**CLASSES CLASSIFICATION**

**Newly created classes**

1. **disease\_name**: this tag contains common disease names (see XML).
2. **gmp**: no specific class already created to represent this.
3. **interaction**: same reason.

**SIO imported classes**

1. **gene:** import *gene* class from SIO (<http://semanticscience.org/resource/SIO_010035>).

Option: Could also import it from EFO (<http://purl.obolibrary.org/obo/SO_0000704>)?

1. **mutant\_phenotype:** import *phenotype* class (<http://semanticscience.org/resource/SIO_010056>) and add the concepts missing in that class?
2. **strain / associated strain:** import *strain* class (<http://semanticscience.org/resource/SIO_010055>)?

Options**:** - *strain accession* from EDAM (<http://edamontology.org/data_2912>)?

* *strain* from EFO (<http://www.ebi.ac.uk/efo/EFO_0005135>)?

1. **pathogen\_species**: *scientific name* class (<http://semanticscience.org/resource/SIO_000120>).

Option: *species name* from EDAM (<http://edamontology.org/data_1045>)?

**EDAM imported classes**

1. **host\_NCBI\_taxonomy\_id / pathogen\_NCBI\_taxonomy\_id:** *NCBI taxonomy ID class* (<http://edamontology.org/data_1179>). PROBLEM: two classes with same URI??
2. **database\_name:** *database name* class (<http://edamontology.org/data_1056>).
3. **accession:** *accession* class (<http://edamontology.org/data_2091>) or *protein accession* (<http://edamontology.org/data_2907)->> see PHI-tag description!
4. **sequence:** *sequence* class (<http://edamontology.org/data_2044>) and then have aa\_sequence and nt\_sequence as subclasses ??
5. **locus\_ID:** *locus ID* class (<http://edamontology.org/data_1893>).
6. **GO\_annotation:** *GO concept ID* class (<http://edamontology.org/data_1176>).
7. **gene\_name:** *gene name* class (<http://edamontology.org/data_2299>).

**EFO imported classes**

1. **experimental\_evidences:** *experimental process* class (<http://www.ebi.ac.uk/efo/EFO_0002694>) and complete with missing processes?
2. **essential\_gene\_lethal\_knockout:** *gene knock-out* class (<http://www.ebi.ac.uk/efo/EFO_0000506>)? Has\_value->yes/no???
3. **function:** *function* class (<http://www.ifomis.org/bfo/1.1/snap#Function>)?? I prefer SIO *function* (<http://semanticscience.org/resource/SIO_000017>).

**Classes imported from other ontologies**

1. **host\_target:** import Cellular Component Ontology (<http://brg.ai.sri.com/CCO/)>??

**Classes newly created but existing/related with PPIO**

1. **host\_response:** could integrate it within *phenotypic process* class?
2. **Experimental\_host:** maybe *host\_plant*, but the problem is that some plant names are not scientific names, they’re common plant names. New creation?
3. **in\_vitro\_growth:** integrate it within *growth\_type*?