fastsemsim Documentation

Release 0.9

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December 10, 2014

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CHAPTER

ONE

CODE

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`Ontology.`**`Ontology`**
alias of `Ontology.Ontology`

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CHAPTER

TWO

FASTSEMSIM PACKAGE

2.1 Subpackages

2.1.1 fastsemsim.Ontology package

Submodules

fastsemsim.Ontology.AnnotationCorpus module

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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 = {}**

fastsemsim.Ontology.CellOntology module

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

alt_ids = None

obsolete_ids = None

fastsemsim.Ontology.DiseaseOntology module

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

alt_ids = None

obsolete_ids = None

fastsemsim.Ontology.FFOntology module

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@mail marco.mina.85@gmail.com @version 2.0 @desc GeneOntology class: extend Ontology to handle the GeneOntology

class fastsemsim.Ontology.FFOntology.**FFOntology**(*terms*, *edges*, *parameters=None*)

Bases: fastsemsim.Ontology.Ontology.Ontology

alt_ids = None

id2name(*codes*, *alt_check=False*)

name2id(*codes*, *alt_check=True*)

obsolete_ids = None

fastsemsim.Ontology.GAF2AnnotationCorpus module

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

Bases: object

int_comment = '!'

int_interpretParameters()

int_separator = '\t'

isOk()

parse(*fname*)

setFields()

fastsemsim.Ontology.GOAnnotationCorpus module

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class fastsemsim.Ontology.GOAnnotationCorpus.**GOAnnotationCorpus**(*go=None*)

class **ECFilter**(*params*)

EC = {}

filter(*EC*)

inclusive = False

name = 'EC'

class GOAnnotationCorpus.**GOFilter**(*params=None*)

GO = None

filter(*GO*)

inclusive = True

int_go = None

name = 'GO'

set(*params*)

class GOAnnotationCorpus.**TaxonomyFilter**(*params*)

filter(*taxonomy*)

inclusive = False

name = 'taxonomy'

taxonomy = {}

GOAnnotationCorpus.**constrain**()

GOAnnotationCorpus.**initCommonFilter**()

GOAnnotationCorpus.**int_checkConsistency**()

GOAnnotationCorpus.**int_exclude_GO_root** = True

GOAnnotationCorpus.**int_resetFields**()

GOAnnotationCorpus.**isConsistent**()

GOAnnotationCorpus.**isOk**(*field*, *value*)

GOAnnotationCorpus.**load**(*fname*, *ftype*, *params={}*)

GOAnnotationCorpus.**parse**(*fname*, *ftype*, *params={}*)

GOAnnotationCorpus.**reset**()

GOAnnotationCorpus.**resetCommonfilter**(*i*)

GOAnnotationCorpus.**resetFilter**(*field*)

GOAnnotationCorpus.**sanitize**()

GOAnnotationCorpus.**setCommonfilters**(*inf*)

GOAnnotationCorpus.**setFilter**(*field*, *selector*)

fastsemsim.Ontology.GeneOntology module

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@mail marco.mina.85@gmail.com @version 2.0 @desc GeneOntology class: extend Ontology to handle the GeneOntology

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

fastsemsim.Ontology.Ontology module

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 contraints 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()

fastsemsim.Ontology.PlainAnnotationCorpus module

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

Bases: object

int_interpretParameters()

isOk()

parse(*fname*)

setFields()

fastsemsim.Ontology.ontologies module

Current implementation can only handle single-scope 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={}*)

Module contents

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2.1.2 fastsemsim.SemSim package

Submodules

fastsemsim.SemSim.BMASemSim module

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

Bases: fastsemsim.SemSim.MixSemSim.MixSemSim

fair = True

fastsemsim.SemSim.CosineSemSim module

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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

fastsemsim.SemSim.CzekanowskiDiceSemSim module

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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

fastsemsim.SemSim.DiceSemSim module

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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

fastsemsim.SemSim.GSESAMESemSim module

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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*)

fastsemsim.SemSim.JaccardSemSim module

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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

fastsemsim.SemSim.JiangConrathSemSim module

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

Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

IC_based = True

SS_type = 'Pairwise'

fastsemsim.SemSim.LinSemSim module

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

Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

IC_based = True

SS_type = 'Pairwise'

fastsemsim.SemSim.MixSemSim module

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

Bases: `object`

`SemSim`(*set1*, *set2*, *TSS*)

fastsemsim.SemSim.ObjSemSim module

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

Bases: `object`

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

fastsemsim.SemSim.ObjSetSemSim module

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

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

fastsemsim.SemSim.ResnikSemSim module

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

Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

IC_based = True

SS_type = 'Pairwise'

fastsemsim.SemSim.SemSimUtils module

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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*)

fastsemsim.SemSim.SetSemSim module

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

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

fastsemsim.SemSim.SimGICSemSim module

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

Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

IC_based = True

SS_type = 'Groupwise'

fastsemsim.SemSim.SimICNDSemSim module

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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*)

fastsemsim.SemSim.SimICNPSemSim module

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class fastsemsim.SemSim.SimICNPSemSim.**ICNPSemSim**(*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*)

fastsemsim.SemSim.SimICSemSim module

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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

fastsemsim.SemSim.SimNTOSemSim module

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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

fastsemsim.SemSim.SimRelSemSim module

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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

fastsemsim.SemSim.SimTOSemSim module

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

Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

IC_based = False

SS_type = 'Groupwise'

fastsemsim.SemSim.SimUISemSim module

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

Bases: fastsemsim.SemSim.TermSemSim.TermSemSim

IC_based = False

SS_type = 'Groupwise'

fastsemsim.SemSim.TermSemSim module

TermSemSim class

This class provides the prototype for a generic Term Semantic Similarity measure (TSS)

There are two types of Term Sem Sim: those which evaluate the semantic similarity between two sets of terms (groupwise - G_TSS), and those which 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 (such as 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 spece requirements and is strongly adviced.

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*)

fastsemsim.SemSim.avgSemSim module

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

fastsemsim.SemSim.maxSemSim module

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

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fastsemsim.SemSim.**select_mix_SemSim**(*mix_name*)

fastsemsim.SemSim.**select_term_SemSim**(*tss_name*)

fastsemsim.SemSim.**term_SemSim_measures = {'G-SESAME': (<class 'fastsemsim.SemSim.GSESAMESemSim.GSES**
Struct mix_strategies. Contains a list of all available mixing strategies It is built as a dictionary. Mixing strategy names are used as keys. Each entry is a tuple with the following structure: (class pointer,)

2.1.3 fastsemsim.data package

Submodules

fastsemsim.data.dataset module

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class fastsemsim.data.dataset.**Dataset**(*descriptor=None*)
Bases: object

get_annotation_corpus(*dataset_name*)

get_annotation_corpus_by_species(*ontology=None*, *species=None*)

get_dataset(*dataset_name*)

get_default_annotation_corpus(*ontology=None*, *species=None*)

get_default_ontology(*ontology_type*)

get_ontology(*dataset_name*)

populate(*descriptor=None*)

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2.1.4 fastsemsim.examples package

Submodules

fastsemsim.examples.load_annotation_corpus module

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fastsemsim.examples.load_ontology module

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2.2 Submodules

2.3 fastsemsim.fastsemsim_cmdline module

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`fastsemsim.fastsemsim_cmdline.`**`build_cmdline_args_parser`**`()`
Build a cmdline arg parser

`fastsemsim.fastsemsim_cmdline.`**`check_parameters`**`()`
Check whether the set of parameters is formally correct to run a query

`fastsemsim.fastsemsim_cmdline.`**`det_ss`**`()`
Determine SS

`fastsemsim.fastsemsim_cmdline.`**`init_parameters`**`()`
Initialize parameters

`fastsemsim.fastsemsim_cmdline.`**`init_ss`**`()`
Initialize SS class

`fastsemsim.fastsemsim_cmdline.`**`load_IC_from_file`**`(`*list_file*, *separator='\t'*`)`

`fastsemsim.fastsemsim_cmdline.`**`load_ac`**`()`
Load the Annotation Corpus

`fastsemsim.fastsemsim_cmdline.`**`load_ontology`**`()`
Load ontology

`fastsemsim.fastsemsim_cmdline.`**`load_params_from_file`**`(`*list_file*`)`
Load parameters from file

`fastsemsim.fastsemsim_cmdline.`**`load_query`**`()`
Load the query

`fastsemsim.fastsemsim_cmdline.`**`load_query_from_file`**`()`
Load query from a file

`fastsemsim.fastsemsim_cmdline.`**`prbool`**`(`*string*`)`
Parse boolean parameters

`fastsemsim.fastsemsim_cmdline.`**`print_IC`**`(`*IC*, *out*, *cut_thres=None*, *cut_nan=False*`)`

`fastsemsim.fastsemsim_cmdline.`**`print_err`**`(`**args*`)`

fastsemsim.fastsemsim_cmdline.**print_parameters**()
Print the parameters selected

fastsemsim.fastsemsim_cmdline.**save_params_to_file**(*list_file*)
Save parameters to file

fastsemsim.fastsemsim_cmdline.**set_parameters**(*args*)
fill the parameter dictionary with the proper parameters

fastsemsim.fastsemsim_cmdline.**ss_pairs**(*out*)
Pairwise Semantic Similarity

fastsemsim.fastsemsim_cmdline.**ss_pairwise**(*out*)

fastsemsim.fastsemsim_cmdline.**start**()
main routine

2.4 Module contents

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