Galaxy [1].

The organism taxa hierarchy is produced by the Galaxy tool NCBITaxonomy2OWL: NCBITaxonomy2OWL gets the user-defined taxa from the NCBO web service

(URL) and injects them in the ontology, respecting the original hierarchy and adding each taxa with an ontology (REF) URI (eg) (ref github repo)

By using Galaxy, the specific workflow we need is defined once and we can execute it at will, each time a new release is set, or also if new tools are needed. The galaxy workflow can be reproduced at biordf.org:8090 with any ontology and OPPL script.

TODO: we need to be able to resolve not only the whole ontology (oclc.purl.org/PPIO), but specific entities (oclc.purl.org/PPIO000023). How? stardog linked data? but then, the redirection is always done with oclc.purl.org!

4. Discussion (comparison with other ontologies on the same topic, pointers to existing applications or use-case experiments)

Acknowledgements

Mikel Egaña Aranguren is funded by the Marie Curie-COFUND Programme (FP7) of the EU.

References

- [1] M. E. Aranguren, J. T. F. Breis, E. Antezana, C. Mungall, A. R. González, and M. Wilkinson. OPPL-Galaxy, a Galaxy tool for

*Corresponding author. Email: alejandroriglesias@gmail.com

¹<http://www.w3.org/TR/owl2-new-features/>

Punning

²<http://oppl.sf.net>

- enhancing ontology exploitation as part of bioinformatics workflows. *Journal of Biomedical Semantics*, 4(1):2+, 2013.
- [2] J. Goecks, A. Nekrutenko, J. Taylor, and Galaxy Team. Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. *Genome biology*, 11(8):R86+, 2010.