
fastsemsim Documentation

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Marco Mina

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Contents:

FASTSEMSIM LIBRARY

1.1 fastsemsim.Ontology module

This module contains all the classes and scripts used to load and represent ontologies and annotation corpora by fastSemSim

1.1.1 Ontology.ontologies

Set of functions to parse and handle ontologies.

class fastsemsim.Ontology.ontologies.**OboParser** (*ontology_class*, *parameters*={})

```
alt_id_tag = 'alt_id'
comment_tag = '!'
consider_tag = 'consider'
def_tag = 'def'
delimiter_tag = ':'
find_next_term()
has_tag_structure(st)
id_tag = 'id'
is_a_tag = 'is_a'
is_obsolete_tag = 'is_obsolete'
name_tag = 'name'
namespace_tag = 'namespace'
parse(_handle)
relationship_delimiter_tag = ''
relationship_tag = 'relationship'
replaced_by_tag = 'replaced_by'
split_rel_tag(st)
split_tag(st)
term_tag = '[Term]'
```

```
typedef_tag = ['Typedef']

class fastsemsim.Ontology.ontologies.OboXmlParser(ontology_class, parameters={})
    Bases: xml.sax.handler.ContentHandler

    alt_id_tag = 'alt_id'

    characters(ch)

    comment_tag = '!'

    consider_tag = 'consider'

    def_tag = 'def'

    delimiter_tag = ':'

    endElement(name)

    id_tag = 'id'

    is_a_tag = 'is_a'

    is_obsolete_tag = 'is_obsolete'

    name_tag = 'name'

    namespace_tag = 'namespace'

    part_of_tag = 'part_of'

    relationship_delimiter_tag = ''

    relationship_tag = 'relationship'

    relationship_to_tag = 'to'

    relationship_type_tag = 'type'

    replaced_by_tag = 'replaced_by'

    startElement(name, attrs)

    term_tag = 'term'

fastsemsim.Ontology.ontologies.load(source=None, source_type='obo', ontology_type='GeneOntology', parameters={})
fastsemsim.Ontology.ontologies.parse(source=None, source_type='obo', ontology_type='GeneOntology', parameters={})
```

1.1.2 Ontology.Ontology

Supported ontologies are those representable as multirooted DAGs. It is not required DAGs to be disconnected, but 'inter-DAG' edges are required to be specified. Class Ontology provides a function `is_consistent` that checks whether this constraints is satisfied. Inconsistent DAGs are NOT currently usable.

Different datastructures can be used to represent ontologies. The section Variables lists a set of different alternatives. Currently Ontology is tuned for using a parent-children and a node-edge representation.

Superclasses can extend the basic datastructure with additional layers of information.

```
class fastsemsim.Ontology.Ontology.Ontology(terms, edges, parameters=None)
    Bases: object

    Base class for the representation of an ontology. It currently supports any multi-rooted DAG (Directed Acyclic Graph).
```



```

debug = False
det_roots ()
edge_number ()
gen_error = False
id2node (codes, alt_check=True)
is_consistent ()
is_valid (term)
name2node (codes)
node2id (codes, alt_check=False)
node_number ()

```

1.1.3 Ontology.GeneOntology

Gene Ontology class

```

class fastsemsim.Ontology.GeneOntology.GeneOntology (terms, edges, parameters)
    Bases: fastsemsim.Ontology.Ontology.Ontology

```

1.1.4 Ontology.CellOntology

@mail marco.mina.85@gmail.com @version 2.0 @desc CellOntology class handles CellOntology

Cell Ontology class

```

class fastsemsim.Ontology.CellOntology.CellOntology (terms, edges, parameters)
    Bases: fastsemsim.Ontology.Ontology.Ontology

    alt_ids = None
    obsolete_ids = None

```

1.1.5 Ontology.DiseaseOntology

@mail marco.mina.85@gmail.com @version 2.0 @desc DiseaseOntology class handles DiseaseOntology

Disease Ontology class

```

class fastsemsim.Ontology.DiseaseOntology.DiseaseOntology (terms, edges, parameters)
    Bases: fastsemsim.Ontology.Ontology.Ontology

    alt_ids = None
    obsolete_ids = None

```

1.1.6 Ontology.AnnotationCorpus

This class provides a unified interface to handle Annotation Corpora.

annotations: dict with protein ids as primary key. Each key is associated with a dictionary of GO Terms annotated for the protein. Detailed information, when available, are included as values within the latter dictionary.

`reverse_annotations`: dict with GO Terms as primary key. Each key is associated with a dict of proteins/gene products annotated with the GO term.

`obj_set`: set of proteins/gene products present in the annotation table, connected with the taxon id of the organism they belong to, when this information is available. This table is useful to filter out proteins from uninteresting species.

`term_set`: set of terms present in the annotation table.

If a GO object is passed as input data, annotation corpus is corrected removing obsolete annotations and resolving alternative ids. This can be done later by calling `sanitize` method after supplying a valid GO object.

`general_parameters`: filtering options and parameters that apply in general `specific_parameters`: parameter that should be used to load a particular file format

Each type of file carries different types of information. How to deal with that? Every operation is rerouted to the original file parser, that will take care of it. This is good since it avoids to duplicate data.

Constraint: an Ontology MUST be loaded and provided as an `AnnotationCorpus` object is instantiated.

```
class fastsemsim.Ontology.AnnotationCorpus.AnnotationCorpus (go)
```

```
    Bases: object
```

```
    class ECFilter (params)
```

```
        EC = {}
```

```
        filter (EC)
```

```
        inclusive = False
```

```
        name = 'EC'
```

```
    class AnnotationCorpus.GOFilter (params=None)
```

```
        GO = None
```

```
        filter (GO)
```

```
        inclusive = True
```

```
        int_go = None
```

```
        name = 'GO'
```

```
        set (params)
```

```
    class AnnotationCorpus.TaxonomyFilter (params)
```

```
        filter (taxonomy)
```

```
        inclusive = False
```

```
        name = 'taxonomy'
```

```
        taxonomy = {}
```

```
    AnnotationCorpus.annotations = {}
```

```
    AnnotationCorpus.annotations_field2pos = {}
```

```
    AnnotationCorpus.annotations_fields = []
```

```
    AnnotationCorpus.constrain ()
```

```
    AnnotationCorpus.initCommonFilter ()
```

```

AnnotationCorpus.int_checkConsistency ()
AnnotationCorpus.int_resetFields ()
AnnotationCorpus.isConsistent ()
AnnotationCorpus.isOk (field, value)
AnnotationCorpus.load (fname, ftype, params={})
AnnotationCorpus.obj_field2pos = {}
AnnotationCorpus.obj_fields = []
AnnotationCorpus.obj_set = {}
AnnotationCorpus.parse (fname, ftype, params={})
AnnotationCorpus.reset ()
AnnotationCorpus.resetCommonfilter (i)
AnnotationCorpus.resetFilter (field)
AnnotationCorpus.reverse_annotations = {}
AnnotationCorpus.reverse_annotations_field2pos = {}
AnnotationCorpus.reverse_annotations_fields = []
AnnotationCorpus.sanitize ()
AnnotationCorpus.setCommonfilters (inf)
AnnotationCorpus.setFilter (field, selector)
AnnotationCorpus.term_field2pos = {}
AnnotationCorpus.term_fields = []
AnnotationCorpus.term_set = {}

```

1.1.7 Ontology.GAF2AnnotationCorpus

#@desc Class to parse Annotation Corpus files in GAF-2.0 format [i.e. Gene Ontology Annotation files] tab separated file. Format as defined in <http://geneontology.org/page/go-annotation-file-gaf-format-20>

class fastsemsim.Ontology.GAF2AnnotationCorpus.**GAF2AnnotationCorpus** (*ac*, *parameters=None*)

```

Bases: object

int_comment = '!'
int_interpretParameters ()
int_separator = '\t'
isOk ()
parse (fname)
setFields ()

```

1.1.8 Ontology.PlainAnnotationCorpus

Plain annotation corpus files parsing utility. Plain format 1: object (eg. gene) ID - Term ID Plain format 1: Term ID - object (eg. gene) ID

```
class fastsemsim.Ontology.PlainAnnotationCorpus.PlainAnnotationCorpus (ac,
                                                                    parameters=None)

    Bases: object

    int_interpretParameters ()

    isOk ()

    parse (fname)

    setFields ()
```

1.2 fastsemsim.data module

This module contains a set of embedded ontologies and annotation corpora, and a class for keeping track and easily find the required datasets.

1.2.1 fastsemsim.data.dataset submodule

```
class fastsemsim.data.dataset.Dataset (descriptor=None)

    Bases: object

    This class keeps track of the dataset of ontologies and annotation corpora included in fastSemSim. The file
    data/dataset.txt is read to collect the list of embedded ontologies and annotation corpora.

    get_annotation_corpus (dataset_name)
        Return the required annotation corpus

    get_annotation_corpus_by_species (ontology=None, species=None)
        Return the annotation corpus for the selected species, and compatible with the ontology specified by the
        ontology parameter.

    get_dataset (dataset_name)
        Return the required dataset

    get_default_annotation_corpus (ontology=None, species=None)
        Return the default annotation corpus for the selected species, and compatible with the ontology specified
        by the ontology parameter.

    get_default_ontology (ontology_type)
        Return the default embedded ontology of the ontology_type type

    get_ontology (dataset_name)
        Return the required ontology

    populate (descriptor=None)
        Initialize class structures. Use the descriptor parameter to specify a dataset descriptor file. By default, the
        file data/dataset.txt will be used.
```

1.3 fastsemsim.SemSim module

This module contains the classes for the evaluation of the Semantic Similarity. Please refer to the single classes for details on the implemented measures.

1.3.1 SemSim.TermSemSim

This class provides the prototype for Term semantic similarity measures (TSS)

There are two types of Term semantic similarity: a first group that can evaluate the semantic similarity between two sets of terms (groupwise - G_TSS), and a second group that can only evaluate the similarity between pairs of GO terms (pairwise - P_TSS). Each class extending TermSemSim should declare whether it is groupwise or pairwise.

TermSemSim relies on SemSimUtils to perform a lot of tasks (e.g. evaluating Term IC or common ancestors). A SemSimUtils object can be passed to the constructor as input data. Otherwise, a new instance will be created. Using only one copy of SemSimUtils helps reducing time and space requirements and is strongly recommended.

exception fastsemsim.SemSim.TermSemSim.**MissingAcException** (*message*)

Bases: exceptions.Exception

class fastsemsim.SemSim.TermSemSim.**TermSemSim** (*ontology*, *ac=None*, *util=None*, *do_log=False*)

Bases: object

G_TSS = 'Groupwise'

IC_based = None

P_TSS = 'Pairwise'

SS_type = None

SemSim (*term1*, *term2*, *ontology=None*)

format_and_check_data = True

setSanityCheck (*en*)

1.3.2 SemSim.ObjSemSim

This class provides the prototype for a generic Object Semantic Similarity measure

class fastsemsim.SemSim.ObjSemSim.**ObjSemSim** (*ontology*, *ac*, *TSS=None*, *MSS=None*, *util=None*, *do_log=False*)

Bases: object

SemSim (*obj1*, *obj2*, *root=None*)

1.3.3 SemSim.ObjSetSemSim

This class provides the prototype for a generic Object Set Semantic Similarity measure (PSS)

class fastsemsim.SemSim.ObjSetSemSim.**ObjSetSemSim** (*ontology*, *ac*, *TSS=None*, *MSS=None*, *util=None*, *do_log=False*)

SemSim (*obj1*, *obj2*, *root=None*)

1.3.4 SemSim.SetSemSim

This class provides the prototype for a generic Pairwise Object Semantic Similarity measure

```
class fastsemsim.SemSim.SetSemSim.SetSemSim(ontology, ac=None, TSS=None, MSS=None,
                                           util=None, do_log=False)

    SemSim(obj1, obj2, root=None)
```

1.3.5 Specific Semantic Similarity measures

SemSim.ResnikSemSim

Resnik Semantic Similarity Measure

Reference: Resnik, P. (1999). Semantic similarity in a taxonomy: An information-based measure and its application to problems of ambiguity in natural language. *Journal of Artificial Intelligence Research*, 11, 95-130.

```
class fastsemsim.SemSim.ResnikSemSim.ResnikSemSim(ontology, ac=None, util=None,
                                                  do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = True
    SS_type = 'Pairwise'
```

SemSim.CosineSemSim

Cosine Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.CosineSemSim.CosineSemSim(ontology, ac=None, util=None,
                                                  do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = False
    SS_type = 'Groupwise'
    dotprod(vector1, vector2)
    extend_annotations = True
```

SemSim.CzekanowskiDiceSemSim

Czekanowski and Dice Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.CzekanowskiDiceSemSim.CzekanowskiDiceSemSim(ontology,
                                                                      ac=None,
                                                                      util=None,
                                                                      do_log=False)

    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = False
    SS_type = 'Groupwise'
```

```
extend_annotations = True
```

SemSim.DiceSemSim

Dice Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.DiceSemSim.DiceSemSim(ontology, ac=None, util=None,
                                              do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = False
    SS_type = 'Groupwise'
    extend_annotations = True
```

SemSim.GSESAMESemSim

G-SESAME Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.GSESAMESemSim.GSESAMESemSim(ontology, ac=None, util=None,
                                                      do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = False
    SS_type = 'Pairwise'
    generic_score = 0.5
    is_a_score = 0.8
    neg_regulates_score = 0.6
    part_of_score = 0.6
    pos_regulates_score = 0.6
    regulates_score = 0.6
    score_ancestors(term)
    score_edge(tp, t)
```

SemSim.JaccardSemSim

Jaccard Index based Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.JaccardSemSim.JaccardSemSim(ontology, ac=None, util=None,
                                                     do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = False
    SS_type = 'Groupwise'
    extend_annotations = True
```

SemSim.JiangConrathSemSim

Jiang and Conrath Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.JiangConrathSemSim.JiangConrathSemSim(ontology, ac=None,
                                                                util=None,
                                                                do_log=False)

    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

    IC_based = True

    SS_type = 'Pairwise'
```

SemSim.LinSemSim

Lin Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.LinSemSim.LinSemSim(ontology, ac=None, util=None, do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

    IC_based = True

    SS_type = 'Pairwise'
```

SemSim.SimGICSemSim

SimGIC Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.SimGICSemSim.SimGICSemSim(ontology, ac=None, util=None,
                                                    do_log=False)

    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

    IC_based = True

    SS_type = 'Groupwise'
```

SemSim.SimICNDSemSim

ICND Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.SimICNDSemSim.ICNDSemSim(ontology, ac=None, util=None,
                                                    do_log=False)

    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

    IC_based = True

    SS_type = 'Pairwise'

    generic_score = 1.0

    is_a_score = 1.0

    neg_regulates_score = 1.0
```



```

part_of_score = 1.0
pos_regulates_score = 1.0
regulates_score = 1.0
score_ancestors (term)
score_edge (tp, t)

```

SemSim.SimICNPSSemSim

ICNP Semantic Similarity Measure

Reference:

```

class fastsemsim.SemSim.SimICNPSSemSim.ICNPSSemSim (ontology,      ac=None,      util=None,
                                                    do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = True
    SS_type = 'Pairwise'
    generic_score = 1.0
    is_a_score = 1.0
    neg_regulates_score = 1.0
    part_of_score = 1.0
    pos_regulates_score = 1.0
    regulates_score = 1.0
    score_ancestors (term)
    score_edge (tp, t)

```

SemSim.SimICSemSim

Information Content Semantic Similarity Measure

Reference:

```

class fastsemsim.SemSim.SimICSemSim.SimICSemSim (ontology,      ac=None,      util=None,
                                                    do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = True
    SS_type = 'Pairwise'
    use_Lin = True

```

SemSim.SimNTOSemSim

Normalized Term Overlap Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.SimNTOSemSim.SimNTOSemSim(ontology, ac=None, util=None,
                                                    do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = False
    SS_type = 'Groupwise'
    extend_annotations = True
```

SemSim.SimRelSemSim

SimRel Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.SimRelSemSim.SimRelSemSim(ontology, ac=None, util=None,
                                                    do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = True
    SS_type = 'Pairwise'
    use_Lin = True
```

SemSim.SimTOSemSim

SimTO Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.SimTOSemSim.SimTOSemSim(ontology, ac=None, util=None,
                                                    do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = False
    SS_type = 'Groupwise'
```

SemSim.SimUISemSim

SimUI Semantic Similarity Measure

Reference:

```
class fastsemsim.SemSim.SimUISemSim.SimUISemSim(ontology, ac=None, util=None,
                                                    do_log=False)
    Bases: fastsemsim.SemSim.TermSemSim.TermSemSim
    IC_based = False
    SS_type = 'Groupwise'
```

1.3.6 SemSim.MixSemSim

This class provides the prototype for a generic mixing strategy for pairwise Term Semantic Similarity measures

```
class fastsemsim.SemSim.MixSemSim.MixSemSim(ontology, ac, util=None, do_log=False)
    Bases: object
```

SemSim (*set1, set2, TSS*)

1.3.7 SemSim.avgSemSim

This class defines the prototype for a generic mixing strategy for pairwise term Protein Semantic Similarity measures

```
class fastsemsim.SemSim.avgSemSim.avgSemSim (ontology, ac, util=None, do_log=False)
    Bases: fastsemsim.SemSim.MixSemSim.MixSemSim
```

1.3.8 SemSim.maxSemSim

Max mixing strategy

```
class fastsemsim.SemSim.maxSemSim.maxSemSim (ontology, ac, util=None, do_log=False)
    Bases: fastsemsim.SemSim.MixSemSim.MixSemSim
```

1.3.9 SemSim.BMASemSim

Best Match Average (BMA) mixing strategy for pairwise term Protein Semantic Similarity measures

```
class fastsemsim.SemSim.BMASemSim.BMASemSim (ontology, ac, util=None, do_log=False)
    Bases: fastsemsim.SemSim.MixSemSim.MixSemSim

    fair = True
```

1.3.10 SemSim.SemSimUtils

This class provides some routines to calculate basic properties used by different SS measures. In particular this class provides code for evaluating:

- term ICs
- term frequency within an annotation corpus
- term's ancestors
- term's offspring
- terms's children
- terms's parents
- MICA/DCA/LCA
- term's distance

```
class fastsemsim.SemSim.SemSimUtils.SemSimUtils (ontology, ac=None)
    Bases: object

    det_IC (term)
    det_IC_table ()
    det_MICA (term1, term2)
    det_ancestors_union (term1, term2)
    det_common_ancestors (term1, term2)
    difference (set1, set2)
```

```
get_ancestors(term1)
int_det_IC(term_id)
int_det_IC_table()
int_det_ancestors(goid, temp_intra)
int_det_ancestors_table()
int_det_freq(term_id)
int_det_freq_table()
int_det_lineage()
int_det_offspring(goid, temp_intra)
int_det_offspring_table()
int_det_p(term_id)
int_det_p_table()
int_merge_sets(set1, set2)
intersection(set1, set2)
```

COMMAND LINE INTERFACE

The FastSemSim package includes a command line utility to load ontologies and annotation corpora, and to evaluate the available semantic similarity measures.

After installation, you may run the command line utility just by typing `fastsemsim` in your console.

Please use `fastsemsim -h` to visualize the full set of parameters.

GRAPHICAL USER INTERFACE

Still to be implemented

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