BPO: The Bioassay Protocol Ontology, a semantic approach to elevate reusability of AMR-related drug discovery data

IMI AMR Accelerator
Tackling antibiotic resistance together

COMBINE

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INTRODUCTION: To enhance the reproducibility and usability of bioassays in antimicrobial resistance associated drug discovery and development, there is an **increasing need for standardisation of bioassay metadata into machine-readable formats**.

At the study result output level, **general ontologies such as the BioAssay Ontology (BAO) already exist, but antibacterial drug discovery specific ontologies that can aid in the standardisation process at the protocol level are missing**.

METHODOLOGY: We tested **10 existing experimental assay** specific ontologies within this project to check the extend of extraction of information from natural language processing (NLP) models. But **none of them were able to provide a complete overview of underlying information**.

BPO was constructe with help of ontology creation tool like ROBOT (http://robot.obolibrary.org/) and the Ontology Development Kit ODK (https://github.com/INCATools/ontology-development-kit) to programmatically develop the ontology.

RESULTS: The BPO was initially established in order to extend the **interoperability and reusability of in-vivo AMR bioassay protocol data** generated within COMBINE.
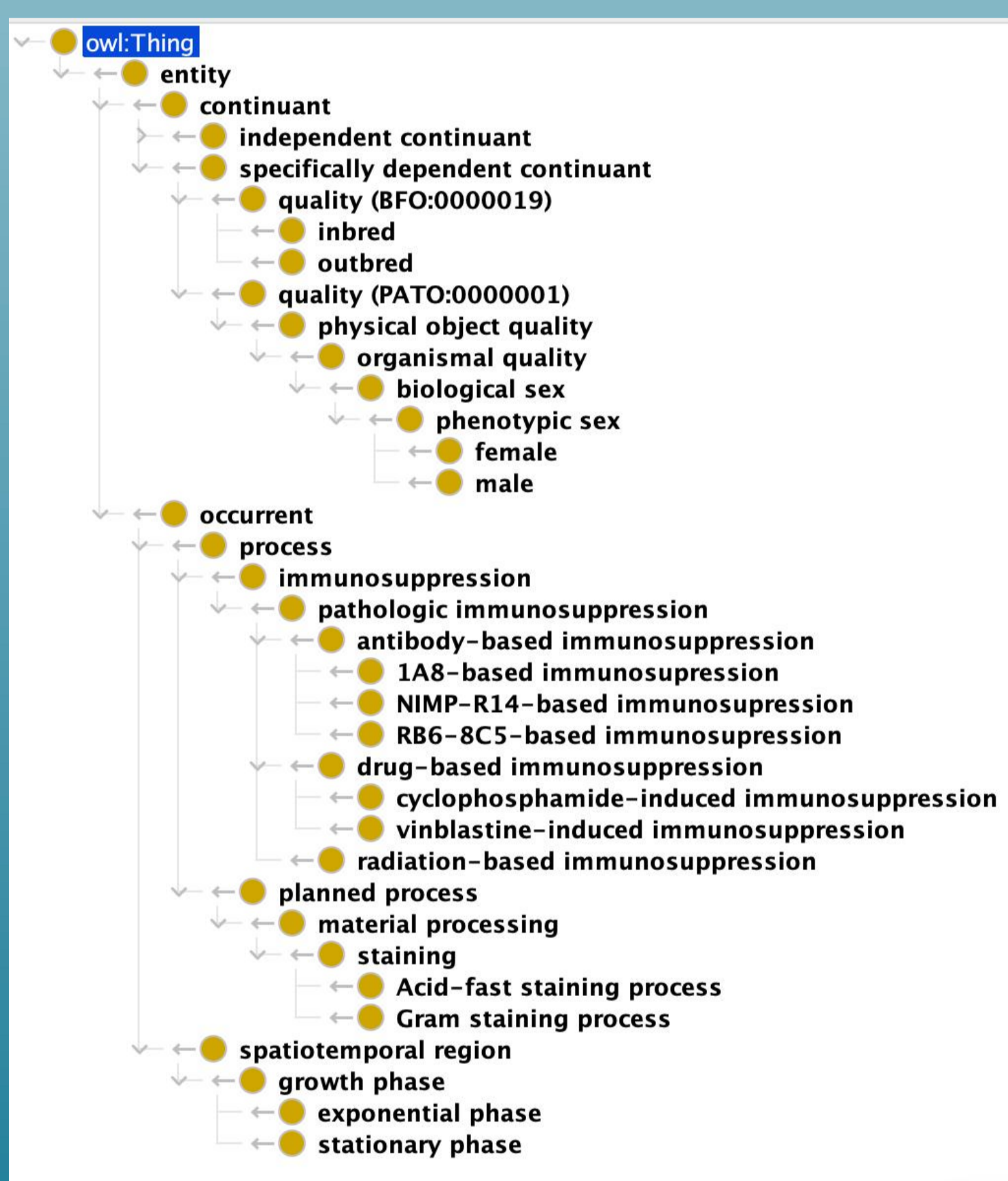
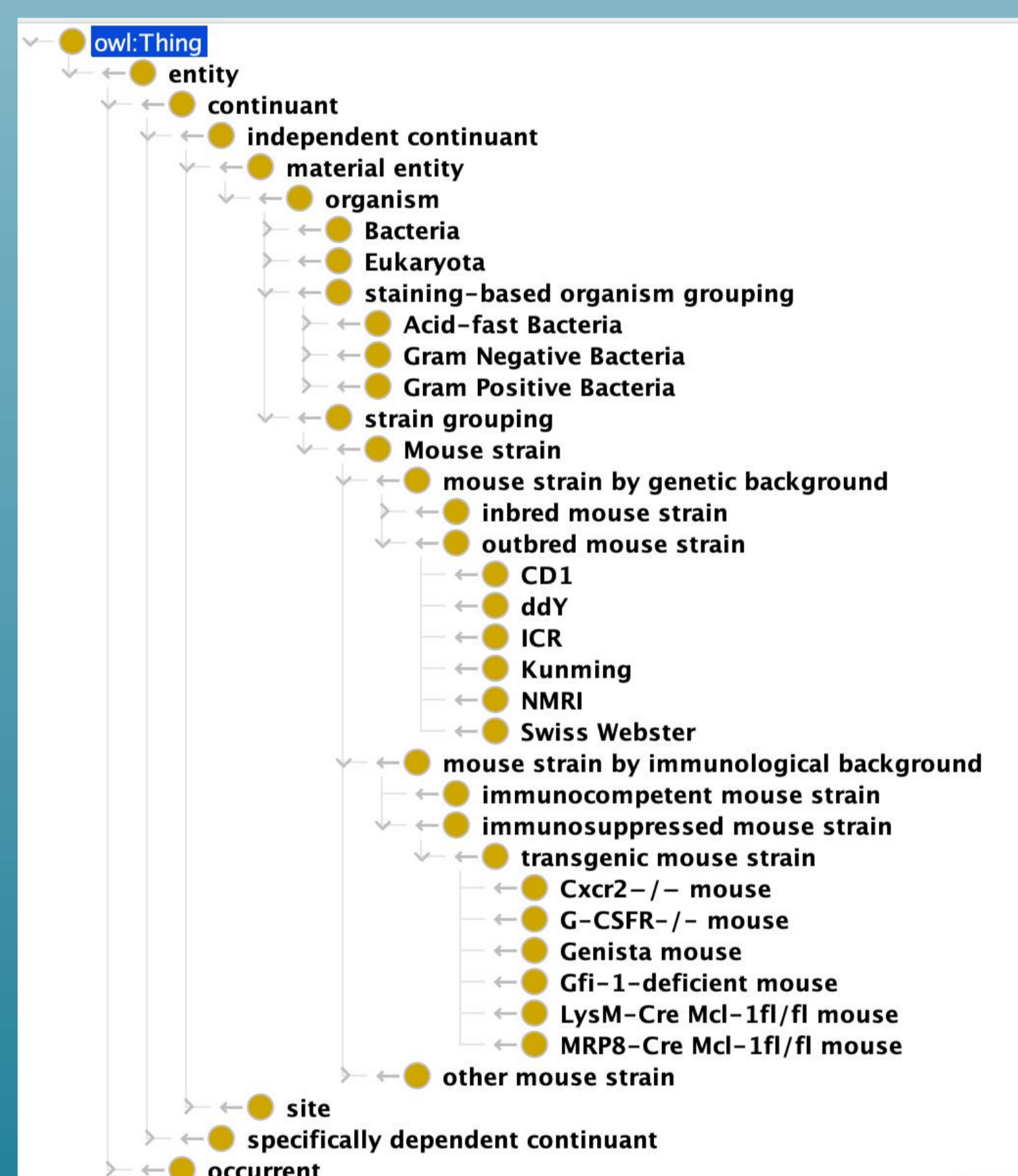Figure 1: The overview of the major classes included in the BPO ontology.

Figure 2: The additional classification and metadata annotation in BPO ontology. This includes the classification of bacteria strain and annotation of mouse strains based on their breeding or immunological classification

We created an **application ontology** through the combination of existing terms from prominent ontologies such as NCBI Taxonomy and PATO along with new terms around the animal model-specific details, such as mouse inbred and outbred status. Alongside addition of new terms, several terms have additional been requested to the parent reference ontologies.

Overall, BPO ontology has **209 classes** and **2,242 axioms**. In the coming months, we aim to integrate BPO into our information retrieval environment (GRIT42) for protocol-level annotation of bioassays.

CONCLUSION: The development of BPO is a first attempt to standardise and organise information within in-vivo AMR-related drug discovery bioassay protocol data in a structured manner. BPO will allow researchers to capture information regarding experimental details such as the type of mouse model, the bacterial strain, and the sex and growth phases of mouse and bacteria respectively from the protocol.

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