NEW PPIO-PHI integration schema

We have tried to re-use classes and concepts from other well-known ontologies, allowing interoperability between PPIO, PHI and these ontologies. In the Excel spreadsheet, the colors correspond to:

* Blue: the new modeling structure according to Mark’s comments.
* Yellow: PHI- tags we are interested in.
* White: domain, property and range of the different terms.

The new modeling changes include (starting from the top left of the Excel sheet):

1. The **interaction** class will be created *de novo*, as we initially thought. The changes in this part are:
   1. phenotypic process renamed as phenotypic consequence.
   2. The “comments” tag from PHI could be modeled using the “description” term from Dublin Core. Comments? Suggestions?
2. The **gene** class will also be created *de novo*, but in this case there are a few changes with respect to the first modeling idea we had.
   1. has\_function would remain as an Object Property.
   2. gene\_name would be discarded. We would use EDAM ->GeneID + SIO has\_value Data Property.
   3. GO\_annotation : db\_xref (although we could somehow link to EDAM - > GO concept ID + SIO) Comments?
   4. locusID would be modeled the same as in b.
   5. For the aa\_sequence and the nt\_sequences, we could use the EDAM classes referring to sequence (*sequence, sequence features*) + SIO.
   6. accession and db\_type would also be modeled using EDAM existing classes.
   7. The two remaining properties (has gene mutation parametersand is related with/belongs to) would be created from scratch. These need to be created to relate the gene with the mutation features, and also to relate the gene features with the plant pathogens.
3. The **gmp** (gene mutation parameters) class will be also created, but with some modifications:
   1. For the lethal knockout property, we could reuse a similar class from EFO (*gene knockout)*, although is not the exactly the same concept, so I will think of another idea. Comments?
   2. experimental\_evidences could be modeled using EFO classes (*experimental process*, probably). It’s the best approach.
   3. The mutant\_phenotype is still an enigma. I am looking for similar things in SO (any suggestions?)
4. In the **plant pathogen** class:
   1. The associated strainand the strain properties would be modeled using EFO related classes.
   2. in vitro growth type would be created. The data in PHI concerning this tag is quite diverse and contains lots of different terms, and I think it would be difficult to try and link it with existing classes in other ontologies. Comments?
   3. has\_gene would be created. This, as mentioned before, would allow clarifying that the genes features described belong to the plant pathogen domain.
5. The rest of the terms/properties are related with the taxonomy. The taxonomy part is being done as it was when the ontology started developing, that is, taking advantage of the NCBI taxonomy site.