The Ontology for Avida digital evolution platform (OntoAvida)

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The Ontology for Avida (OntoAvida) aims to develop an integrated vocabulary for the description of Avida, the most widely used computational approach for performing experiment evolution using digital organisms.

The Problem is that: The lack of a clearly defined vocabulary makes some biologists feel reluctant to embrace the field of digital evolution.
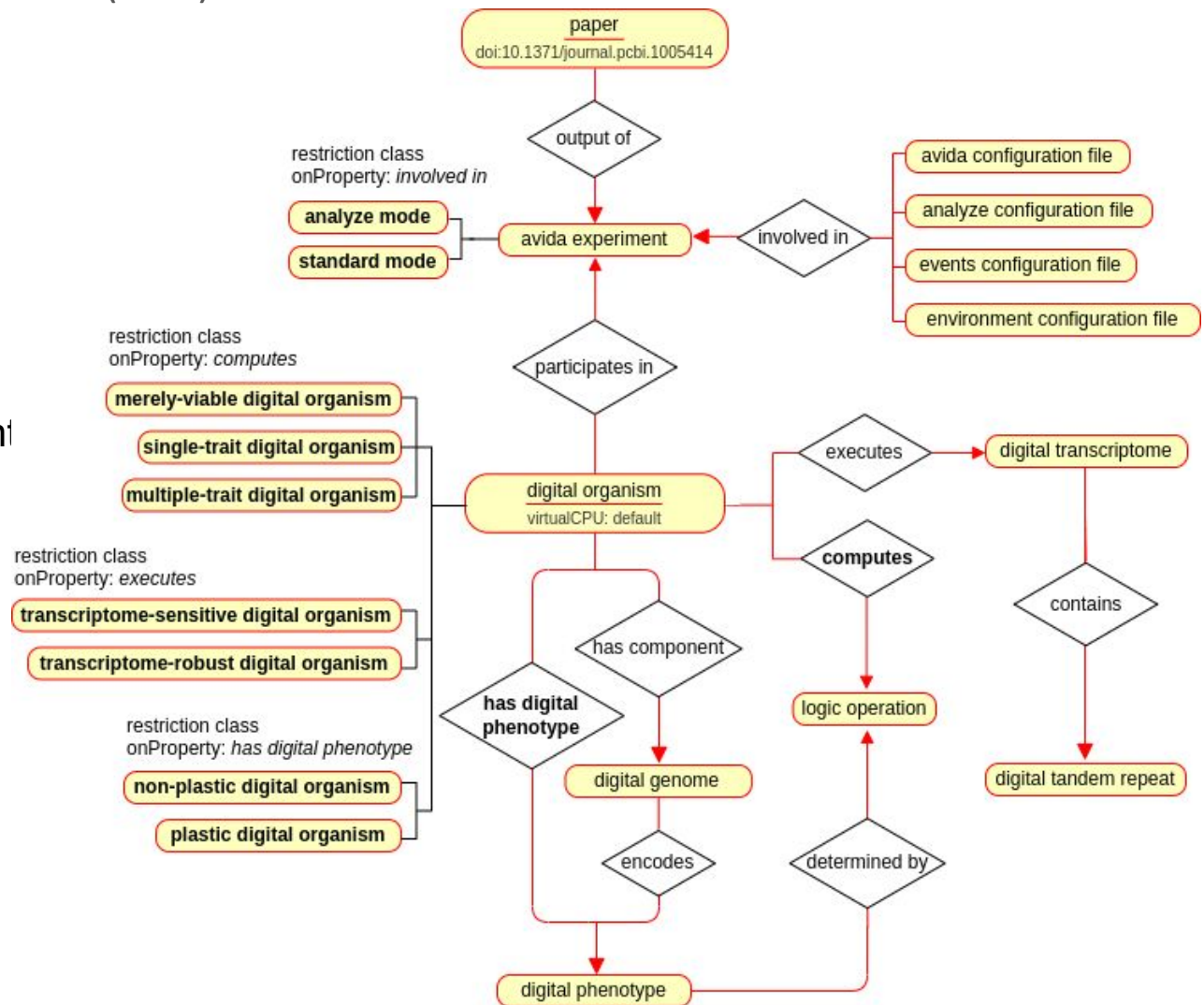

Fig.1. Subset of the ontology showing inference, reproducibility, and provenance

By using ROBOT commands the process of developing OntoAvida ontology was automatized (Fig.2).

For the development of the ontology we used the following ROBOT pipeline (from top to bottom): selecting terms from external ontologies to reuse them (extract); integrating new terms proposed by contributors (template); merging imported and template modules with the core ontology (merge); checking the logical consistency of the ontology (reason, reduce, and annotate); and releasing the ontology (convert).

OntoAvida is listed in the OBO registry (http://obofoundry.org) after passing the validation checks performed by the ROBOT software suite
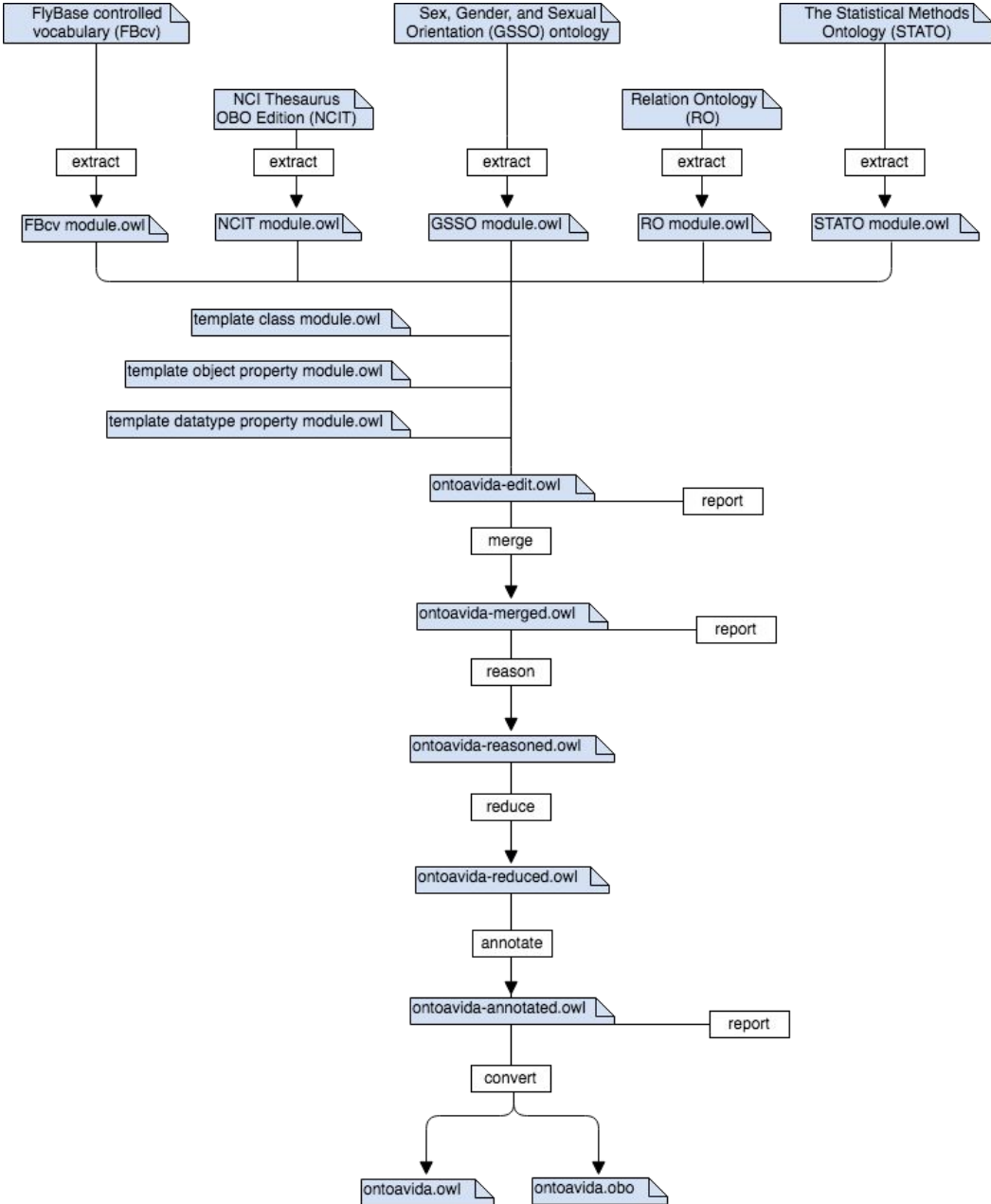
Fig.2. Ontology workflow.

SPARQL Querying AvidaDB for phenotypic plasticity

How an universal developmental property of phenotypes, such as plasticity, can be reported by using the containers in OntoAvida? (Fig.3).

The phenotypic plasticity of the digital organisms (i.e., the capability of the genome of a digital organism to encode different phenotypes in distinct computational environments.

The Ontology for Avida (OntoAvida) provides semantics to AvidaDB (a database that stores genomes, transcriptomes, and phenotypes of more than a million digital organisms).

Summary

OntoAvida will allow researchers to:
- make inferences (e.g. regarding phenotypic plasticity) based on certain rules and constraints,
- facilitate the reproducibility of in silico evolution experiments described in the scientific literature
- verify the origin of the stored Track data in AvidaDB.

Fig.3. The SPARQL query retrieves the 229 phenotypes encoded by the genome #273485 in 1000 distinct environments.