Ontologies tutorial:OPA2VEC

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Semantic similarity (Limitations)

- Uses only a limited set of axioms from the ontology.
- Pre-defined measure for all datasets and applications.
- Reduces all information to one single value.

OPA2Vec: An Alternative ...

- What is it?
- How does it work?
- How to use it?

OPA2Vec

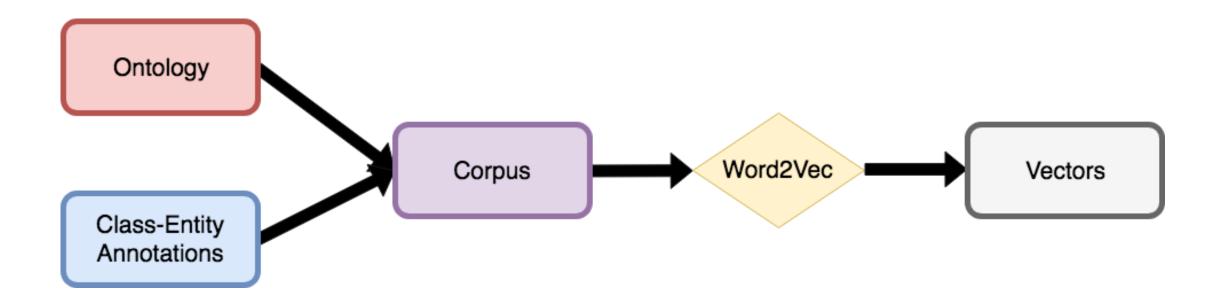
- Produces vector representations for biological entities from:
 - Ontologies: axioms + metadata (GO)
 - Their annotations to biological entities (proteins).

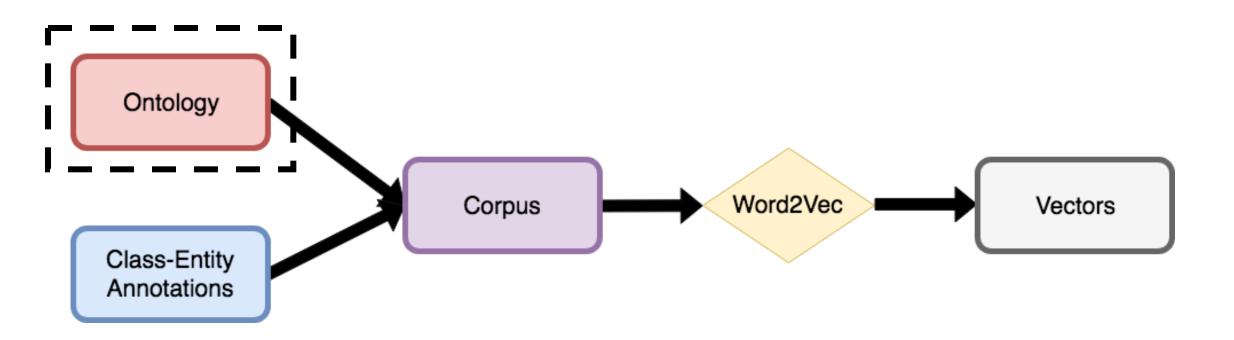
What can it be used for ?

• A trained and data-specific semantic similarity measure.

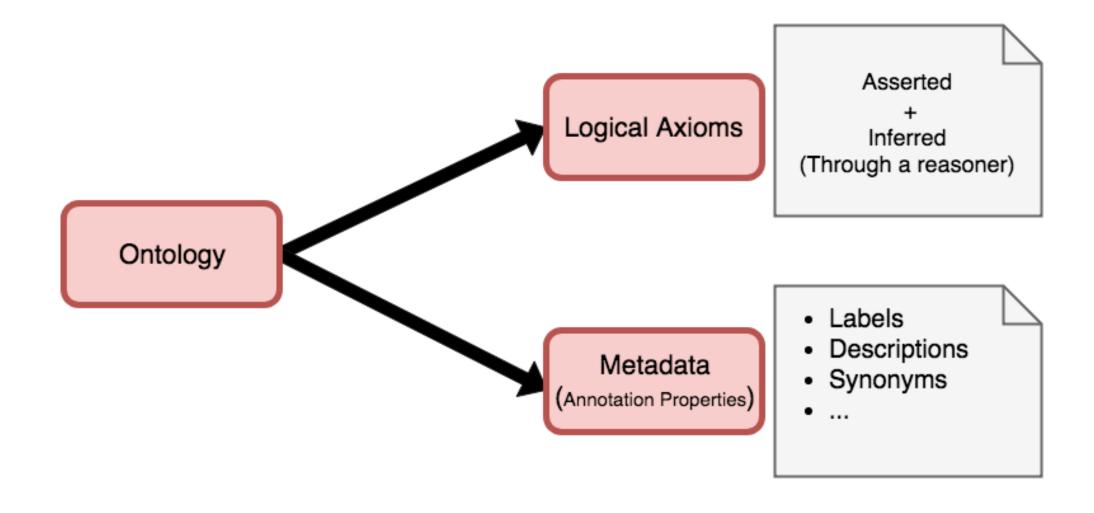
Set of features for machine learning algorithms.

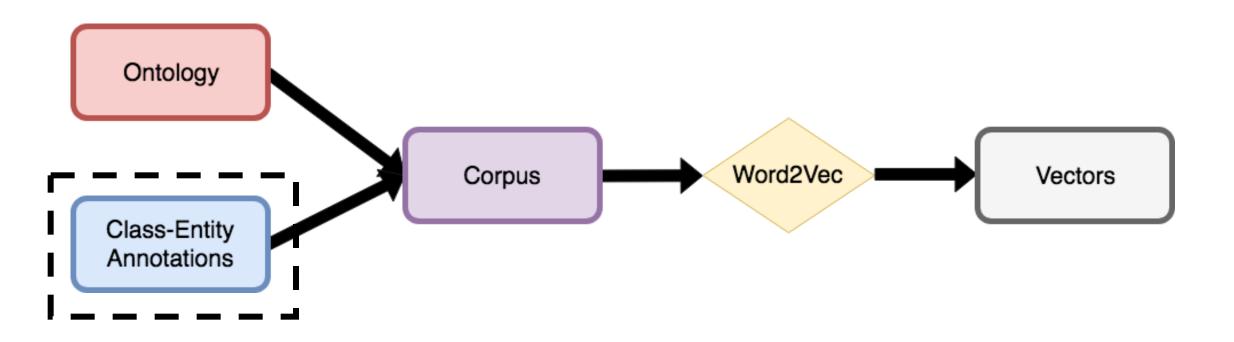
Can be used to visualize the data.



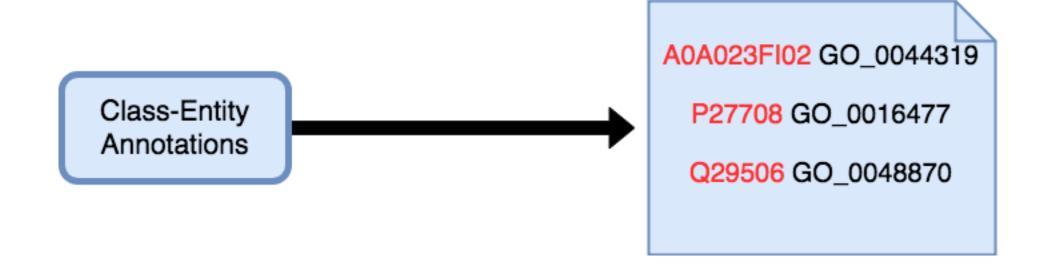


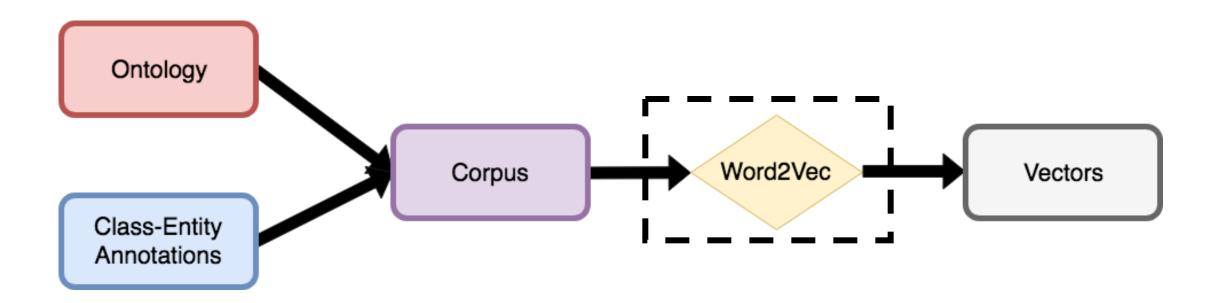
Ontology Information





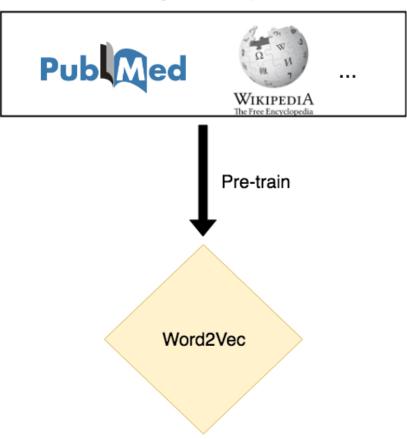
Annotation Information





Word2Vec

Background Corpus



How to use OPA2Vec

- Mandatory input:
 - Owl Ontology
 - Class-entity annotations (e.g.: GO-protein annotation)
- Optional parameters:
 - Metadata annotations: labels, description, synonyms ... (default value: all)
 - e.g: <http://purl.obolibrary.org/obo/IAO 0000115>
 - Vector size (default 200)
 - Word2vec parameters:
 - Model: cbow or sg (default value: sg)
 - Window size (default value: 5)
 - Mincount (default value: 25)
 - Pre trained model: Corpus used to pre-train Word2Vec for some background information (Have to be pre-trained already).
 - List of entities for which you want to get the vector representation (default: all classes and entities)

How to run OPA2Vec?

- Download package from:
 - https://github.com/bio-ontology-research-group/opa2vec
 - Get your ontology (e.g. go.owl) and annotation file (e.g. protein-GO annotation).

• To run with default parameters, use command:

python runOPA2Vec.py go.owl SampleAssociationFile.lst

You can also modify the default values as shown below: