MacSyFinder

Release 2.0

Sophie Abby, Bertrand Néron

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CONTENTS

A **new version of MacSyFinder (v2)** is available, see *here for an overview of the novelties*. The search engine was improved, and some bugs/unwanted behaviors corrected. MacSyFinder's models for V2 are very similar, yet not compatible with those from V1. See here for details on *how to carry your models to V2*.

MacSyFinder is a program to **model and detect macromolecular systems, genetic pathways**... in protein datasets. In prokaryotes, these systems have often evolutionarily conserved properties: they are made of **conserved components**, and are encoded in **compact loci** (conserved genetic architecture). The user models these systems with MacSyFinder to reflect these conserved features, and to allow their efficient detection.

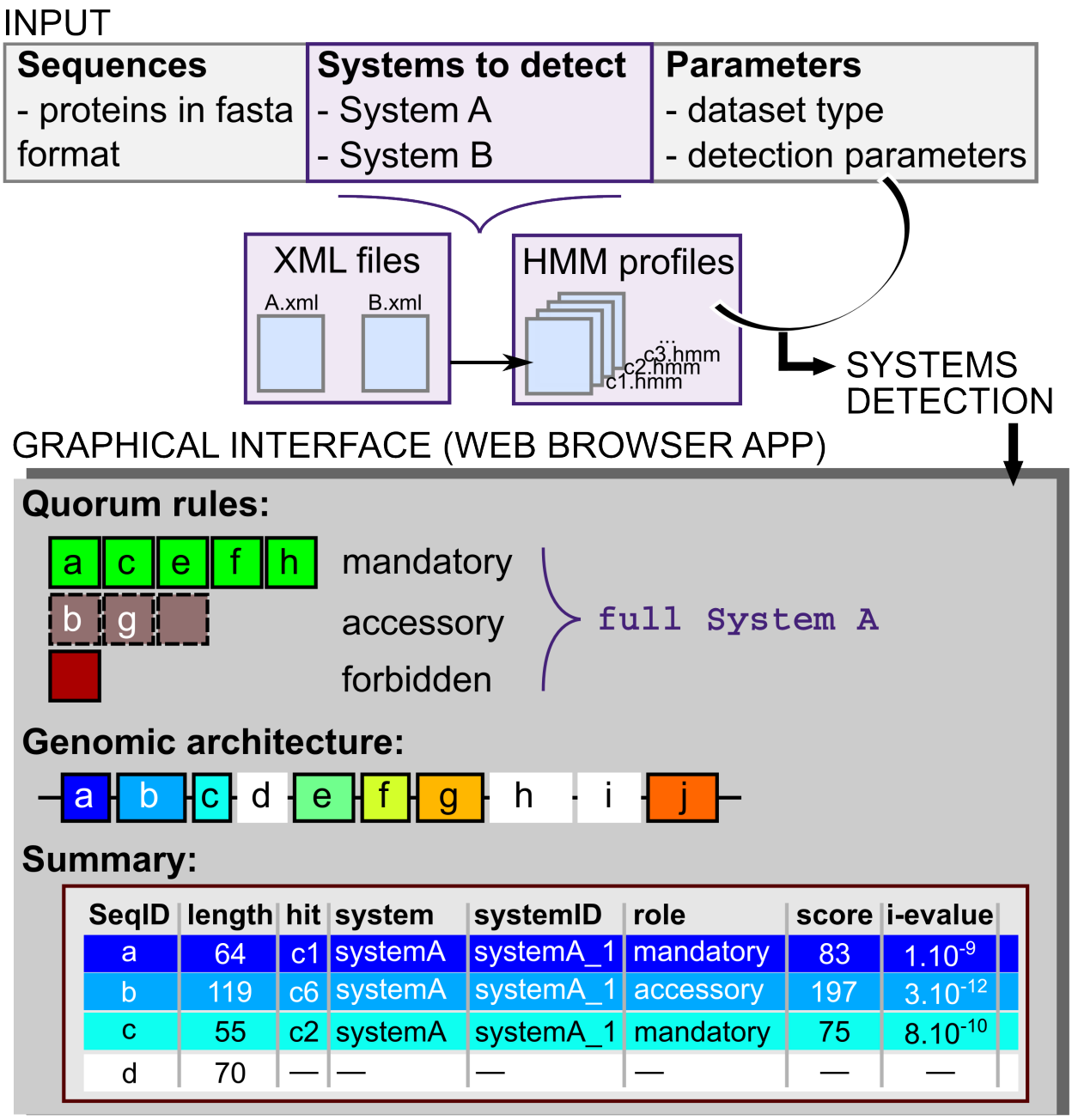
Criteria for systems detection include **component content (quorum)**, and **genomic co-localization**. Each component corresponds to a hidden Markov model (HMM) protein profile to perform sequence similarity searches with the program Hmmer.

In order to model macromolecular systems, the user:

- builds or gather from databanks **HMM protein profiles** for components of interest,
- defines **decision rules** for each system in a dedicated XML grammar (see *Macromolecular models*).

Note: If you use MacSyFinder, please cite:

Abby SS, Néron B, Ménager H, Touchon M, Rocha EPC (2014). MacSyFinder: A Program to Mine Genomes for Molecular Systems with an Application to CRISPR-Cas Systems. PLoS ONE 9(10): e110726. doi:10.1371/journal.pone.0110726



SeqID	length	hit	system	systemID	role	score	i-evalue
a	64	c1	systemA	systemA_1	mandatory	83	1.10^{-9}
b	119	c6	systemA	systemA_1	accessory	197	3.10^{-12}
c	55	c2	systemA	systemA_1	mandatory	75	8.10^{-10}
d	70	—	—	—	—	—	—

CHAPTER

ONE

USER GUIDE

1.1 User Guide

1.1.1 Running MacSyFinder

What's new in MacSyFinder v2?

For Version 2, MacSyFinder was carried under Python 3

New features and search engine

The **search engine** was changed for a more intuitive and comprehensive exploration of putative systems.

The search is now more thorough and avoid undesirable side-effects of the previous search engine. Being more thorough, it now also includes a **scoring scheme** to build candidate systems from sets of detected components (clusters), and can offer several optimal "solutions" (sets of detected systems) based on a combinatorial exploration of detected clusters. See *here for more details*.

Several **new features** were added, including:

- a **new type of gene component** "neutral" was added in order to provide more possibilities for systems' modelling in macsy-models. *See here* for more details.
- more flexibility was introduced in the **search for systems' components using HMMER**. It is now possible to use the *cut_ga* threshold when provided in the HMM profiles used for components' similarity search. This enables to have a search tailored for each HMM profile, and thus component. *See here* for more details.
- a **new file structure** was created to better organize MacSyFinder's packages (i.e. that include systems' models and corresponding HMMER profiles). *See here* for details.
- a **tool** to easily install and distribute MacSyFinder's packages was created. *See here* for more details on *macsy-data*.
- the **format for MacSyFinder's models** has slightly changed, in order to offer more possibilities, and more readibility. To see how to carry models from v1 to v2, *see below*.

Also, the search modes corresponding to "unordered" and "unordered_replicon" were merged into the **"unordered"** search mode - as they basically correspond to the same behaviour.

Note: In v2, output files were also re-defined. See *here for more details*.

Dependencies

MacSyFinder v2 no longer requires the *formatdb* or *makeblastdb* tools from NCBI. However, new dependencies are used, but as they are Python libraries, it should be transparent for the user, and not require manual installations. See *here for details*.

Carrying models from v1 to v2

Models from v1 are not compatible straight away with v2. For those who had designed MacSyFinder's models for Version 1 and would like to carry them for Version 2, here are the changes to consider:

- the keyword "system" was changed: <*system*> ::arrow:: <*model*>
- the keyword <*system_ref*> was removed. For a given systems' package, each gene has to be defined only once in a macsy-model. There is no need anymore to reference which model it is from, when used as a component in another system's model.
- now the version of the macsy-models' type has to be documented as a feature of the "model" keyword, like this: *vers = "2.0"*
- the following keywords have been replaced (but see *below* for more details):
  - homologs => exchangeables
  - analogs => exchangeables

Note: "exchangeable" is not a feature anymore, but is replaced by the keyword "exchangeables".

Examples

Here follow some examples of updates from v1 to v2.

1. A very simple model.

T1SS.xml under **v1**:

```
<system inter_gene_max_space="5" min_mandatory_genes_required="3" min_genes_required=
↪"3">
    <gene name="T1SS_abc" presence="mandatory"/>
    <gene name="T1SS_mfp" presence="mandatory"/>
    <gene name="T1SS_omf" presence="mandatory" loner="1" multi_system="1"/>
</system>
```

T1SS.xml under **v2**:

```
<model inter_gene_max_space="5" min_mandatory_genes_required="3" min_genes_required="3
↪" vers = "2.0">
    <gene name="T1SS_abc" presence="mandatory"/>
    <gene name="T1SS_mfp" presence="mandatory"/>
    <gene name="T1SS_omf" presence="mandatory" loner="1" multi_system="1"/>
</model>
```

Note: In a nutshell, the minimal changes from v1 to v2 for a simple macsy-model listing components are the following: - <system> => <model> - *vers = "2.0"*

2. A model with homologs.

Tad.xml under **v1**:

```
<system inter_gene_max_space="5" min_mandatory_genes_required="4" min_genes_required=
↪"6" multi_loci="0">
    <gene name="Tad_rcpA" presence="mandatory">
        <homologs>
                <gene name="T2SS_gspD" system_ref="T2SS"/>
                <gene name="T4P_pilQ" system_ref="T4P"/>
                <gene name="T3SS_sctC" system_ref="T3SS"/>
        </homologs>
    </gene>
    <gene name="Tad_tadA" presence="mandatory"/>
    <gene name="Tad_tadB" presence="mandatory"/>
    <gene name="Tad_tadC" presence="mandatory"/>
    <gene name="Tad_tadV" presence="mandatory"/>
    <gene name="Tad_tadZ" presence="mandatory"/>
    <gene name="Tad_flp" presence="accessory"/>
    <gene name="Tad_tadE" presence="accessory"/>
    <gene name="Tad_tadF" presence="accessory"/>
</system>
```

Tad.xml under **v2**:

```
<model inter_gene_max_space="5" min_mandatory_genes_required="4" min_genes_required="6
↪" multi_loci="0" vers="2.0">

    <gene name="Tad_rcpA" presence="mandatory"/>
    <gene name="Tad_tadA" presence="mandatory"/>
    <gene name="Tad_tadB" presence="mandatory"/>
    <gene name="Tad_tadC" presence="mandatory"/>
    <gene name="Tad_tadV" presence="mandatory"/>
    <gene name="Tad_tadZ" presence="mandatory"/>
    <gene name="Tad_flp" presence="accessory"/>
    <gene name="Tad_tadE" presence="accessory"/>
    <gene name="Tad_tadF" presence="accessory"/>

</model>
```

Note: The *homologs* and *analogs* keyword having disappeared, it is not necessary anymore to list homologous components (e.g., those that may match several HMM profiles during the sequence similarity search), unless they are *exchangeables*.

3. A model with exchangeable homologs.

T3SS.xml under **v1**:

```
<system inter_gene_max_space="10" min_mandatory_genes_required="7" min_genes_required=
↪"7" multi_loci="1">
    <gene name="T3SS_sctC" presence="mandatory" exchangeable="1">
        <homologs>
            <gene name="T2SS_gspD" system_ref="T2SS"/>
            <gene name="T4P_pilQ" system_ref="T4P"/>
            <gene name="Tad_rcpA" system_ref="Tad"/>
        </homologs>
    </gene>
    <gene name="T3SS_sctJ" presence="mandatory">
        <homologs>
            <gene name="Flg_sctJ_FLG" system_ref="Flagellum"/>
        </homologs>
    </gene>
    <gene name="T3SS_sctN" presence="mandatory">
        <homologs>
            <gene name="Flg_sctN_FLG" system_ref="Flagellum"/>
        </homologs>
    </gene>
    <gene name="T3SS_sctQ" presence="mandatory">
        <homologs>
            <gene name="Flg_sctQ_FLG" system_ref="Flagellum"/>
        </homologs>
    </gene>
    <gene name="T3SS_sctR" presence="mandatory">
        <homologs>
            <gene name="Flg_sctR_FLG" system_ref="Flagellum"/>
        </homologs>
    </gene>
    <gene name="T3SS_sctS" presence="mandatory">
        <homologs>
            <gene name="Flg_sctS_FLG" system_ref="Flagellum"/>
        </homologs>
    </gene>
    <gene name="T3SS_sctT" presence="mandatory">
        <homologs>
            <gene name="Flg_sctT_FLG" system_ref="Flagellum"/>
        </homologs>
    </gene>
    <gene name="T3SS_sctU" presence="mandatory">
        <homologs>
            <gene name="Flg_sctU_FLG" system_ref="Flagellum"/>
        </homologs>
    </gene>
    <gene name="T3SS_sctV" presence="mandatory">
        <homologs>
            <gene name="Flg_sctV_FLG" system_ref="Flagellum"/>
        </homologs>
    </gene>
    <gene name="Flg_fliE" presence="forbidden" system_ref="Flagellum"/>
    <gene name="Flg_flgB" presence="forbidden" system_ref="Flagellum"/>
    <gene name="Flg_flgC" presence="forbidden" system_ref="Flagellum"/>
</system>
```

T3SS.xml under **v2**:

```
<model inter_gene_max_space="10" min_mandatory_genes_required="7" min_genes_required=
↪"7" multi_loci="1" vers="2.0">
    <gene name="T3SS_sctC" presence="mandatory">
        <exchangeables>
            <gene name="T2SS_gspD"/>
            <gene name="T4P_pilQ"/>
            <gene name="Tad_rcpA"/>
        </exchangeables>
    </gene>
    <gene name="T3SS_sctJ" presence="mandatory"/>
    <gene name="T3SS_sctN" presence="mandatory"/>
    <gene name="T3SS_sctQ" presence="mandatory"/>
    <gene name="T3SS_sctR" presence="mandatory"/>
    <gene name="T3SS_sctS" presence="mandatory"/>
    <gene name="T3SS_sctT" presence="mandatory"/>
    <gene name="T3SS_sctU" presence="mandatory"/>
    <gene name="T3SS_sctV" presence="mandatory"/>
    <gene name="Flg_fliE" presence="forbidden"/>
    <gene name="Flg_flgB" presence="forbidden"/>
    <gene name="Flg_flgC" presence="forbidden"/>
</model>
```

Note:

- As only the secretin component 'T3SS_sctC' was exchangeable in its role within T3SS with its homologs T2SS_gspD, T4P_pilQ and Tad_rcpA, these three components are now set as *exchangeables* (they can functionally *replace* the component 'T3SS_sctC'), and all other *homologs* do not need to be listed anymore.
- The keyword *system_ref* is not needed anymore. Therefore, the **v2** definition of T3SS is way more compact than that for **v1**.

Installation

MacSyFinder works with models for macromolecular systems that are not shipped with it, you have to install them separately. See the *macsydata section* below.

MacSyFinder dependencies

Python version >=3.7 is required to run MacSyFinder: https://docs.python.org/3.7/index.html

MacSyFinder has one program dependency:

- the *Hmmer* program, version 3.1 or greater (http://hmmer.org/).

The *hmmsearch* program should be installed (*e.g.*, in the PATH) in order to use MacSyFinder. Otherwise, the paths to this executable must be specified in the command-line: see the *command-line options*.

MacSyFinder also relies on four Python library dependencies:

- colorlog
- pyyaml
- packaging

- networkx

These dependencies will be automatically retrieved and installed when using *pip* for installation (see below).

MacSyFinder Installation procedure

It is recommended to use *pip* to install the MacSyFinder package.

Archive overview

- **doc** => the documentation in html and pdf
- **etc** => a template of macsyfinder configuration file
- **test** => all what is needed for unitary tests
- **macsypy** => the macsyfinder python library
- **setup.py** => the installation script
- **requirements.txt** => the python dependencies
- **requirements_dev.txt** => the python dependencies for developers
- **COPYING** => the licensing
- **COPYRIGHT** => the copyright
- **README.md** => very brief macsyfinder overview
- **CONTRIBUTORS** => list of people who contributed to the code

Installation steps:

Make sure every required dependency/software is present.

By default MacSyFinder will try to use *hmmsearch* in your PATH. If *hmmsearch* is not in the PATH, you have to set the absolute path to *hmmsearch* in a *configuration file* or in the *command-line* upon execution. If the tools are not in the path, some test will be skipped and a warning will be raised.

Perform the installation.

```
pip install --no-binary macsyfinder macsyfinder
```

If you do not have the privileges to perform a system-wide installation, you can either install it in your home directory or use a virtual environment.

installation in your home directory

```
pip install --user --no-binary macsyfinder macsyfinder
```

installation in a virtualenv

```
python3.7 -m venv macsyfinder
cd macsyfinder
source bin/activate
pip install --no-binary macsyfinder macsyfinder
```

To exit the virtualenv just execute the *deactivate* command. To run *macsyfinder*, you need to activate the virtualenv:

```
source macsyfinder/bin/activate
```

Then run *macsyfinder* or *macsydata*.

Note: Super-user privileges (*i.e.*, `sudo`) are necessary if you want to install the program in the general file architecture.

Note: If you do not have the privileges, or if you do not want to install MacSyFinder in the Python libraries of your system, you can install MacSyFinder in a virtual environment (http://www.virtualenv.org/).

Warning: When installing a new version of MacSyFinder, do not forget to uninstall the previous version installed !

Uninstalling MacSyFinder

To uninstall MacSyFinder (the last version installed), run:

```
(sudo) pip uninstall macsyfinder
```

If you install it in a virtualenv, just delete the virtual environment. For instance if you create a virtualenv name macsyfinder:

```
python3.7 -m venv macsyfinder
```

To delete it, remove the directory:

```
rm -R macsyfinder
```

Models installation with *macsydata*

Once MacSyFinder is installed you have access to an utility program to manage the models: *macsydata*

This script allows to search, download, install and get information from MacSyFinder models stored on github or locally installed. The general syntax for *macsydata* is:

```
macsydata <general options> <subcommand> <sub command options> <arguments>
```

To list all models available:

```
macsydata available
```

To search for models:

```
macsydata search TXSS
```

you can also search in models description:

```
macsydata search -S secretion
```

To install a model package:

```
macsydata install <model name>
```

To install a model when you have not the right to install it system-wide:

```
macsydata install --user <model name>
```

To know how to cite a model package:

```
macsydata cite <model name>
```

To list all *macsydata* subcommands:

```
macsydata --help
```

To list all available options for a subcommand:

```
macsydata <subcommand> --help
```

MacSyFinder Quick Start

1. We recommend to install MacSyFinder using *pip* in a virtual environment (for further details see *Installation*).

   ```
   python3 -m venv MacSyFinder
   cd MacSyFinder
   source bin/activate
   pip install macsyfinder
   ```

   Warning: *hmmsearch* from the HMMER package (http://hmmer.org/) must be installed.

2. Prepare your data. You need a file containing all protein sequences of your genome of interest in fasta format (for further details see *Input dataset*).

Fig. 1: This page is still under construction

3. You need to have models to search in your input data. Please refer to *Macromolecular models* to create your own package of models. We will soon provide a set of predefined models for you to test.
4. Command lines:
   - Type: `macsyfinder -h`

     To see all options available. All command-line options are described in the *Command-line options section*. In order to run MacSyFinder on your favorite dataset as soon as you have installed it, you can simply follow the following steps:
   - On a "metagenomic" (unordered) dataset for example: `macsyfinder --db-type unordered --sequence-db metagenome.fasta --models-dir my-models --models model_family all`

     will detect all models of model_family modelled in .xml files placed in the *"my-models"* folder without taking into account any gene order.
   - On a completely assembled genome (where the gene order is known, and is relevant for systems' detection):

     ```
     macsyfinder --db-type ordered-replicon --sequence-db mygenome.fasta
     --models-dir my-models --models model_family ModelA ModelB
     ```

     will detect the macromolecular systems described in the two models *"ModelA"* and *"ModelB"* in a complete genome from the *"ModelA.xml"* and *"ModelB.xml"* definition files placed in the folder *"my-models/model_family/definitions"*.

Note: Systems names have to be spelled in a case-sensitive way to run their detection from the command-line. The name of the System corresponds to the suffix defined for xml files (.xml by default), for example *"toto"* for a model defined in *"toto.xml"*.

The *"all"* keyword allows to detect all models available in the definitions folder in a single run. See the *Command-line options*.

Input and Options of MacSyFinder

Input dataset

The input dataset must be a set of protein sequences in **Fasta format** (see http://en.wikipedia.org/wiki/FASTA_format).

The *base section* in the configuration file (see *Configuration file*) can be used to specify **the path** and the **type of dataset** to deal with, as well as the *–sequence_db* and *–db_type* parameters respectively, described in the *Command-line options* (see *Input options*).

Four types of protein datasets are supported:

- *unordered* : a set of sequences corresponding to a complete genome (*e.g.* an unassembled complete genome)
- *ordered_replicon* : a set of sequences corresponding to an ordered complete replicon (*e.g.* an assembled complete genome)
- *gembase* : a set of multiple ordered replicons, which format follows the convention described in *Gembase format*.

For "ordered" ("ordered_replicon" or "gembase") datasets only, MacSyFinder can take into account the **shape of the genome**: "linear", or "circular" for detection. The default is set to "circular".

This can be set with the *–replicon_topology* parameter from *Command-line options* (see *Input options*), or in the configuration in the *base section*.

With the "gembase" format, it is possible to specify a topology per replicon with a topology file (see *Gembase format* and *Topology files*).

Command-line options

Optional arguments:

```
-h, --help            Show the help message and exit

-m [MODELS [MODELS ...]], --models [MODELS [MODELS ...]]
                      The models to search. The --models option can be set several␣
↪times.'
                      For each --models options the first element must be the name of␣
↪family models,
                      followed by the name of the models.
                      If the name 'all' is in the list all models from the family␣
↪will be searched.'
                      '--models TXSS Flagellum T2SS'
                                means MSF will search for models TXSS/Flagellum and␣
↪TXSS/T2SS
                      '--models TXSS all'
                                means for all models found in model package TXSS
                      '--models CRIPRcas/subtyping all'
                               means MSF will search for all models described in the␣
↪CRISPRCas/subtyping subfamily.
                      (required unless --previous-run is set)
```

Input dataset options:

```
--sequence-db SEQUENCE_DB
                      Path to the sequence dataset in fasta format.
                      (required unless --previous-run is set)
--db-type {ordered_replicon,gembase,unordered}
                      The type of dataset to deal with. "unordered" corresponds
                      to a non-assembled genome,
                      "ordered_replicon" to an assembled genome,
                      and "gembase" to a set of replicons where sequence identifiers
                      follow this convention: ">RepliconName SequenceID".
                      (required unless --previous-run is set)
--replicon-topology {linear,circular}
                      The topology of the replicons
                      (this option is meaningful only if the db_type is
                      'ordered_replicon' or 'gembase'.
--topology-file TOPOLOGY_FILE
                      Topology file path. The topology file allows to specify a␣
↪topology
                      (linear or circular) for each replicon (this option is␣
↪meaningful only if
                      the db_type is 'ordered_replicon' or 'gembase'.
                      A topology file is a tabular file with two columns:
                      the 1st is the replicon name, and the 2nd the corresponding␣
↪topology:
                      "RepliconA      linear"
--idx                 Forces to build the indexes for the sequence dataset even
                      if they were previously computed and present at the dataset␣
↪location.
                      (default: False)
```

Systems detection options:

```
--inter-gene-max-space INTER_GENE_MAX_SPACE INTER_GENE_MAX_SPACE
                      Co-localization criterion: maximum number of components non-
↪matched by a
                      profile allowed between two matched components
                      for them to be considered contiguous.
                      Option only meaningful for 'ordered' datasets.
                      The first value must match to a model, the second to a number␣
↪of components.
                      This option can be repeated several times:
                          "--inter-gene-max-space TXSS/T2SS 12 --inter-gene-max-space␣
↪TXSS/Flagellum 20
--min-mandatory-genes-required MIN_MANDATORY_GENES_REQUIRED MIN_MANDATORY_GENES_
↪REQUIRED
                      The minimal number of mandatory genes required for model␣
↪assessment.
                      The first value must correspond to a model fully qualified name,
↪ the second value to an integer.
                      This option can be repeated several times:
                          "--min-mandatory-genes-required TXSS/T2SS 15 --min-
↪mandatory-genes-required TXSS/Flagellum 10"
--min-genes-required MIN_GENES_REQUIRED MIN_GENES_REQUIRED
                      The minimal number of genes required for model assessment "
                      (includes both 'mandatory' and 'accessory' components).
                      The first value must correspond to a model fully qualified name,
↪ the second value to an integer.
                      This option can be repeated several times:
```

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```
                        "--min-genes-required TXSS/T2SS 15 --min-genes-required␣
↪TXSS/Flagellum 10
--multi-loci MULTI_LOCI
                      Specifies if the system can be detected as a 'scattered' system.
                      The models are specified as a comma separated list of fully␣
↪qualified name
                        "--multi-loci model_familyA/model_1,model_familyB/model_2"
```

Options for Hmmer execution and hits filtering:

```
 --hmmer HMMER         Path to the hmmsearch program.
                       If it is not specify rely on the PATH
                       (default: hmmsearch)
--e-value-search E_VALUE_SEARCH
                       Maximal e-value for hits to be reported during hmmsearch␣
↪search.
                       By default MF set per profile threshold for hmmsearch run (--
↪cut_ga option)
                       for profiles containing the GA bit score threshold.
                       If a profile does not contains the GA bit score the --e-value-
↪search (-E in hmmsearch)
                       is applied to this profile.
                       To applied the --e-value-search to all profiles use the --no-
↪cut-ga option.
                       (default: 0.1)
 --no-cut-ga           By default the Mf try to applied a threshold per profile by␣
↪using the
                       hmmer -cut-ga option. This is possible only if the Ga bit␣
↪score is present in the profile otherwise MF switch to use the
                       the --e-value-search (-E in hmmsearch).
                       If this option is set the --e-value-search option is used for␣
↪all profiles regardless
                       the presence of the a GA bit score in the profiles.
                       (default: False)
 --i-evalue-sel I_EVALUE_SEL
                       Maximal independent e-value for Hmmer hits to be selected for␣
↪system detection.
                       (default:0.001)
 --coverage-profile COVERAGE_PROFILE
                       Minimal profile coverage required in the hit alignment to allow
                       the hit selection for system detection.
                       (default: 0.5)
```

Options for cluster and systems scoring:

```
--mandatory-weight MANDATORY_WEIGHT
                      the weight of a mandatory component in cluster scoring
                      (default:1.0)
--accessory-weight ACCESSORY_WEIGHT
                      the weight of a mandatory component in cluster scoring
                      (default:0.5)
--exchangeable-weight EXCHANGEABLE_WEIGHT
                      the weight modifier for a component which code for exchangeable␣
↪cluster scoring
                          (default:0.75)
--redundancy-penalty REDUNDANCY_PENALTY
                      the weight modifier for cluster which bring a component already␣
↪presents in other
```

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```
                      clusters (default:1.5)
```

Path options:

```
--models-dir MODELS_DIR
                      specify the path to the models if the models are not installed␣
↪in the canonical place.
                      It gather definitions (xml files) and hmm profiles in a specific
                      structure. A directory with the name of the model with at least␣
↪two directories
                      profiles" which contains all hmm profile for gene describe in␣
↪definitions and
                      models" which contains either xml file of definitions or␣
↪subdirectories
                      to organize the model in subsystems.
-o OUT_DIR, --out-dir OUT_DIR
                      Path to the directory where to store results.
                      if out-dir is specified res-search-dir will be ignored.
--res-search-suffix RES_SEARCH_SUFFIX
                      The suffix to give to Hmmer raw output files. (default: .search_
↪hmm.out)
--res-extract-suffix RES_EXTRACT_SUFFIX
                      The suffix to give to filtered hits output files. (default: .
↪res_hmm_extract)
--profile-suffix PROFILE_SUFFIX
                      The suffix of profile files. For each 'Gene' element, the␣
↪corresponding profile is
                      searched in the 'profile_dir', in a file which name is based on␣
↪the
                      Gene name + the profile suffix.
                      For instance, if the Gene is named 'gspG' and the suffix is '.
↪hmm3',
                      then the profile should be placed at the specified location
                      and be named 'gspG.hmm3'
                      (default: .hmm)
```

General options:

```
-w WORKER, --worker WORKER
                      Number of workers to be used by MacSyFinder.
                      In the case the user wants to run MacSyFinder in a multi-thread␣
↪mode.
                      (0 mean all cores will be used).
                      (default: 1)
-v, --verbosity       Increases the verbosity level. There are 4 levels:
                      Error messages (default), Warning (-v), Info (-vv) and Debug.(-
↪vvv)
--mute                mute the log on stdout.
                      (continue to log on macsyfinder.log)
                      (default: False)
--version             show program's version number and exit
-l, --list-models     display the all models installed in generic location and quit.
--cfg-file CFG_FILE   Path to a MacSyFinder configuration file to be used.
--previous-run PREVIOUS_RUN
                      Path to a previous MacSyFinder run directory.
                      It allows to skip the Hmmer search step on same dataset,
                      as it uses previous run results and thus parameters regarding␣
↪Hmmer detection.
```

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```
                    The configuration file from this previous run will be used.
                    Conflict with options
                        --config, --sequence-db, --profile-suffix, --res-extract-
↪suffix, --e-value-res, --db-type, --hmmer
```

Configuration file

Options to run MacSyFinder can be specified in a configuration file. The *Config object* handles all configuration options for MacSyFinder. Three locations are parsed to find configuration files:

- $PREFIX/etc/macsyfinder/macsyfinder.conf
- $(HOME)/.macsyfinder/macsyfinder.conf
- ./macsyfinder.conf

Moreover these three locations options can be passed on the command-line.

Each file can define options, and in the end all options are integrated. If an option is specified several times:

Note: The precedence rules from the least to the most important priority are:

$PREFIX/etc/macsyfinder/macsyfinder.conf < $(HOME)/.macsyfinder/macsyfinder.conf < ./macsyfinder.conf < "command-line" options

---

This means that command-line options will always bypass those from the configuration files. In the same flavor, options altering the definition of systems found in the command-line or the configuration file will always overwhelm values from systems' *XML definition files*.

The configuration files must follow the Python "ini" file syntax. The *Config object* provides some default values and performs some validations of the values.

In MacSyFinder, six sections are defined and stored by default in the configuration file:

- **base** : all information related to the protein dataset under study
  - *sequence_db* : the path to the dataset in Fasta format (*no default value*)
  - *db_type* : the type of dataset to handle, four types are supported:
    - *unordered* : a set of sequences corresponding to a complete replicon (*e.g.* an unassembled complete genome)
    - *ordered_replicon* : a set of sequences corresponding to a complete replicon ordered (*e.g.* an assembled complete genome)
    - *gembase* : a set of multiple ordered replicons.

    (*no default value*)
  - *replicon_topology* : the topology of the replicon under study. Two topologies are supported: 'linear' and 'circular' (*default* = 'circular'). This option will be ignored if the dataset type is not ordered (*i.e.* "unordered_replicon" or "unordered").
- **models** * list of models to search in replicon
- **models_opt**
  - *inter_gene_max_space* = list of models' fully qualified names and integer separated by spaces (see example below). These values will supersede the values found in the model definition file.

  - *min_mandatory_genes_required* = list of models' fully qualified name and integer separated by spaces. These values will supersede the values found in the model definition file.
  - *min_genes_required* = list of models' fully qualified name and integer separated by spaces. These values will supersede the values found in the model definition file.

- **hmmer**
  - *hmmer_exe* (default= *hmmsearch*)
  - *e_value_res* = (default= *1*)
  - *i_evalue_sel* = (default= *0.5*)
  - *coverage_profile* = (default= *0.5*)
- **score_opt**
  - *mandatory_weight* (default= *1.0*)
  - *accessory_weight* (default= *0.5*)
  - *exchangeable_weight* (default= *0.8*)
  - *redundancy_penalty* (default= *1.5*)
  - *loner_multi_system_weight* (default= *0.7*)
- **directories**
  - *res_search_dir* = (default= *./datatest/res_search*)
  - *res_search_suffix* = (default= *.search_hmm.out*)
  - *models_dir* = (default= *./models*)
  - *res_extract_suffix* = (default= *.res_hmm_extract*)
- **general**
  - ***log_level*: (default= *debug*) This corresponds to an integer code:**

Level	Numeric value
CRITICAL	50
ERROR	40
WARNING	30
INFO	20
DEBUG	10
NOTSET	0

  - *log_file* = (default = macsyfinder.log in directory of the run)

Example of a configuration file

```
[base]
prefix = /path/to/macsyfinder/home/
file = %(prefix)s/data/base/prru_psae.001.c01.fasta
db_type = gembase
replicon_topology = circular

[models]
models_1 = TFF-SF_final all
```

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```
 [models_opt]
 inter_gene_max_space = TXSS/T2SS 22 TXSS/Flagellum 44
 min_mandatory_genes_required = TXSS/T2SS 6 TXSS/Flagellum 4
 min_genes_required = TXSS/T2SS 8 TXSS/Flagellum 4

 [hmmer]
 hmmer = hmmsearch
 e_value_res = 1
 i_evalue_sel = 0.5
 coverage_profile = 0.5

 [score_opt]
 mandatory_weight = 1.0
 accessory_weight = 0.5
 exchangeable_weight = 0.8
 redundancy_penalty = 1.5
 loner_multi_system_weight = 0.7

 [directories]
 prefix = /path/to/macsyfinder/home/
 data_dir = %(prefix)s/data/
 res_search_dir = %(prefix)s/dataset/res_search/
 res_search_suffix = .raw_hmm
 models_dir = %(data_dir)/data/models
 profile_suffix = .fasta-aln.hmm
 res_extract_suffix = .res_hmm

[general]
log_level = debug
worker = 4
```

Note: After a run, the corresponding configuration file ("macsyfinder.conf") is generated as a (re-usable) output file that stores every options used in the run. It is stored in the results' directory (see *the output section*).

In-house input files

Gembase format

In order to allow the users to run MacSyFinder on **several genomes at once**, we propose to adopt the following convention to fulfill the requirements for the "gembase db_type".

It consists in providing for each protein, both the replicon name and a protein identifier separated by a "_" in the first field of fasta headers. "_" are accepted in the replicon name, but not in the protein identifier. Hence, the last "_" is the separator between the replicon name and the protein identifier. As such, MacSyFinder will be able to treat each replicon separately to assess macromolecular systems' presence.

For instance:

```
>PlasmidA_0001 YP_003225072.1 | putative stcE protein
MKLKYLSCMILASLAMGAFAATAADNNSAIYFNTTQPVNDLQGGLAAEVK
FAQSQILSAHPKEGESQQHLTSLRKSLLLVRLVKADDKTPVQVEARDAND
KILGTLTLSPPSSLPDTVYHLDGVPADGIDFTPQNGTKKIINTVAEVNKL
SDASGSSIKSYLANNALVEIQTANGRWIRDMYLPQGAELEGKMVRFVSYA
```

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```
GYNSTVFYGDRKVTLSVGNTLLFKYVNGQWFRSGELENNRIAYAQHTWSA
ELPAHWIVPGLNLVIKQGNLSGSLNDINVGAPGELLLHTIDIGMLTTPRG
RFDFAKDKEAHREYFQTIPVSRMIVNNYAPLHLKEVMLPTGTLLTDADPG
>PlasmidA_0002 YP_003225073.1 | type II secretion protein EtpC
MLFFLSSRRDRNLFIKDIALKMLTPNWVLCVILLIAGYQLVSVIRHFWLT
PATSASDLSHVSVSETAVTDEHTEENFVFTLFGTASPPLSEGKVQKTTSS
LSDDLLSGGDLDVRGILYSSVTEHSVAIFAHNNRQFSLGIGEKVPGYDAT
ISAIFSDHIVINYQGKNASLPLRYDNPAKRNAQDDNNLIVGPVTTQANFR
VKNIFDIMSLSPVTVNNTLSGYRLSPGKASSLFYNAGLHDNDLAVLLNGS
ELRDTRQAKQIMKQLTELKEIKITVERDGQLYDAFIAVGEN
....
>ChromosomeA_0001 YP_003573410.1 | adhesin-like protein
MKKLFLFAALLMTGFAFYSCEDVVDNPAQDPAQSWNYSVSVKFADFDFNG
AVDENSVPYTYKAPTTLYVLNEENTLMGTITTDAAPAIGDYGTYAGTLTG
SIGNNLIITTKIGNDLTKQDGTLKSAIENGIVQTAEVPIKIYNANSGTLT
TASAKMDNTAAIAYTSLGYIKGGDKILFVEGNQTFEWTVNEEFDPYTSTD
LYIALPMNTDPETEYTISSDSKDGYTRGGTFKLADYPTLAAGKVSNYIGG
IPFIQTGVDLTKWDAYMRTDPNNTWYMNNINNGWPATFSQEVEDGKSFIV
TQSGPTLDSLNVVVGGVTGKEVNVTLNNIRLGKDRSINIGDKHGWVEYDG
THDIYGWGAKANVTLIGENECETLYIQCPATKKGEGTLNYKNLSIDSYGS
>ChromosomeA_0020 YP_003573411.1 | hypothetical protein
MKRIVLITLVSILTTFQAIAQVANGFYRVQNNASSRYITLRDNAVGTVDY
SSTNVDLSNIVTWSGFDKVKSNPASIIYVEQHDSKYDLKVQGTGIYAITG
GRTYLELRPKDSGYILAVTYNGMEGRLYDSEEDVDGEGYVKRSGNSAYQY
WSFIPVDTENNYIGLQPTVQVGDNYYGTLYASYPFKAASSGIKFYYVDAI
....
>NC_001548_0015 YP_003225080.1 | type II secretion protein EtpJ  (translation)
MSQQRVKGFTLLEMLLALAVFAALSISAFQVLQSGIRAHELSQDKVRRLA
ELQRGGSQIERDLMQMIPRHSRGSEGLLLAAPHLLKSDDWGISFTRNSWL
NPAGMLPRPELQWVGYRLRQQKLERLSYFYVDHPSGIAPDVRVVLEGVHA
FRLRFFVNGTWQARWDSTSILPQAVEVTLVMDDFAELTRLFLVSKETAE
```

This input file contains 3 replicons: PlasmidA (which 2 first protein identifiers are 0001 and 0002), ChromosomeA (which 2 first protein identifiers are 0001 and 0020) and NC_001548 (which first protein identifier is 0015). MacSyFinder search results will thus be reported for each of these three replicons.

Topology files

To be able to attribute a topology per replicon/genome when using the Gembase format, we propose the user to build a "topology file" in the form of a tabular file with two columns separated by a ":". The 1st column is the replicon name, and the 2nd the corresponding topology. Comments can be written after a "#".

For example:

```
# comment line
PlasmidA : circular
ChromosomeA : linear
ChromosomeB : circular
```

Note: A topology file can be specified on the command-line with the `--topology-file` parameter.

Output format

MacSyFinder provides different types of output files. At each run, MacSyFinder creates a new folder, whose name is based on a fixed prefix and a random suffix, for instance "macsyfinder-20130128_08-57-46". MacSyFinder output files are stored in this run-specific folder.

Hmmer results' output files

Raw Hmmer outputs are provided, as long with processed tabular outputs that include hits filtered as specified by the user. For instance, the Hmmer search for SctC homologs with the corresponding profile will result in the creation of two output files: "sctC.search_hmm.out" for the raw HMMER output file and "sctC.res_hmm_extract" for the output file after processing/filtering of the HMMER results by MacSyFinder.

The processed output file "sctC.res_hmm_extract" recalls on the first lines the parameters used for hits filtering and relevant information on the matches, as in this example:

```
# gene: sctC extract from /Users/bob/macsyfinder_results/
      macsyfinder-20130128_08-57-46/sctC.search_hmm.out hmm output
# profile length= 544
# i_evalue threshold= 0.001000
# coverage threshold= 0.500000
# hit_id replicon_name position_hit hit_sequence_length gene_name gene_system i_eval␣
↪score
      profile_coverage sequence_coverage begin end
PSAE001c01_006940       PSAE001c01      3450    803     sctC    T3SS    1.1e-41 141.6
      0.588235  0.419676        395     731
PSAE001c01_018920       PSAE001c01      4634    776     sctC    T3SS    9.2e-48 161.7
      0.976103  0.724227        35      596
PSAE001c01_031420       PSAE001c01      5870    658     sctC    T3SS    2.7e-52 176.7
      0.963235  0.844985        49      604
PSAE001c01_051090       PSAE001c01      7801    714     sctC    T3SS    1.9e-46 157.4
      0.571691  0.463585        374     704
```

Note: Each tabular output file contains a header line describing each column in the output.

Output files for the "ordered replicon(s)" search modes

These output files are provided when MacSyFinder search proceeds on a set of proteins that are deemed to follow the order of their genes on replicons. This corresponds to the two search modes *gembase* and *ordered_replicon*.

Systems detection results

Different types of output files are provided, human-readable files ".txt", and tabulated files ".tsv". For the latter, headers are provided with the content of the lines in the file.

- **best_solution.tsv** - This file contains the **best solution found by MacSyFinder** in terms of systems detected, under the form of a per-component, tabulated report file. A **solution** consists in a set of compatible systems (no components' overlap allowed). If multiple solutions showed a maximal score, the solution maximizing
  1. the number of components in systems and
  2. the number of systems detected is proposed.

To see potential other best solutions (in case several obtained the same highest score), see file *all_best_solutions.tsv*.

To see all possible, candidate systems without further processing, see files *all_systems.txt* and *all_systems.tsv*.

The *best_solution.tsv* file is the most similar to former V1 file *macsyfinder.report*.

- **all_systems.txt** - This file describes the search process of all possible candidate systems given the definitions in systems' models - without processing of the potential overlaps between candidate systems. This set of possible candidate systems are also given under the form of a tabulated file in *all_systems.tsv*.
- **rejected_clusters.txt** - This file lists candidate clusters of systems' components that were rejected by MacSyFinder during the search process, and were thus not assigned to a candidate system.
- **all_best_solutions.tsv** - This file contains all possible best solutions under the form of a per-component, tabulated report file. To retrieve a single best solution as proposed by MacSyFinder, see file *best_solution.tsv*.
- **all_systems.tsv** - This file contains all possible candidate systems given the definitions - without processing of the potential overlaps between candidate systems, under the form of a per-component, tabulated report file. It corresponds to the tabulated version of the *all_systems.txt* file.

all_systems.txt

The file starts with some comments:

- the version of MacSyFinder used
- the command line used to produce this file

Then for each replicon, the systems detected are listed along with their description:

- **system_id** - the unique identifier of a system
- **model** - the model assigned to this system
- **replicon** - the name of the replicon harbouring the system
- **clusters** - the clusters composition of this system
  - each clusters is a list of tuple
  - each tuple is composed of:
    - the name of the matching gene(s) in the replicon
    - the name of the corresponding gene profile(s)
    - the position of the corresponding sequence(s) along the replicon
- **occurrence** - the average number of occurrences of each components of the system (as a potential proxy to estimate whether there's the genetic potential for multiple systems in one)
- **wholeness** - the percentage of the model's components that were found in this system
- **loci nb** - the number of different loci constituting this system
- **score** - the score of the system. See *here* for more details
- **systems components** - the number of occurrences of each model components in parenthesis the name of the matching profile in square brackets the name of other putative systems that would involve this gene

Here is an example of the *all_systems.txt* file:

```
# macsyfinder 20200217.dev
# macsyfinder --sequence-db DATA_TEST/sequences.prt --db-type=gembase --models-dir␣
↪data/models/ --models TFF-SF_final all -w 4
# Systems found:

system id = VICH001.B.00001.C001_MSH_1
model = TFF-SF_final/MSH
replicon = VICH001.B.00001.C001
clusters = [('VICH001.B.00001.C001_00406', 'MSH_mshI', 366), ('VICH001.B.00001.C001_
↪00407', 'MSH_mshJ', 367), ('VICH001.B.00001.C001_00408', 'MSH_mshK', 368), (
↪'VICH001.B.00001.C001_00409', '
MSH_mshL', 369), ('VICH001.B.00001.C001_00410', 'MSH_mshM', 370), ('VICH001.B.00001.
↪C001_00411', 'MSH_mshN', 371), ('VICH001.B.00001.C001_00412', 'MSH_mshE', 372), (
↪'VICH001.B.00001.C001_0041
3', 'MSH_mshG', 373), ('VICH001.B.00001.C001_00414', 'MSH_mshF', 374), ('VICH001.B.
↪00001.C001_00415', 'MSH_mshB', 375), ('VICH001.B.00001.C001_00416', 'MSH_mshA',␣
↪376), ('VICH001.B.00001.C001
_00417', 'MSH_mshC', 377), ('VICH001.B.00001.C001_00418', 'MSH_mshD', 378), ('VICH001.
↪B.00001.C001_00419', 'MSH_mshO', 379), ('VICH001.B.00001.C001_00420', 'MSH_mshP',␣
↪380), ('VICH001.B.00001
.C001_00421', 'MSH_mshQ', 381)]
occ = 1
wholeness = 0.941
loci nb = 1
score = 10.500

mandatory genes:
        - MSH_mshA: 1 (MSH_mshA)
        - MSH_mshE: 1 (MSH_mshE)
        - MSH_mshG: 1 (MSH_mshG)
        - MSH_mshL: 1 (MSH_mshL)
        - MSH_mshM: 1 (MSH_mshM)

accessory genes:
        - MSH_mshB: 1 (MSH_mshB)
        - MSH_mshC: 1 (MSH_mshC)
        - MSH_mshD: 1 (MSH_mshD)
        - MSH_mshF: 1 (MSH_mshF)
        - MSH_mshI: 1 (MSH_mshI)
        - MSH_mshI2: 0 ()
        - MSH_mshJ: 1 (MSH_mshJ)
        - MSH_mshK: 1 (MSH_mshK)
        - MSH_mshN: 1 (MSH_mshN)
        - MSH_mshO: 1 (MSH_mshO)
        - MSH_mshQ: 1 (MSH_mshQ)
        - MSH_mshP: 1 (MSH_mshP)

neutral genes:

============================================================
system id = VICH001.B.00001.C001_T4P_14
model = TFF-SF_final/T4P
replicon = VICH001.B.00001.C001
clusters = [('VICH001.B.00001.C001_00476', 'T4P_pilT', 427), ('VICH001.B.00001.C001_
↪00477', 'T4P_pilU', 428)], [('VICH001.B.00001.C001_00847', 'T4P_pilO', 778), (
↪'VICH001.B.00001.C001_00850',
 'T4P_pilE', 781), ('VICH001.B.00001.C001_00851', 'T4P_fimT', 782), ('VICH001.B.00001.
↪C001_00852', 'T4P_pilW', 783), ('VICH001.B.00001.C001_00853', 'T4P_pilX', 784), (
↪'VICH001.B.00001.C001_00
```

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```
854', 'T4P_pilV', 785)], [('VICH001.B.00001.C001_02305', 'T4P_pilA', 2202), ('VICH001.
↪B.00001.C001_02306', 'T4P_pilB', 2203), ('VICH001.B.00001.C001_02307', 'T4P_pilC',␣
↪2204), ('VICH001.B.000
01.C001_02308', 'T4P_pilD', 2205)], [('VICH001.B.00001.C001_02502', 'MSH_mshM', 2391),
↪ ('VICH001.B.00001.C001_02505', 'T4P_pilQ', 2394), ('VICH001.B.00001.C001_02506',
↪'T4P_pilP', 2395), ('VI
CH001.B.00001.C001_02507', 'T4P_pilO', 2396), ('VICH001.B.00001.C001_02508', 'T4P_pilN
↪', 2397), ('VICH001.B.00001.C001_02509', 'T4P_pilM', 2398)]
occ = 1
wholeness = 0.944
loci nb = 4
score = 12.000

mandatory genes:
        - T4P_pilE: 1 (T4P_pilE)
        - T4P_pilB: 1 (T4P_pilB)
        - T4P_pilC: 1 (T4P_pilC)
        - T4P_pilO: 2 (T4P_pilO, T4P_pilO)
        - T4P_pilQ: 1 (T4P_pilQ)
        - T4P_pilN: 1 (T4P_pilN)
        - T4P_pilT: 1 (T4P_pilT)
        - T4P_pilD: 1 (T4P_pilD [VICH001.B.00001.C001_T2SS_4])

accessory genes:
        - T4P_pilA: 1 (T4P_pilA)
        - T4P_pilV: 1 (T4P_pilV)
        - T4P_pilY: 0 ()
        - T4P_pilW: 1 (T4P_pilW)
        - T4P_pilX: 1 (T4P_pilX)
        - T4P_fimT: 1 (T4P_fimT)
        - T4P_pilM: 1 (T4P_pilM)
        - T4P_pilP: 1 (T4P_pilP)
        - T4P_pilU: 1 (T4P_pilU)
        - MSH_mshM: 1 (MSH_mshM)

neutral genes:
```

all_systems.tsv

This corresponds to the tabulated version of the systems listed in *all_systems.txt*. Each line corresponds to a "hit" that has been assigned to a detected system. It includes:

- **replicon** - the name of the replicon it belongs to
- **hit_id** - the unique identifier of the hit
- **gene_name** - the name of the component identified by the hit
- **hit_pos** - the position of the sequence in the replicon
- **model_fqn** - the model fully-qualified name
- **sys_id** - the unique identifier attributed to the detected system
- **sys_loci** - the number of loci
- **sys_wholeness** - the wholeness of the system
- **sys_score** - the system score

- **sys_occ** - the estimated number of system occurrences that could be potentially "filled" with this system's occurrence, based on the average number of each component found. A proxy for the genetic potential ton encode several systems from the set of components found in this one occurrence.
- **hit_gene_ref** - the gene in the model whose this hit plays the role of
- **hit_status** - the status of the component in the assigned system's definition
- **hit_seq_len** - the length of the protein sequence matched by this hit
- **hit_i_eval** - Hmmer statistics, the independent-evalue
- **hit_score** - Hmmer score
- **hit_profile_cov** - the percentage of the profile covered by the alignment with the sequence
- **hit_seq_cov** - the percentage of the sequence covered by the alignment with the profile
- **hit_begin_match** - the position in the sequence where the profile match begins
- **hit_end_match** - the position in the sequence where the profile match ends
- **used_in** - whether the hit could be used in another system's occurrence

This file can be easily parsed using the Python pandas library.

```
import pandas as pd

systems = pd.read_cvs("path/to/systems.tsv", sep='\t', comment='#')
```

Note: each system reported is separated from the others with a blank line to ease human reading. These lines are ignored during the parsing with pandas.

best_solution.tsv and all_best_solutions.tsv

Since MacSyFinder 2.0, a combinatorial exploration of solutions using sets of systems found is performed. We call best solution, the combination of systems offering the highest score.

The *best_solution.tsv* and *all_best_solutions.tsv* files have the same structure as the file *all_systems.tsv*, except that there is an extra column **sol_id** which is a solution identifier added to the file *all_best_solutions.tsv*. The systems that have the same "sol_id" belong to a same solution.

As the files have the same structure as *all_systems.tsv*, they can also be parsed with pandas as shown above.

For the description of the fields of *best_solution.tsv*, see *above* those of the *all_systems.tsv* file.

For the *all_best_solutions.tsv*, each line corresponds to a "hit" that has been assigned to a detected system. It includes:

- **sol_id** - the name of the solution it is part of
- **replicon** - the name of the replicon it belongs to
- **hit_id** - the unique identifier of the hit
- **gene_name** - the name of the component identified by the hit
- **hit_pos** - the position of the sequence in the replicon
- **model_fqn** - the model fully-qualified name
- **sys_id** - the unique identifier attributed to the detected system
- **sys_loci** - the number of loci

- **sys_wholeness** - the wholeness of the system
- **sys_score** - the system score
- **sys_occ** - the estimated number of system occurrences that could be potentially "filled" with this system's occurrence, based on the average number of each component found. A proxy for the genetic potential ton encode several systems from the set of components found in this one occurrence.
- **hit_gene_ref** - the gene in the model whose this hit plays the role of
- **hit_status** - the status of the component in the assigned system's definition
- **hit_seq_len** - the length of the protein sequence matched by this hit
- **hit_i_eval** - Hmmer statistics, the independent-evalue
- **hit_score** - Hmmer score
- **hit_profile_cov** - the percentage of the profile covered by the alignment with the sequence
- **hit_seq_cov** - the percentage of the sequence covered by the alignment with the profile
- **hit_begin_match** - the position in the sequence where the profile match begins
- **hit_end_match** - the position in the sequence where the profile match ends
- **used_in** - whether the hit could be used in another system's occurrence

rejected_clusters.txt

This file records all clusters or cluster combinations (if the "multi_loci" search mode is on) which have been discarded and the reason why they were not selected as systems.

The header is composed of the MacSyFinder version and the command line used followed by the description of the cluster(s). The list of the hits composing the cluster is presented at the end of the cluster or clusters' combination, followed by the reason why it has been discarded.

```
# macsyfinder 20200511.dev
# /macsyfinder --sequence-db data/base/GCF_000006745.fasta --models TFF-SF all --
↪models-dir data/models/ --db-type gembase -w 4
# Rejected clusters:

Cluster:
    - model: T4P
    - hits: (GCF_000005845_025680, T4P_pilW, 2568), (GCF_000005845_025690, T4P_fimT,␣
↪2569)
Cluster:
    - model: T4P
    - hits: (GCF_000005845_026930, T2SS_gspO, 2693)
Cluster:
    - model: T4P
    - hits: (GCF_000005845_030080, T2SS_gspO, 3008)
These clusters have been rejected because:
The quorum of mandatory genes required (4) is not reached: 1
The quorum of genes required (5) is not reached: 3
============================================================
Cluster:
    - model: Archaeal-T4P
    - hits: (GCF_000005845_019260, Archaeal-T4P_arCOG00589, 1926), (GCF_000005845_
↪019310, Archaeal-T4P_arCOG02900, 1931)
These clusters have been rejected because:
```

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```
The quorum of mandatory genes required (3) is not reached: 0
The quorum of genes required (3) is not reached: 2
============================================================
```

Output files for the "unordered replicon" search mode

Systems detection results

As for ordered replicons, several output files are provided.

- **all_possible_systems.txt** - This file contains the description of candidate systems found.
- **all_possible_systems.tsv** - The same information as in *all_possible_systems.txt* but in the tabulated tsv format.
- **uncomplete_systems.txt** - This file contains occurrences for systems that did not complete models' definitions and that were therefore not kept as candidate systems.

In this *unordered* search mode, there is no notion of order or distance of the components along the replicon. The clustering step is skipped by MacSyFinder, and it is therefore "only" checked for each type of system being searched whether there is the genetic potential to fulfil its model definition.

all_systems.txt

This file contains potential systems for unordered replicon in human readable format.

In this file, for each component of each searched system's model, we report the number of hits found. For the description of the fields, see *above*.

Warning: In this mode the *forbidden* genes are reported here to the user. As we do not know if they co-localize (cluster) with the other genes they could be present in the replicon, yet far away - or very close on the contrary - to the potential system.

```
# macsyfinder 20201028.dev
# macsyfinder --sequence-db tests/data/base/one_replicon.fasta --db-type unordered --
↪models-dir tests/data/models -m TFF-SF T4P_single_locus
# Systems found:

This replicon contains genetic materials needed for system TFF-SF/T4P_single_locus


system id = Unordered_T4P_single_locus_1
model = TFF-SF/T4P_single_locus
replicon = Unordered
hits = [('GCF_000006845_000250', 'T4P_pilY', 25), ('GCF_000006845_000700', 'T4P_pilY',
↪ 70), ('GCF_000006845_001030', 'T4P_pilQ', 103), ('GCF_000006845_001040', 'T4P_pilP
↪', 104), ('GCF_000006845_001050', 'T4P_pilO', 105), ('GCF_000006845_001060', 'T4P_
↪pilN', 106), ('GCF_000006845_001070', 'T4P_pilM', 107), ('GCF_000006845_003200',
↪'T4P_pilU', 320), ('GCF_000006845_004190', 'T4P_fimT', 419), ('GCF_000006845_004200
↪', 'T4P_pilV', 420), ('GCF_000006845_004210', 'T4P_pilW', 421), ('GCF_000006845_
↪004220', 'T4P_pilX', 422), ('GCF_000006845_004230', 'T4P_pilA', 423), ('GCF_
↪000006845_010160', 'T4P_pilA', 1016), ('GCF_000006845_012440', 'T4P_pilA', 1244), (
↪'GCF_000006845_014270', 'T4P_pilC', 1427), ('GCF_000006845_014280', 'T4P_pilD',␣
↪1428), ('GCF_000006845_014310', 'T4P_pilB', 1431), ('GCF_000006845_016430', 'T4P_
↪pilT', 1643), ('GCF_000006845_016440', 'T4P_pilU', 1644)]
```

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```
wholeness = 0.889

mandatory genes:
    - T4P_pilE: 0 ()
    - T4P_pilB: 1 (T4P_pilB)
    - T4P_pilC: 1 (T4P_pilC)
    - T4P_pilO: 1 (T4P_pilO)
    - T4P_pilQ: 1 (T4P_pilQ)
    - T4P_pilN: 1 (T4P_pilN)
    - T4P_pilT: 1 (T4P_pilT)
    - T4P_pilD: 1 (T4P_pilD)

accessory genes:
    - T4P_pilA: 3 (T4P_pilA, T4P_pilA, T4P_pilA)
    - T4P_pilV: 1 (T4P_pilV)
    - T4P_pilY: 2 (T4P_pilY, T4P_pilY)
    - T4P_pilW: 1 (T4P_pilW)
    - T4P_pilX: 1 (T4P_pilX)
    - T4P_fimT: 1 (T4P_fimT)
    - T4P_pilM: 1 (T4P_pilM)
    - T4P_pilP: 1 (T4P_pilP)
    - T4P_pilU: 2 (T4P_pilU, T4P_pilU)
    - MSH_mshM: 0 ()

neutral genes:

forbidden genes:

Use ordered replicon to have better prediction.
```

all_systems.tsv

This file contains the same information as in *all_systems.txt* but in *tsv* format. For the description of the fields, see *above*.

Note: This file can be easily parsed with pandas:

```
import pandas as pd
pot_systems = pd.read_csv('all_possible_systems.tsv', sep='\t', comment='#')
```

```
# macsyfinder 20201028.dev
# macsyfinder --sequence-db tests/data/base/one_replicon.fasta --db-type unordered --
↪models-dir tests/data/models -m TFF-SF T4P_single_locus
# Likely Systems found:

replicon    hit_id  gene_name       hit_pos model_fqn       sys_id  sys_wholeness  ␣
↪hit_gene_ref    hit_status      hit_seq_len     hit_i_eval      hit_score       hit_
↪profile_cov hit_seq_cov     hit_begin_match hit_end_match   used_in
Unordered   GCF_000006845_014310    T4P_pilB        1431    TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilB        mandatory       558     3.
↪8e-178         589.000 0.964   0.731   146     553
Unordered   GCF_000006845_014270    T4P_pilC        1427    TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilC        mandatory       410     1.
↪9e-131         434.800 0.997   0.817   72      406
```

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```
Unordered   GCF_000006845_014280    T4P_pilD        1428    TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilD        mandatory       286     2.
↪8e-82 272.300 1.000   0.829   28      264
Unordered   GCF_000006845_001060    T4P_pilN        106     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilN        mandatory       199     2.
↪3e-33 112.200 0.986   0.714   7       148
Unordered   GCF_000006845_001050    T4P_pilO        105     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilO        mandatory       215     2.
↪9e-37 124.800 0.980   0.693   23      171
Unordered   GCF_000006845_001030    T4P_pilQ        103     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilQ        mandatory       723     1.
↪9e-62 206.600 0.935   0.238   548     719
Unordered   GCF_000006845_016430    T4P_pilT        1643    TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilT        mandatory       347     6.
↪9e-167        551.400 0.997   0.983   2       342
Unordered   GCF_000006845_004190    T4P_fimT        419     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_fimT        accessory       221     2.
↪7e-23 78.900  0.985   0.294   7       71
Unordered   GCF_000006845_004230    T4P_pilA        423     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilA        accessory       162     8.
↪6e-20 67.800  0.744   0.389   9       71
Unordered   GCF_000006845_010160    T4P_pilA        1016    TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilA        accessory       149     1.
↪3e-15 54.300  0.821   0.430   5       68
Unordered   GCF_000006845_012440    T4P_pilA        1244    TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilA        accessory       129     1.
↪5e-19 67.000  0.859   0.519   6       72
Unordered   GCF_000006845_001070    T4P_pilM        107     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilM        accessory       371     3.
↪3e-43 144.300 0.988   0.429   30      188
Unordered   GCF_000006845_001040    T4P_pilP        104     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilP        accessory       181     2.
↪7e-34 115.600 1.000   0.735   13      145
Unordered   GCF_000006845_003200    T4P_pilU        320     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilU        accessory       376     2.
↪2e-170        562.600 0.985   0.896   16      352
Unordered   GCF_000006845_016440    T4P_pilU        1644    TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilU        accessory       408     1.
↪5e-127        421.800 0.994   0.833   40      379
Unordered   GCF_000006845_004200    T4P_pilV        420     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilV        accessory       203     9.
↪6e-16 54.600  1.000   0.276   14      69
Unordered   GCF_000006845_004210    T4P_pilW        421     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilW        accessory       326     1.
↪7e-10 38.000  0.517   0.190   17      78
Unordered   GCF_000006845_004220    T4P_pilX        422     TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilX        accessory       203     2.
↪8e-18 62.600  0.983   0.286   17      74
Unordered   GCF_000006845_000250    T4P_pilY        25      TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilY        accessory       1006    2.
↪2e-57 191.700 0.728   0.389   463     853
Unordered   GCF_000006845_000700    T4P_pilY        70      TFF-SF/T4P_single_locus␣
↪Unordered_T4P_single_locus_1    0.889   T4P_pilY        accessory       1047    1.
↪9e-57 191.900 0.721   0.362   516     894
```

uncomplete_systems.txt

This file is created when a search is performed in the *unordered replicon* mode. This file list models that probably do not have not full systems in the replicon(s). For each model, the reason why it is not fulfilled is reported, followed by the model description and the components found.

```
# macsyfinder 20201113.dev
# macsyfinder --sequence-db tests/data/base/one_replicon.fasta --db-type unordered --
↪models-dir tests/data/models -m TFF-SF all
# Unlikely Systems found:

This replicon probably not contains a system TFF-SF/T2SS:
The quorum of mandatory genes required (4) is not reached: 1
The quorum of genes required (6) is not reached: 2

system id = Unordered_T2SS_3
model = TFF-SF/T2SS
replicon = Unordered
hits = [('GCF_000006845_002600', 'Tad_tadD', 260), ('GCF_000006845_014280', 'T4P_pilD
↪', 1428), ('GCF_000006845_016430', 'T4P_pilT', 1643)]
wholeness = 0.143

mandatory genes:
        - T2SS_gspD: 0 ()
        - T2SS_gspE: 0 ()
        - T2SS_gspF: 0 ()
        - T2SS_gspG: 0 ()
        - T2SS_gspC: 0 ()
        - T2SS_gspO: 1 (T4P_pilD)

accessory genes:
        - T2SS_gspM: 0 ()
        - T2SS_gspH: 0 ()
        - T2SS_gspI: 0 ()
        - T2SS_gspJ: 0 ()
        - T2SS_gspK: 0 ()
        - T2SS_gspN: 0 ()
        - T2SS_gspL: 0 ()
        - Tad_tadD: 1 (Tad_tadD)

neutral genes:

forbidden genes:
        - T4P_pilT: 1 (T4P_pilT)

Use ordered replicon to have better prediction.

============================================================
```

Logs and configuration files

Three specific output files are systematically built, whatever the search mode, to store information on MacSyFinder's execution:

- **macsyfinder.conf** - contains the configuration information of the run. It is useful to recover all the parameters used for the run.
- **macsyfinder.log** - the log file, contains raw information on the run. Please send it to us with any **bug report**.

1.1.2 MacSyFinder functioning

Macromolecular models

MacSyFinder relies on the definition of models of macromolecular systems as a **set of models' components** to be searched by similarity search, and a **set of rules** regarding their genomic organization and their requirement level to make a complete system (mandatory, accessory components, number of components required).

See *below* for more details on MacSyFinder's modelling scheme and the section on *Functioning* for the principles of the MacSyFinder's search engine.

A **MacSyFinder model** (macsy-model for short) is the association of several elements:

- a **definition** which describes the system to detect with a specific **XML grammar** that is described *below*.
- a set of *HMM profiles* (one per component/gene in the model) to enable the similarity search of the systems' components with the HMMER program.

The models are grouped by *family* possibly gathering *sub-families* (multiple levels allowed), for instance *Secretion*, *Cas-proteins*... A set of models from a same family (coherent set) of systems to detect is called hereafter a **macsy-model package** `NEW in V2`.

Structure of a macsy-model package

A macsy-model package follows the following structure

```
family_name
    |________ metadata.yml
    |________ LICENCE
    |________ README.md
    |________ definitions
    |             |_________ model_1.xml
    |             |_________ model_2.xml
    |             :
    |
    |________ profiles
                  |_________ geneA.hmm
                  |_________ geneB.hmm
```

If the package contains sub-families

```
family_name
    |________ metadata.yml
    |________ LICENCE
    |________ README.md
    |________ definitions
```

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```
    |              |_________ subfamilyA
    |              |              |_________ model_1.xml
    |              |              |_________ model_2.xml
    |              |
    |              |_________ subfamilyB
    |              |              |_________ model_3.xml
    |              |              |_________ model_4.xml
    |              |
    |              :
    |
    |________ profiles
                   |_________ geneA.hmm
                   |_________ geneB.hmm
```

For examples of macsy-model packages, please visit https://github.com/macsy-models

Principles, and how to write macsy-models definitions

Macsy-models are written as XML files, and should be named with the name of the system to detect as a prefix, and the XML file extension as a suffix. For example, 'T1SS.xml' for T1SS (Type I Secretion System).

A macsy-model defines a macromolecular System as:

- A set of **components** (*i.e.* proteins, or protein-coding genes given the context) with different attributes that are used for system's **content description**.
- Features regarding the **genomic architecture** of the systems' components for system detection.
- Rules for **quorum** specifying how many components are required to infer the presence of a complete system.

Macsy-model Components

Four distinct **types of components** can be used to model the System's content. Components correspond to Gene objects in MacSyFinder's implementation, and point to corresponding HMM protein profiles.

- **mandatory** components represent components that are essential to be found to infer the system's presence.
- **accessory** components correspond to components that can be found in some systems' occurrence (or quickly evolving components that are hard to detect with a single HMM profile and thus can be missed along similarity search).
- **neutral** components are used to build/extend clusters of proximal genes/components on the replicon analysed, but are not part of the quorum (i.e., not taken into account to assess the system's presence). `NEW in V2`
- **forbidden** components are components which presence is eliminatory for the system's presence assessment.

Specifying a genomic organization

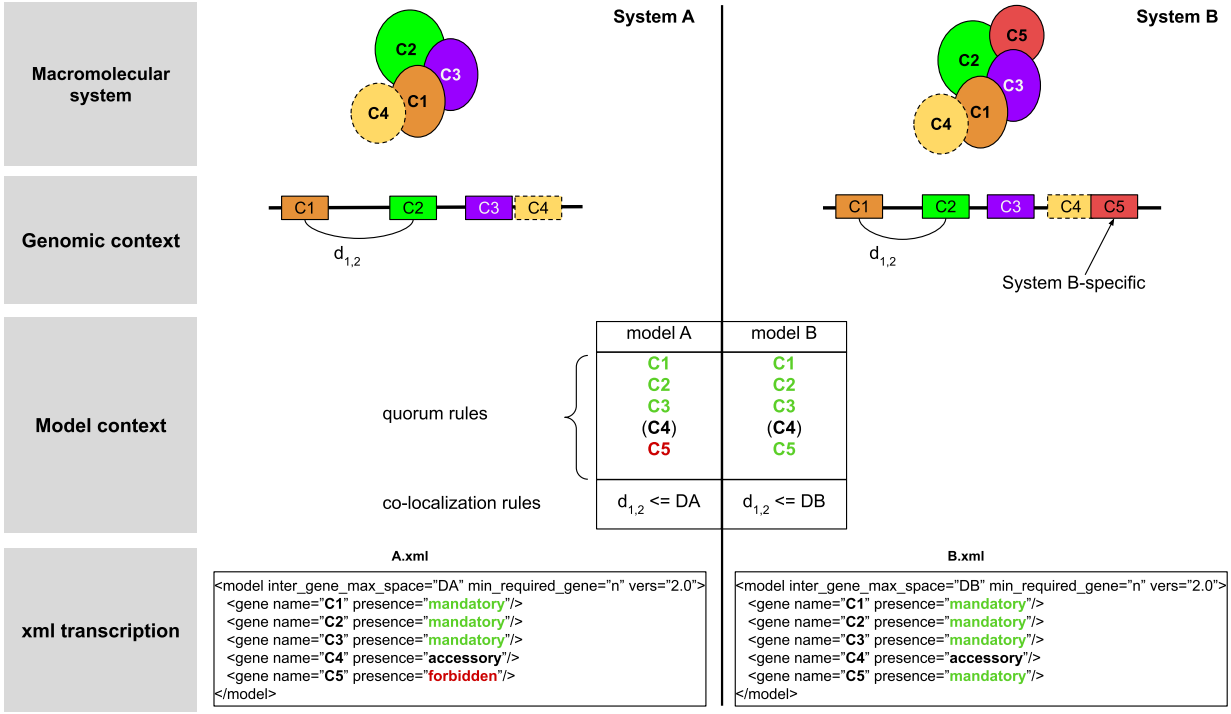
Beyond its list of Components, a MacSyFinder's model of a System is defined by the genomic organization of its components. This genomic organization can be defined in several ways:

- the general System's architecture, whether it is *single-locus* or *multi-loci* (encoded at one or several loci)
- the co-localization criteria defined either at the System level or at the Gene (component) level:
  - the *inter-gene-max-space* parameter (system- or gene- wise)
  - the *loner* parameter (gene- wise)

See *below* for more details on how to specify these parameters in a macsy-model.

The XML hierarchy

A System's model is defined using a specific XML grammar that is hereby described. It consists in a hierarchic view of a Model that has specific features described through parameters, and is made of a set of Genes that have specific features themselves. All these elements and corresponding parameters will parametrize the search of Systems matching the search by MacSyFinder, in terms of Gene content and genomic architecture criteria.



- The element root of a System's model is "model".
  - It has a mandatory attribute: "inter_gene_max_space", an integer representing the maximal number of components without a match between two components with a match for a component profile in order to consider them contiguous (part of a same *Cluster*).
  - The version of the XML grammar (the actual version is "2.0")
  - The element "model" may have attributes:

        * **min_mandatory_genes_required**: an *integer* representing the minimal number of mandatory genes required to infer the system's presence.
        * **min_genes_required**: an *integer* representing the minimal number of mandatory or accessory genes (whose corresponding proteins match a profile of the model) required to infer the system's presence.
        * **multi_loci**: a *boolean* set to True ("1", "true" or "True") to allow the definition of "scattered" systems (i.e., systems encoded at different genomic loci or by different gene *clusters*). If not specified, *default value is false*.
    - The model contains one or more element(s) "gene" that correspond(s) to the genetic components of the macromolecular system.

- The element "gene" has several mandatory attributes:
    - **name**: a *string* representing the name of the component/gene which must match that of a profile enclosed in the profile directory of the macsy-model package (see *below*).
    - **presence**: a *string* representing the status of the gene's presence in the system. It can take four values among "mandatory", "accessory", "neutral", "forbidden" (see above).

  The element "gene" may have other attributes:

    - **loner**: a *boolean*. A *loner* gene can be isolated on the genome and does not have to be part of a cluster of genes to be considered for system's assessment (*default false*).
    - **multi_system**: a *boolean*. If a gene has the feature "multi_system" (value set to "1", "true" or "True"), it means that it can be used to fill multiple systems' occurrences - and thus be considered part of several systems. (*default false*).
    - **inter_gene_max_space**: an *integer* that defines gene-wise value of system's "inter_gene_max_space" parameter (see above). It supersedes the system-wise parameter to give the gene a specific co-localization parameter.

  The element "gene" may have one "exchangeables" child element:

    - The element "exchangeables" can contain one or more elements "gene".

    For a Gene to have "exchangeables" Genes listed, means that this Gene can be replaced *in the quorum* by the listed child Genes.

Note: If not specified by the user, several features will have their values assigned **by default**:

- the **genomic architecture** of the System being searched will consist in a **single locus**. If a System may be made of Genes from multiple loci, consider setting the *multi_loci* parameter to *True*.
- the **quorum parameters** *min_mandatory_genes_required* and *min_genes_required* will be set to the number of mandatory Genes listed - the *accessory* Genes being deemed not required to infer a complete System.

Example of a macsy-model definition in XML:

```
<model inter_gene_max_space="5" ver="2.0">
  <gene name="gspD" presence="mandatory">
     <exchangeables>
         <gene name="sctC"/>
     </exchangeables>
  </gene>
  <gene name="sctN_FLG" presence="mandatory" loner="1"/>
     <exchangeables>
         <gene name="gspE"/>
         <gene name="pilT"/>
```

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```
    </exchangeables>
  <gene name="sctV_FLG" presence="mandatory"/>
  <gene name="flp" presence="accessory"/>
</model>
```

In this example, the described System consists of three mandatory and one accessory components:

- Two components, the Gene "GspD" and the Gene "sctN_FLG" can respectively be replaced by sctC, and gspE and pilT genes in the quorum.
- To be considered as part of such System, the components should be co-localized in loci (Clusters of Genes), which in this case would amount to being located from each other at a distance of 5-Genes maximum, except for the Gene "sctN_FLG" that is allowed to be located "alone" in the genome being investigated, by a *loner* parameter being set to True. As the *multi_loci* parameter is not set, by default the System should be made of a single locus (Cluster of co-localized Genes - except for the ones listed as *loners*).
- To be considered a complete System, the quorum of Genes should be reached. In this case, the *min_genes_required* and *min_mandatory_genes_required* are not specified and therefore assigned to their default values: *min_mandatory_genes_required* is set to the number of mandatory Genes listed as well as the *min_genes_required* parameter (see above).

Warning:

- a gene is identified by its name.
- this name is case sensitive.
- this name must be unique inside a family of models.
- a HMM profile with a gene-based name must exist in the *profiles* directory of the macsy-model package (see *below*).

Providing HMM profiles

For each gene mentioned in each model you have to provide **a HMM profile** to enable the similarity search of this gene. The HMM profile must have been created by the user from a curated multiple sequence alignment with the *hmmbuild* program from the HMMER package, or can have been obtained from HMM profiles' databases such as TIGRFAM or PFAM .

This profile *MUST* have the same name as the name of the gene mentioned in the definition. For instance, a component named "GeneA" in the macsy-model would correspond by default to a HMM profile "GeneA.hmm" enclosed in the macsy-model package. The names are **case-sensitive**. All HMM profiles must be placed in the *profiles* directory of the macsy-model package.

Note: For a detailed tutorial on how to define your macsy-model's features, parameters and HMM profiles, you can have a look at our cookbook in this book chapter .

Installing and sharing models

How to install new models

MacSyFinder does not provide models. You must install models before using it. The `macsydata` utility tool is shipped with *MacSyFinder* to deal with macsy-models:

macsydata <subcommand> [options]

The main sub-commands are

- `macsydata available` to get the list of macsy-models available
- `macsydata search` to search a model given its name or a pattern in its description
- `macsydata install` to install a macsy-model package (the installed version can be set see –help)
- `macsydata cite` to retrieve information on how to cite the model
- `macsydata --help` to get the extended list of available subcommands
- `macsydata <subcommand> --help` to get help about the specified subcommand

macsydata is `NEW in V2`

Where the models are located

MacSyFinder looks at several locations to find macsy-models.

system-wide installation

By default *macsydata* installs models in a shared location (set by –install-data option) that is */usr/share/macsyfinder/* or */usr/local/share/macsyfinder* depending on your Operating System distribution. If you use a *virtualenv*, the shared resources are located in the *<virtualenv>/share/macsyfinder* directory.

user-wide installation

If you don't own rights to install system-wide, you can install models in the MacSyFinder's cache located in your home: *$HOME/.macsyfinder/data/*. *macsydata* installs packages in this location when you use the *–user* option. The packages installed in user land is added to the system-wide packages.

Note: If two packages have the same name, the package in the user land supersedes the system-wide package.

---

project-wide installation

If you cannot install macsy-model packages in system or user land locations, you can specify a specific location with the `--models-dir` *command-line option*. The path must point at a directory that contains macsy-model packages as described *above*.

Writing my own macsy-model package

The whole package structure is described *above* and requires five different types of files described below to be complete:

- a metadata file
- a README.md file
- a LICENCE file
- macsy-models definition(s)
- HMM profiles

metadata file

This file contains some meta information about the package itself. It is in YAML format and must have the following structure:

```
---
maintainer:
  name: The name of the person who maintains/to contact for further information.␣
↪(required)
  email: The email of the maintainer (required)
short_desc: A one line description of the package (can e.g. be used for *macsydata*␣
↪searches) (required)
vers: The package version (required)
cite: The publication(s) to cite by the user when the package is used (optional, used␣
↪by `macsydata cite`)
doc: Where to find extended documentation (optional)
licence: The licence under the package is released (optional but highly recommended)
copyright: The copyright of the package (optional)
```

For example:

```
---
maintainer:
   name: first name last name
   email: login@my_domain.com
short_desc: Models for 15 types of secretion systems or bacterial appendages (T1SS,␣
↪T2SS, T3SS, T4P, pT4SSt, pT4SSi, T5aSS, T5bSS, T5bSS, T6SSi, T6SSii, T6SSiii,␣
↪Flagellum, Tad, T9SS).
vers: 0.0a1
cite:
   - |
     Abby Sophie S., Cury Jean, Guglielmini Julien, Néron Bertrand, Touchon Marie,␣
↪Rocha Eduardo P. C. (2016).
     Identification of protein secretion systems in bacterial genomes.
     In Scientific Reports, 6, pp. 23080.
     http://dx.doi.org/10.1038/srep23080
doc: https://github.com/macsy-models/TXSS
licence: CC BY-NC-SA 4.0 (https://creativecommons.org/licenses/by-nc-sa/4.0/)
copyright: 2014-2020, Institut Pasteur, CNRS
```

Warning: This *metadata.yml* file is **mandatory**. Without this file your archive/repository will not be considered as a *macsy-model package*.

Note:

- - specify an item of yaml list
- | is used to specify a single item but over multiple lines.

README.md

A description of the package: what kind of systems the package models, how to use it etc... in markdown format.

LICENCE

The licence use to protect and share your work. If you don't know which licence to choose, have a look at CreativeCommons *This file is optional, but highly recommended.*

Share your models

If you want to share your models you can create a *macsy-model package* in your github repository.

1. check the validity of your package with the `macsydata check` command.
2. create a tag, and submit a pull request to https://github.com/macsy-models organization.
3. when your pull request (PR) is accepted, the model package becomes automatically available to the community through the *macsydata* tool.

If you don't want to submit a PR you can provide the tag release tarball (tar.gz) as is to your collaborators. This archive will also be usable with the *macsydata* tool.

MacSyFinder's functioning

Functioning overview

MacSyFinder is run from the command-line using a variety of input files and options. See *Input dataset* for more details. Below follows a description of its overall functioning.

A. Searching for Systems' components

Initially, MacSyFinder **searches for the components** of the *System(s)* to detect by sequence similarity search.

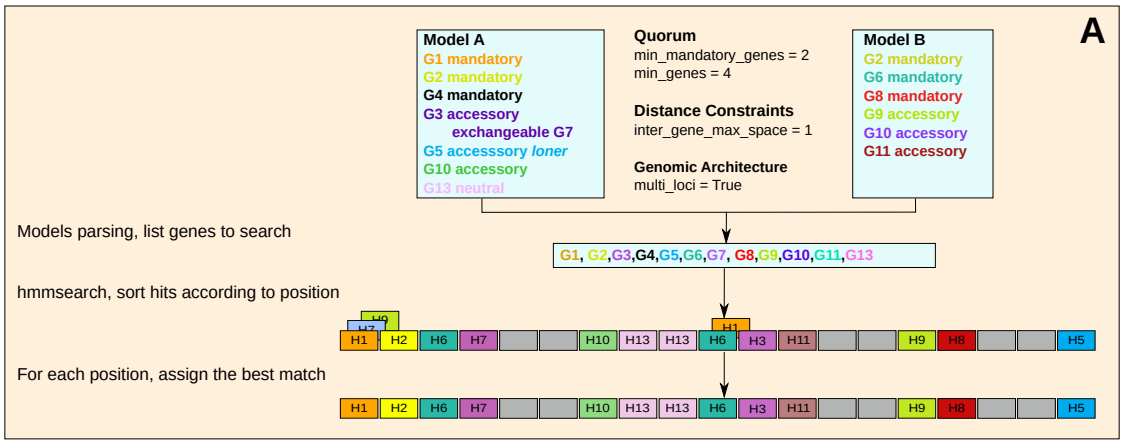
1. From the list of *System(s)* to detect, a **non-redundant list of components to search** is built. For each system, the list can include:

- mandatory components
- accessory components
- neutral components

- forbidden components
- exchangeable components that can be functionally replaced by other components (usually by analogs or homologs). These other components are thus also added to the list of components to search.

See *here for more details on writing MacSyFinder's models.*

2. HMMER is run on the corresponding set of components' HMM profiles, and the hits are filtered according to the criteria defined by the user or by default (see *Hmmer options* and for more, the API *report* object page). This step, and the extraction of significant hits can be performed in parallel (*-w* command-line option). See the *Command-line options*, and the *search_genes API* for more details.



B. Hits browsing

The following steps depend on whether the input dataset is **ordered** (complete or nearly complete genome(s)), or **unordered** (metagenomes, or unassembled genome(s)) (see the *Input dataset* section).

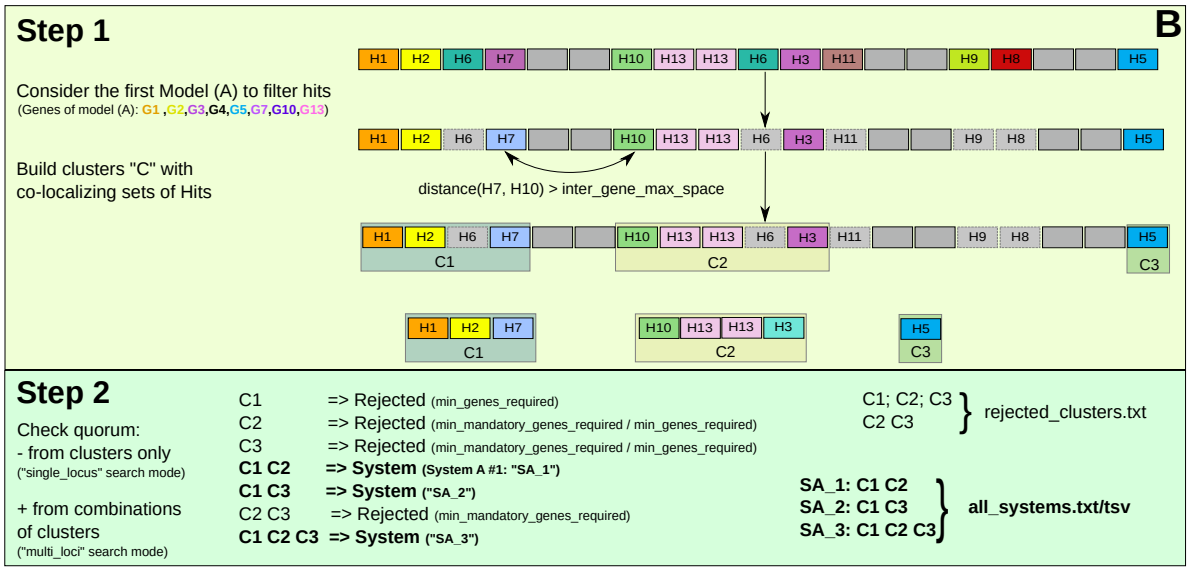
In the case of **ordered datasets** (*ordered_replicon* or *gembase* search mode), the hits are filtered to keep only hits related to the system's model we are looking for. These hits are used to build **clusters of co-localized genes** as defined *in the macsy-model files*. These clusters are then screened to check for the model specifications such as the minimal quorum of "Mandatory" or "Accessory" genes, or the absence of "Forbidden" components.

When the **gene order is unknown** (*unordered* search mode) the power of the analysis is more **limited**. In this case, the presence of systems can only be suggested on the basis of the **quorum** of components - and not based on genomic context information.

For *ordered* datasets: building clusters of components

The following two steps are reiterated for each model being searched.

1. The search starts with the filtering of hits to only keep the **hits that are listed in the model** (mandatory, accessory, neutral, forbidden, exchangeable).
2. MacSyFinder searches for sets of contiguous hits to build **clusters**, following the **(co-localization criterion)** for each replicon, as defined in the MacSyFinder's model. Two hits are deemed contiguous if their genomic location is separated by less than *d* protein-encoding genes, *d* being the maximum of the two *inter_gene_max_space* parameters from the two genes with hits (system-wise, or gene-specific parameter). The *loner* components may form a cluster on their own.



Once performed for each model searched, the *next step* is performed.

Note: The clusters that do not fulfill the quorum requirements are stored in the *rejected_clusters.txt* file.

For *unordered* datasets:

For each model being searched:

1. The Hits are filtered by model.
2. They are used to check if they reach the quorum (i.e., the clustering step is skipped as there is no notion of genetic distance in this search mode).
3. For each system, if the quorum is reached, hits are reported in the *all_systems.tsv* output file. It has to be noted that forbidden components are listed too, as they can also be informative for the user.

Note: The "unordered" mode of detection is less powerful, as a single occurrence of a given model is filled for an entire dataset with hits that origin is unknown. Please consider the assessment of systems with caution in this mode.

For unordered datasets, the **search so ends**, and MacSyFinder generates the final *output files*.

C. Computing candidate Systems' scores (ordered mode)

This step only applies to the most powerful search mode, i.e., on **ordered datasets**. The whole step is `NEW in V2`

The **new search engine** implemented since version 2.0 of MacSyFinder better explores the space of possible Solutions regarding the presence of Systems in replicons analysed. It creates clusters of hits for Systems' components separately for each System searched, and therefore might find **candidate occurrences of Systems that overlap** in terms of components. Moreover, if a System is possibly encoded at several locations on the replicon analysed (option *multi_loci* set to "True" in the model), this calls for a **combinatorial screening** of the different clusters to assemble them into coherent systems regarding the macsy-models.

- For a given model, clusters are used to "fill up" Systems' occurrence(s) according to the **quorum criteria** defined in the System's model (see function `macsypy.system.match()`):

  The *min_genes_required* and *min_mandatory_genes_required* thresholds must be reached.

  - In the case of the *single-locus system* search mode (default), each cluster in addition to potential loners are evaluated for System's assessment separately.
  - In the case of the *multi-loci system* search mode (`multi_loci=True`), each possible combination of clusters is confronted to the quorum of the System being examined.

  The sets of clusters that fulfill the quorum are reported as candidate Systems in the *all_systems.txt* and *all_systems.tsv* output files (see *Output format*), and they obtain a **System's score** (see below).

  The clusters that do not allow to form a candidate System are reported in the *rejected_clusters.txt* output file.

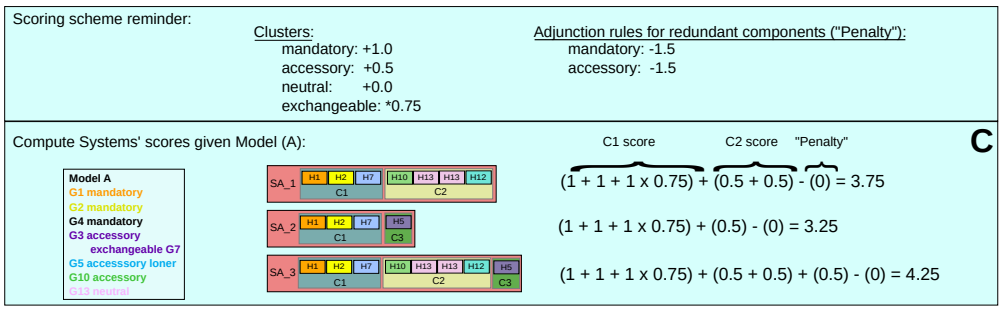
- We introduce a **scoring scheme for candidate Systems**, to easily separate combinations of clusters that are readily more similar to a system's model than others.

  The assumptions behind this scoring scheme are the following:

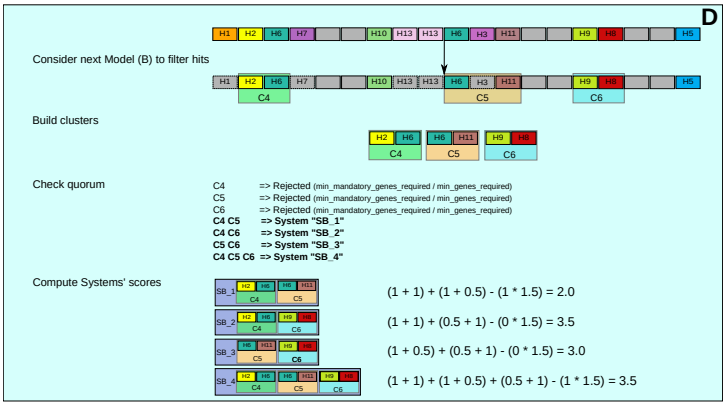
  - We set a score for the different types of genes/components when defining a **cluster's score**:
    - +1.0 is added when a *mandatory* gene is present
    - +0.5 is added when an *accessory* gene is present
    - +0.0 is added when a *neutral* gene is present
    - *0.8 (a factor of 0.8) is applied to the above-scores when the function is fulfilled by an *exchangeable* gene
    - *0.7 (a factor of 0.7) is applied to the above scores if the hit is a *loner multi system*.
  - When combinations of clusters are explored in order to fulfill macsy-models' requirements and build candidate systems ("multi_loci" mode, several clusters can make a complete *System*), we sum the score of clusters to assign a *System*'s score.
  - In addition, we want to **favor concise sets of clusters** to fulfill a *System*'s model. We thus **penalize the adjunction of a cluster** to a candidate *System* when this cluster does not bring any new components to the *System*'s quorum, or when it brings **redundant components**. Thus:
    - -1.5 is added when a **redundant** mandatory gene is added when adjuncting the cluster to a candidate *System*
    - -1.5 is added when a **redundant** accessory gene is added when adjuncting the cluster to a candidate *System*
    - for the loner multi system the score of loner is added only if the function is not fulfilled in the others culsters. In this case, even there is several occurrences the score is added only once (but no penaltiy is applied).

– Only candidate sets of clusters that fulfill a macsy-model and that are thus designated candidate *Systems*, obtain a **System's score**

In summary, a Systems's score is made of two parts: the **sum of the scores** of the Clusters it is made of, plus **a penality part** to avoid too much component's redundancy in Cluster's combinations. The systems' scoring step is exemplified in this figure:



D. Repeat operations B and C for the other models being searched



This search for candidate *Systems* from different models results in a number of possible *Solutions* representing combinations of putative sets of *Systems* in the analysed dataset.

E. Computing possible Solutions, defining the best one (ordered mode)

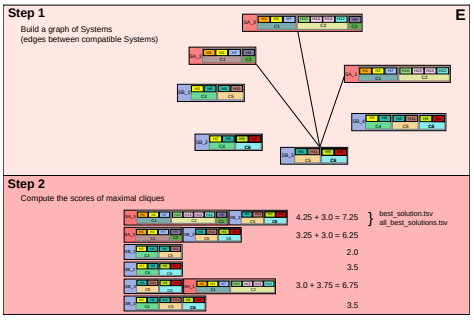
At the end of the previous step MacSyFinder has computed all potential *Systems* present in the replicon, made of combinations of Clusters and *loner* components that fulfill the model's requirements, which are themselves made of a subset of Hits (remember, Hits are at 1st filtered and treated separately for each model of System to be detected). Candidate *Systems* may thus overlap by being partly made of the same components, or even partly being made of the same Clusters.

We define a *Solution* as being **a set of compatible Systems**, i.e. that do not have any overlaps between their components. All possible *Solutions* are combinatorially explored and consist in all possible sets of compatible *Systems*.

A scoring scheme enables to separate between sets of *Solutions*. A **Solution's score** is basically the **sum of its Systems' scores**. The overall procedure of exploring the space of all possible *Solutions* while finding the optimal one, i.e. that with the maximal score, is performed at once using a graph solution to this problem, implemented in the `networkx package`.

We create a graph where each potential *System* is a vertex, and we create an edge between pairs of vertices if they do

not share any components (compatible *Systems*). Once the graph is created we look for the maximum clique which maximizes the score. This allows to provide the user with one, or multiple *Solutions* that have the **best score possible** among all combinations of compatible *Systems*.



CHAPTER

TWO

DEVELOPER GUIDE

2.1 Developer Guide

2.1.1 MacSyFinder implementation overview

MacSyFinder is implemented with an object-oriented architecture. Below a short glossary to fix the vocabulary used in MacSyFinder

Cluster Is a "contiguous" set of hits. two hits are considered contiguous if the number of genes between the 2 genes matching the 2 hits in the replicon is lesser than inter-genes-max-space.

Model Is a formal description of a macromolecular system. Is composed of a definition and a list of profiles. at each gene of the Model must correspond a profile

Model family A set of models, on the same topic. It is composed of several definitions which can be sorted in hierachical structure and profiles. A profile is a hmm profile file.

ModelDefinition Is a definition of model, it's serialize as a xml file

Solution It's a systems combination for one replicon. Technically it's a list of Systems. The best solution for a replicon, is the combination of all systems found in this replicon which maximize the score.

System It's an occurrence of a specific Model on a replicon. Basically, it's a cluster or set of clusters which satisfy the Model quorum.

MacSyFinder project structure

A brief overview of the files and directory constituting the MacSyFinder project

doc The project is documented using sphinx. All sources files needed to generate this documentation is in the directory *doc*

etc This directory contains a template to configure macsyfinder. It's allow to set some configuration available for each run and avoid to specify them at each run on the command line. This file is in *ini* format.

macsypy This the MacSyFinder python library Inside macsypy there is a subdirectory *scripts* which are the entry points for *macsyfinder* and *macsydata*

tests The code is tested using *unittests*. In *tests* the directory *data* contains all data needed to perform the tests.

utils Contains a binary *setsid* needed macsyfinder to parallelize some steps. Usually *setsid* is provides by the system, but some macOS version does not provide it.

CITATION.yml A file indicating how to cite macsyfinder in yaml format.

CONTRIBUTORS A file containing the list of code contributors.

CONTRIBUTING A guide on how to contribute to the project.

COPYRIGHT The macsyfinder copyrights.

COPYING The licencing. MacSyFinder is released under GPLv3.

README.md Brief information about the project.

requirements.txt The list of python dependencies needed by macsyfinder. do not forget to install hmmsearch which is not handle by python packet manager *pip*

requirements_dev.txt The list of extra dependencies needed if you want to contribute to the code.

setup.py The installation recipe.

MacSyFinder architecture overview

An overview of the main classes.

Note: use *view image* of your browser to zoom in the diagram

---

MacSyFinder functioning overview

In this section I'll give you an idea of the macsyfinder functioning at very high grain coarse.

As all program the entrypoint is the main function The goal of *macsyfinder.main* is to parse the command line. Then to creates a *configuration* object and also initialize the logger. After that it call main_search_systems which contains the macsyfinder logic

The first main_search_systems task is to create models asked by the user on the command line. So a DefinitionParser is instantiated and the ModelBank and GeneBank are populated

Once all models are created, we gather all genes and search them in the replicons. This step is done in parallel. The search is done by profile object associated to each gene and rely on the external software *hmmsearch*. The parallelization is ensure by search_genes function The results of this step is a list of hits.

This list is sorted by position and score. this list is filtered to keep only one hit for each position, the one with the best score (position is a gene product in a replicon)

For each model asked by the user, we filter the hits list to keep only those related to the model. Those which are link to mandatory, accessory, neutral or forbidden genes included the exchangeables.

This hits are clustered based on distance constraints describe in the models:

- **inter_gene_max_space** : the maximum genes allowed between to genes of a system.
- **loner** : allow a gene to participate to system even if it does not clusterize with some other genes.

Then we check if each cluster satisfy the quorum described in the model.

- **min_mandatory_genes** : the minimum of mandatory genes requisite to have a system.
- **min_genes_required** : the minimum of genes (mandatory + accessory) requisite to have a system.
- **forbidden_genes** : no forbidden genes may appear in the cluster.

If the model is multi_loci we generate a combination of the clusters and check the quorum for each combination. If the cluster or combination satisfy the quorum a `macsypy.systems.System` is created otherwise a `macsypy.cluster.RejectedCluster`.

The Systems from the same replicon are sort against their position, score.

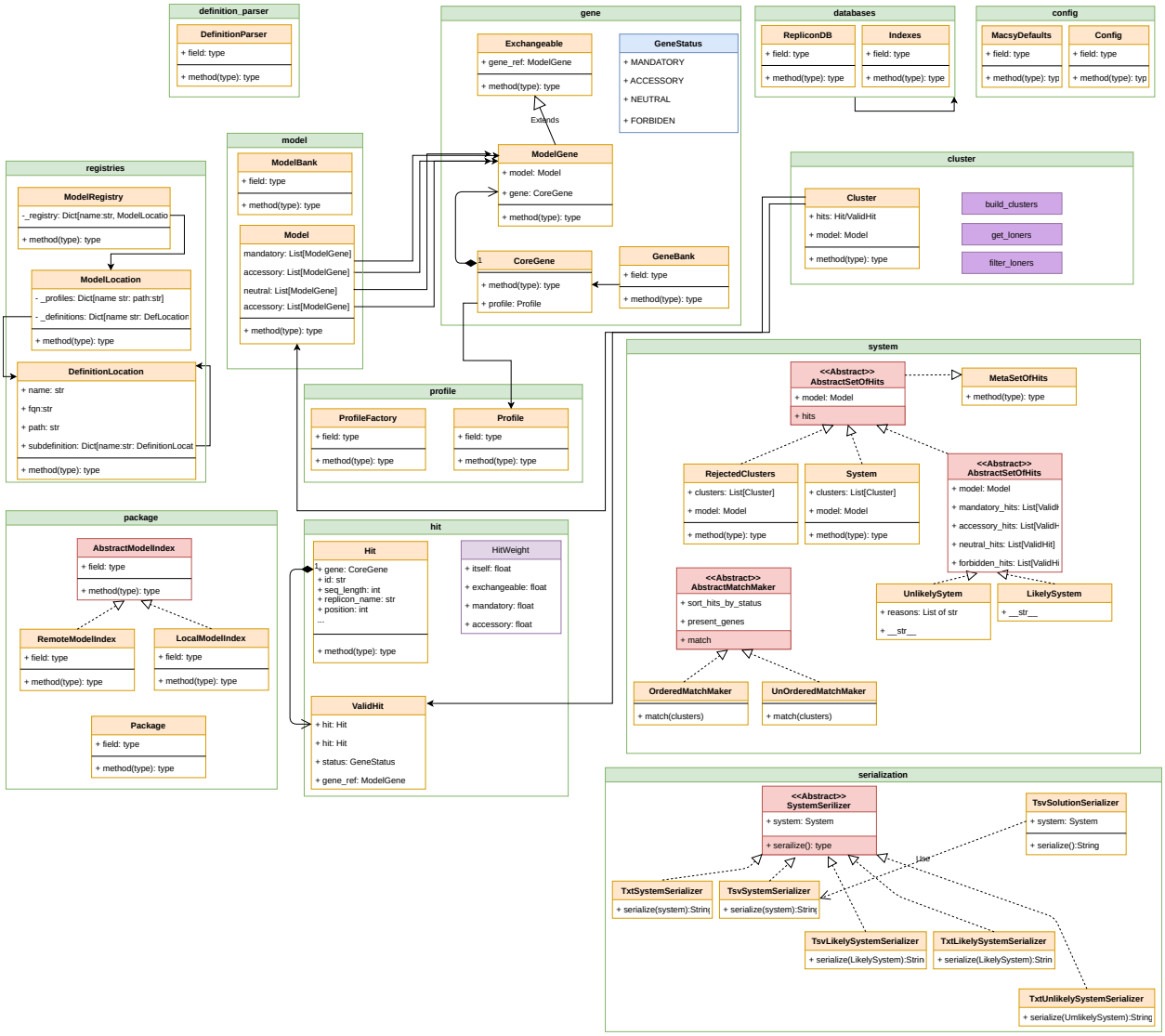


Fig. 1: The macsyfinder classes diagram. The classes are not details. only the main attributes allowing us to understand the interaction are mentioned.

- in green the modules
- in orange, the concrete class
- in red the abstract classes
- in blue the enumeration
- in purple the dataclass
- in purple/pink functions

Note: The neutral genes are used to build clusters. But not to fulfill the quorum.

Among all this potential systems, MSF compute the best combination. *macsypy.solution.find_best_solutions()*. The best combination is the set of compatible systems (do not share common hits) which maximize the score. It's possible to have several equivalent "best solutions". The results of this step is reported in the *best_systems.tsv* file.

The Model object

The *Model object* represents a macromolecular model to detect. It is defined *via* a definition file in XML stored in a dedicated location that can be specified *via* the configuration file, or the command-line (*-d* parameter). See *The XML hierarchy* for more details on the XML grammar.

An object *ModelDefinitionParser* is used to build a model object from its XML definition file.

A model is named after the file tree name of its XML definition. A model has an attribute *inter_gene_max_space* which is an integer, and four kind of components are listed in function of their presence in the system:

- The genes that must be present in the genome to define this model ("mandatory").
- The genes that can be present, but do not have to be found in every case ("accessory").
- The genes that are used to build clusters, but not take in account to check the quorum (`min-genes-required` and `min-mandatory-genes-required`) are described as "neutral".
- The genes that must not be present in the system ("forbidden").

Note: A complete description of macromolecular models modelling is available in the section *Macromolecular models*

The Gene object

The *Gene object* represents genes encoding the protein components of a Model. There is 2 kind of gene The `CoreGene` (*macsypy.gene.CoreGene*) which must be unique given a name. A `CoreGene` must have a corresponding HMM protein profile. These profiles are represented by Profile objects (*macsypy.profile.Profile*), and must be named after the gene name. For instance, the gene *gspD* will correspond to the "gspD.hmm" profile file. See *The Profile object*). After hmmsearch step the hits are link the them. The CoreGene must be created by using the GeneBank factory.

A `ModelGene` (*macsypy.gene.ModelGene*) which encapsulate a CoreGene and is linked to a Model. Instead CoreGene, several ModelGene with the same name may coexists in macsyfinder, in different Models and hold different values for attributes as *inter_gene_max_space*, ... Each ModelGene points out its Model of origin (*macsypy.model.Model*). A Gene has several properties described in the *Gene API*.

A ModelGene may be functionally replaced by an other (usually Homologs or Analogs). In this case these genes are described as exchangeables. Exchangeable object encapsulates a ModelGene and has a reference to the ModelGene it is exchangeable to. See the *Exchangeable API* for more details.

Warning: To optimize computation and to avoid concurrency problems when we search several Models, each CoreGene must be instantiated only once, and stored in a *"gene_bank"*. gene_bank is a *macsypy.gene.GeneBank* object. The gene_bank and model_bank are filled by the system_parser (`macsypy.definition_parser.ModelDefinitionParser`)

The Profile object

Each *"CoreGene"* component corresponds to a *"Profile"*. The *"Profile"* object is used for the search of the gene with Hmmer. Thus, a *"Profile"* must match a HMM file, which name is based on the profile name. For instance, the *gspG* gene has the corresponding "gspG.hmm" profile file provided at a dedicated location.

Reporting Hmmer search results

A *"HMMReport"* (`macsypy.report.HMMReport`) object represents the results of a Hmmer program search on the input dataset with a hidden Markov model protein profile. This object has methods to extract and build *"Hits"* that are then analyzed for systems assessment.

It analyses Hmmer raw outputs, and applies filters on the matches (according to *Hmmer options*). See *Hmmer results' output files* for details on the resulting output files. For profile matches selected with the filtering parameters, *"Hit"* objects are built (see *the Hit API*).

2.1.2 MacSyFinder API documentation

configuration

Options to run MacSyFinder can be specified in a *Configuration file*. The API described below handles all configuration options for MacSyFinder.

The `macsypy.config.MacsyDefaults` hold the default values for *macsyfinder* whereas the `macsypy.config.Config` hold the values for a *macsyfinder* run.

Config

class macsypy.config.**Config**(*defaults*, *parsed_args*)

Handle configuration values for macsyfinder. This values come from default and ar superseded by the configuration files, then the command line settings.

__init__(*defaults*, *parsed_args*)

Store macsyfinder configuration options and propose an interface to access to them.

The config object is populated with the defaults then superseded with the value specified in configuration files and finally by the options set on the command line.

Parameters

- **defaults** (a `MacsyDefaults` object) –
- **parsed_args** (a `argspace.Namescape` object) – the command line arguments parsed

__weakref__

list of weak references to the object (if defined)

_config_file_2_dict(*defaults*, *files*, *previous_run=False*)

parse config files files, the last one have precedence on the previous on so on, and return a dict with properties, values. The defaults is just used to know the type of the properties and cast them. It is not used to fill the dict with default values.

Parameters

- **defaults** (a *macsypy.config.MacsyDefaults* object) – the macsyfinder defaults value
- **files** (*list of string*) – the configuration files to parse

Returns dict

_set_db_type(*value*)
set value for 'db_type' option

Parameters **value** (*str*) – the value for db_type, allowed values are : 'ordered_replicon', 'gembase', 'unordered'

Raises **ValueError** – if value is not allowed

_set_inter_gene_max_space(*value*)
set value for 'inter_gene_max_space' option

Parameters **value** (*str*) – the string parse representing the model fully qualified name and it's associated value and so on the model_fqn is a string, the associated value must be cast in int

Raises **ValueError** – if value is not well formed

_set_max_nb_genes(*value*)
set value for 'max_nb_genes' option

Parameters **value** (*str*) – the string parse representing the model fully qualified name and it's associated value and so on the model_fqn is a string, the associated value must be cast in int

Raises **ValueError** – if value is not well formed

_set_min_genes_required(*value*)
set value for 'min_genes_required' option

Parameters **value** (*str*) – the string parse representing the model fully qualified name and it's associated value and so on the model_fqn is a string, the associated value must be cast in int

Raises **ValueError** – if value is not well formed

_set_min_mandatory_genes_required(*value*)
set value for 'min_mandatory_genes_required' option

Parameters **value** (*str*) – the string parse representing the model fully qualified name and it's associated value and so on the model_fqn is a string, the associated value must be cast in int

Raises **ValueError** – if value is not well formed

_set_models(*value*)

Parameters **value** – The models to search as return by the command line parsing or the configuration files

if value come from command_line [['model1', 'def1', 'def2', 'def3'], ['model2', 'def4'], ...]

if value come from config file [('set_1', 'T9SS, T3SS, T4SS_typeI'), ('set_2', 'T4P')] [(model_family, [def_name1, ...]), ...]

_set_models_dir(*path*)

Parameters **path** (*str*) – the path to the models (definitions + profiles) are stored.

_set_multi_loci(*value*)

Parameters **value** (*str*) – the models fqn list separated by comma of multi loc models

_set_replicon_topology(*value*)
set the default replicon topology

Parameters **value** (*str*) – 'circular' or 'linear'

_set_sequence_db(*path*)

Parameters **path** (*str*) – set the path to the sequence file (in fasta format) to analysed

_set_topology_file(*path*)
test if the path exists and set it in config

Parameters **path** (*str*) – the path to the topology file

_str_2_tuple(*value*)
transform a string with syntax {model_fqn int} in list of tuple

Parameters **value** (*str*) – the string to parse

Returns

Return type [(model_fqn, int), ..]

hmmer_dir()

Returns The name of the directory containing the hmmsearch results (output, error, parsing)

inter_gene_max_space(*model_fqn*)

Parameters **model_fqn** (*str*) – the model fully qualifed name

Returns the gene_max_space for the model_fqn or None if it's does not specify

Return type int or None

log_level()

Returns the verbosity output level

Return type int

max_nb_genes(*model_fqn*)

Parameters **model_fqn** (*str*) – the model fully qualifed name

Returns the max_nb_genes for the model_fqn or None if it's does not specify

Return type int or None

min_genes_required(*model_fqn*)

Parameters **model_fqn** (*str*) – the model fully qualifed name

Returns the min_genes_required for the model_fqn or None if it's does not specify

Return type int or None

min_mandatory_genes_required(*model_fqn*)

Parameters **model_fqn** (*str*) – the model fully qualifed name

Returns the min_mandatory_genes_required for the model_fqn or None if it's does not specify

Return type int or None

multi_loci(*model_fqn*)

Parameters **model_fqn** (*str*) – the model fully qualified name

Returns True if the model is multi loci, False otherwise

Return type bool

out_dir()

Returns the path to the directory where the results are stored

save(*path_or_buf=None*)
save itself in a file in ini format.

Note: the undefined options (set to None) are omitted

Parameters **path_or_buf** (*str or file like object*) – where to serialize itself.

working_dir()
alias to `config.Config.out_dir()`

class macsypy.config.**MacsyDefaults**(***kwargs*)
Handle all default values for macsyfinder. the default values must be defined here, **NOT** in argument parser nor in config the argument parser or config must use a MacsyDefaults object

__init__(***kwargs*)

Parameters **kwargs** – allow to overwrite a default value. It mainly used in unit tests

To define a new default value just add an attribute with the default value

__weakref__
list of weak references to the object (if defined)

registries

The registry manage the different location where *macsyfinder* can find models definitions and their associated profiles.

registries API reference

class macsypy.registries.**DefinitionLocation**(*name=None*, *subdefinitions=None*, *path=None*)
Manage were definitions are stored. a Model is a xml definition and associated profiles. It has 3 attributes

name: the fully qualified definitions name like TXSS/T3SS or CRISPR-cas/Typing/Cas path: the absolute path to the definitions or set of definitions subdefinitions: the subdefintions if it exists

__eq__(*other*)
Return self==value.

__gt__(*other*)
Return self>value.

__hash__()
Return hash(self).

__init__(*name=None*, *subdefinitions=None*, *path=None*)
Initialize self. See help(type(self)) for accurate signature.

__lt__(*other*)
Return self<value.

__str__()
Return str(self).

__weakref__
list of weak references to the object (if defined)

add_subdefinition(*subdefinition*)
add new sub category of definitions to this definition

Parameters **subdefinition** (*DefinitionLocation* object) – the new definition to add as subdefinition.

class macsypy.registries.**ModelLocation**(*path=None*, *profile_dir=None*, *def_dir=None*, *profile_suffix='.hmm'*, *relative_path=False*)
Handle where are store Models. Models are organized in families and sub families. each family match to a ModelLocation. a ModelLocation contains the path toward the definitions and the paths to corresponding to the profiles.

__eq__(*other*)
Return self==value.

__gt__(*other*)
Return self>value.

__init__(*path=None*, *profile_dir=None*, *def_dir=None*, *profile_suffix='.hmm'*, *relative_path=False*)

Parameters

- **path** (*str*) – if it's an installed model, path is the absolute path to a model family. otherwise path is None, and profile_dir and def_dir must be specified.
- **profile_dir** (*str*) – the absolute path to the directory which contains the hmm profiles files.
- **def_dir** (*str*) – The absolute path to the directory which contains the models definitions (xml files) or submodels.
- **profile_suffix** (*str*) – the suffix of hmm files
- **relative_path** (*bool*) – True if you want to work with relative path, False to work with absolute path.

Raise MacsypyError if path is set and profile_dir or def_dir is set

Raise MacsypyError if profile_dir is set but not def_dir and vice versa

__lt__(*other*)
Return self<value.

__str__()
Return str(self).

__weakref__
list of weak references to the object (if defined)

_scan_definitions(*model_def=None*, *def_path=None*)
Scan recursively the definitions tree on the file model and store them.

Parameters

- **model_def** (*DefinitionLocation*) – the current model definition to add new submodel location

- **def_path** (*string*) – the absolute path to analyse

Returns a definition location

Return type *DefinitionLocation* object

_scan_profiles(*path*, *profile_suffix='.hmm'*, *relative_path=False*)
Store all hmm profiles associated to the model

get_all_definitions(*root_def_name=None*)

Name root_def_name The name of the root definition to get sub definitions. If root_def is None, return all definitions for this set of models

Parameters **root_def_name** – string

Returns the list of definitions or subdefinitions if root_def is specified for this model.

Return type list of :class: DefinitionLocation` object

Raises **ValueError** – if root_def_name does not match with any definitions

get_definition(*fqn*)

Parameters **fqn** (*string.*) – the fully qualified name of the definition to retrieve. it's complete path without extension. for instance for a file with path like this: models/TXSS/defintions/T3SS.xml the name is: TXSS/T3SS for models/CRISPR-Cas/definitions/typing/CAS.xml: the name is CRISPR-Cas/typing/CAS

Returns the definition corresponding to the given name.

Return type a *DefinitionLocation* object.

Raise valueError if fqn does not match with any model definition.

get_definitions()

Returns

get_profile(*name*)

Parameters **name** (*string.*) – the name of the profile to retrieve (without extension).

Returns the absolute path of the hmm profile.

Return type string.

Raise KeyError if name does not match with any profiles.

class macsypy.registries.**ModelRegistry**
scan canonical directories to register the different models available in global macsyfinder share data location (depending installation /usr/share/data/models) or can be overload with the location specify in the macsyfinder configuration (either in config file or command line)

__getitem__(*name*)

Parameters **name** (*string*) –

Returns the model corresponding to name.

Return type *ModelLocation* object.

Raises **KeyError** – if name does not match any ModelLocation registered.

__init__()
Initialize self. See help(type(self)) for accurate signature.

__str__()
Return str(self).

__weakref__
list of weak references to the object (if defined)

add(*model_loc*)

Parameters **model_loc** (*ModelLocation* object) – the model location to ad to the registry

models()

Returns the list of models

Return type list of *ModelLocation* object

macsypy.registries.**join_def_path**(**args*)
join different elements of the definition path :param str args: the elements of the definition path, each elements must be a string :return: The return value is the concatenation of different elements of args with one separator :rtype: string

macsypy.registries.**scan_models_dir**(*models_dir*, *profile_suffix='.hmm'*, *relative_path=False*)

Parameters

- **models_dir** (*str*) – The path to the directory where are stored the models
- **profile_suffix** – the suffix of the hmm profiles
- **relative_path** – True if models_dir is relative false otherwise

Returns the list of models in models_dir

Return type [*macsypy.registries.ModelLocation*, ...]

macsypy.registries.**split_def_name**(*fqn*)

Parameters **fqn** (*string*) – the fully qualified de name of a DefinitionLocation object the follow the schema model_name/<def_name>*/def_name for instance CRISPR-Cas/typing/cas

Returns the list of components of the def path ['CRISPR-Cas', 'typing', 'cas']

Return type list of string

definition_parser

The model definition parser object "DefinitionParser" instantiates Models and Genes objects from XML model definitions (see *Macromolecular models*). The parsing consists in three phases.

Phase 1.

- For each model to parse
  - create the Model
  - add this Model to the model_bank
  - findall genes defined in this model what are the level in the model definition.
  - create the CoreGene (a Gene which is not bind to a model). For each gene name there is only one instance of CoreGene
  - add these CoreGene in the gene_bank

Phase 2.

- For each model to search

  - For each Gene defined in this System:
    * link the gene to the model. Create a ModelGene by encapsulating CoreGene from the gene_bank It can exists at each run several ModelGene for one CoreGene
    * If a gene has exhangeables create them (an Exchangeable inherits from ModeleGene) and add them to the current ModelGene

For instance:

```
Syst_1
<system inter_gene_max_space="10">
    <gene name=”A” mandatory=”1” loner="1">
        <exchangeables>
            <gene name=”B”>
        </exchangeables>
    </gene>
<system>

Syst_2
<system inter_gene_max_space="15">
    <gene name=”B” mandatory=”1”>
        <exchangeables>
            <gene name=”C”>
        </exchangeables>
    </gene>
<system>

Syst_3
<system inter_gene_max_space="20">
    <gene name=”c” mandatory=”1” />
<system>
```

With the example above:

- the CoreGene A, B, C will be created
- the ModelGene (Syst_1, A) (Syst_1, B), (Syst_2, B), (Syst_2, C), (Syst_3, C)
- The ModeleGene (Syst_1, A), (Syst_2, B) and (Syst_3, C) are directly link to their respective Models
- and where (Syst_1, B) (Syst_2, C) are exchangeables and link respectively to (Syst_1, A) and (Syst_2, B)
- the ModelGene has attributes defined in the model where they appear (Syst_1, B) inter_gene_max_space=”10” (Syst_2, B) inter_gene_max_space=”15”

Note: The only “full” Systems (*i.e.,* with all corresponding Genes created) are those to detect.

DefinitionParser

class macsypy.definition_parser.**DefinitionParser**(*cfg*, *model_bank*, *gene_bank*, *model_registry*, *profile_factory*)

Build a Model instance from the corresponding model definition described in the XML file.

__init__(*cfg*, *model_bank*, *gene_bank*, *model_registry*, *profile_factory*)

Parameters

- **cfg** (*macsypy.config.Config* object) – the configuration object of this run

- **model_bank** (*macsypy.model.ModelBank* object) – the model factory
- **gene_bank** (*macsypy.gene.GeneBank* object) – the gene factory
- **model_registry** (macsypy.registry.ModelRegistry object) – The registry with all model location
- **profile_factory** (macsypy.profil.ProfilFactory object) – The profile factory

__weakref__
list of weak references to the object (if defined)

_check_syntax(*model_node*, *path*)
Check if the definition does not contains logical error which is allow by syntax and absence of explicit grammar.

Parameters

- **model_node** (Et.Element object) – the node correponding to the model
- **path** (*str*) – the path of the definition.

Returns None

Raises ***ModelInconsistencyError*** – if an error is encountered in the document.

_create_model(*def_loc*, *model_node*)

Parameters

- **def_loc** (*macsypy.registries.DefinitionLocation* object) – the definition location to parse.
- **model_node** (Et.ElementTree object.) – the node corresponding to the model.

Returns the model corresponding to the definition location.

Return type *macsypy.model.Model* object.

_fill_gene_bank(*model_node*, *model_location*, *def_loc*)
find all gene node and add them to the gene_bank

Parameters

- **model_node** (Et.ElementTree object.) –

  param model_node the node corresponding to the model.
- **model_location** (class:*macsypy.registries.ModelLocation* object.) –
- **def_loc** (*the node corresponding to the 'model' tag*) – a definition location to parse.

Returns None

_get_model_node(*def_loc*)

Parameters **def_loc** (*return the node corresponding to the 'model' tag*) – a definition location to parse.

_parse_exchangeable(*node*, *gene_ref*, *curr_model*)
Parse a xml element gene child of exchangeable and build the corresponding object

Parameters

- **node** (xml.etree.ElementTree.Element object.) – a "node" corresponding to the gene element in the XML hierarchy

- **gene_ref** (class:*macsypy.gene.ModelGene* object) – the gene which this gene is homolog to
- **curr_model** (*macsypy.model.Model* object) – the model being parsed .

Returns the gene object corresponding to the node

Return type *macsypy.gene.Exchangeable* object

_parse_genes(*model*, *model_node*)

Create genes belonging to the models. Each gene is directly added to the model in it's right category ('mandatory, accessory, . . .)

Parameters

- **model** (*macsypy.model.Model* object) – the Model currently parsing
- **model_node** (:class"*Et.ElementTree* object) – the element 'model'

check_consistency(*models*)

Check the consistency of the co-localization features between the different values given as an input: between XML definitions, configuration file, and command-line options.

Parameters **models** (list of *class:macsypy.model.Model* object) – the list of models to check

Raise *macsypy.error.ModelInconsistencyError* if one test fails

(see feature)

In the different possible situations, different requirements need to be fulfilled ("mandatory_genes" and "accessory_genes" consist of lists of genes defined as such in the model definition):

- **If:** min_mandatory_genes_required = None ; min_genes_required = None
- **Then:** min_mandatory_genes_required = min_genes_required = len(mandatory_genes)

always True by Models design

- **If:** min_mandatory_genes_required = value ; min_genes_required = None
- **Then:** min_mandatory_genes_required <= len(mandatory_genes)
- AND min_genes_required = min_mandatory_genes_required

always True by design

- **If:** min_mandatory_genes_required = None ; min_genes_required = Value
- **Then:** min_mandatory_genes_required = len(mandatory_genes)
- AND min_genes_required >= min_mandatory_genes_required
- AND min_genes_required <= len(mandatory_genes+accessory_genes)

to be checked

- **If:** min_mandatory_genes_required = Value ; min_genes_required = Value
- **Then:** min_genes_required <= len(accessory_genes+mandatory_genes)
- AND min_genes_required >= min_mandatory_genes_required
- AND min_mandatory_genes_required <= len(mandatory_genes)

to be checked

parse(*models_2_detect*)

Parse models definition in XML format to build the corresponding Model objects, and add them to the model factory after checking its consistency. To get the model ask it to model_bank

Parameters **models_2_detect** (list of `macsypy.registry.DefinitionLocation`) – a list of model definition to parse.

model

The model is a formal representation of system. The model is describe in terms of components. There are 3 component classes:

- genes which are mandatory
- genes which are accessory
- genes which are forbiden

each genes can have homolgs or analogs. Analogs and Homolgs refer to genes described in an other model.

The models describe also distance constraints between genes:

- inter_gene_max_space
- loner
- multi_loci

and quorum constraints

- min_mandatory_genes_required
- min_genes_required

ModelBank

class macsypy.model.**ModelBank**

Store all Models objects.

__contains__(*model*)

Implement the membership test operator

Parameters **model** (*macsypy.model.Model* object) – the model to test
Returns True if the model is in the Model factory, False otherwise
Return type boolean

__getitem__(*fqn*)

Parameters **fqn** (*string*) – the fully qualified name of the model
Returns the model corresponding to the fqn.
Return type *macsypy.model.Model* object
Raises **KeyError** – if the model corresponding to the name does not exists

__init__()

Initialize self. See help(type(self)) for accurate signature.

__iter__()

Return an iterator object on the models contained in the bank

__len__()

Returns the number of models stored in the bank
Return type integer

__weakref__

list of weak references to the object (if defined)

add_model(*model*)

Parameters **model** (*macsypy.model.Model* object) – the model to add
Raise KeyError if a model with the same name is already registered.

Model

class macsypy.model.**Model**(**args*, ***kwargs*)
Handles a macromolecular model.

Contains all its pre-defined characteristics expected to be fulfilled to predict a complete model:

- component list (genes that are mandatory, accessory, neutral, forbidden)
- quorum (number of genes)
- genetic architecture

__eq__(*other*)

Parameters **other** – the other model to compare

Returns True if this fully qualified name is equal to other fully qualified name. False otherwise.

Return type boolean

__gt__(*other*)

Parameters **other** – the other model to compare

Returns True if this fully qualified name is greater than to other fully qualified name. False otherwise.

Return type boolean

__hash__()

Returns

__init__(*fqn*, *inter_gene_max_space*, *min_mandatory_genes_required=None*, *min_genes_required=None*, *max_nb_genes=None*, *multi_loci=False*)

Parameters

- **fqn** (*string*) – the fully qualified name of the model CRISPR-Cas/sub-typing/CAS-TypeIE
- **inter_gene_max_space** (*integer*) – the maximum distance between two genes (**co-localization** parameter)
- **min_mandatory_genes_required** (*integer*) – the quorum of mandatory genes to define this model
- **min_genes_required** (*integer*) – the quorum of genes to define this model
- **max_nb_genes** (*integer*) –
- **multi_loci** (*boolean*) –

Raises ***ModelInconsistencyError*** – if an error is found in model logic. For instance *genes_required* > *min_mandatory_genes_required*

__lt__(*other*)

Parameters **other** – the other model to compare

Returns True if this fully qualified name is lesser than to other fully qualified name. False otherwise.

Return type boolean

__str__()
Return str(self).

__weakref__
list of weak references to the object (if defined)

property family_name

Returns the family name of the model for instance 'CRISPRCas' or 'TXSS'

Return type str

filter(*hits*)
filter out the hits according to this model. The filtering is based on the name of CoreGene associated to hit and the name of ModelGene of the model (the name of the ModelGene is the name of the CoreGene embed in the ModelGene) only the hits related to genes implied in the model are kept.

Parameters **hits** (list of `macsypy.report.Hit` object) – list of hits to filter

Returns list of hits

Return type list of `macsypy.report.Hit` object

property genes

Returns all the genes without the exchangeables which are described in the model.

Return type set of *macsypy.gene.ModelGene* objects.

get_gene(*gene_name*)

Parameters **gene_name** (*string*) – the name of the gene to get

Returns the gene corresponding to gene_name.

Return type a *macsypy.gene.ModelGene* object.

Raise KeyError the model does not contain any gene with name gene_name.

property inter_gene_max_space

Returns set the maximum distance allowed between 2 genes for this model

Return type integer

property max_nb_genes

Returns the maximum number of genes to assess the model presence.

Return type int (or None)

property min_genes_required

Returns get the minimum number of genes to assess for the model presence.

Return type integer

property min_mandatory_genes_required

Returns get the quorum of mandatory genes required for this model

Return type integer

property multi_loci

Returns True if the model is authorized to be inferred from multiple loci, False otherwise

Return type boolean

property name

Returns the short name of this model

gene

The *Gene object* represents genes encoding the protein components of a Model. There is 2 kind of gene The `CoreGene` (*`macsypy.gene.CoreGene`*) which must be unique given a name. A `CoreGene` must have a corresponding HMM protein profile. A `ModelGene` encapsulate a CoreGene and is linked to a Model.

Warning: To optimize computation and to avoid concurrency problems when we search several models, each gene must be instantiated only once, and stored in gene_bank. gene_bank is a *`macsypy.gene.GeneBank`* object. The gene_bank and model_bank (*`macsypy.model.ModelBank`* object) are instantiated in `macsypy.scripts.macsyfinder.main()` function and filled by a definition_parser (`macsypy.defintion_parser.DefinitionParser`)

Example to get a CoreGene object:

```
# get a model object
model_a = model_bank("TXSS/model_a")
model_b = model_bank("TXSS/model_b")

# get of a <CoreGene> object
t2ss =  gene_bank[("TXSS", "T2SS")]
pilO = gene_bank[("TXSS", "pilO")]
```

to create a ModelGene

```
modelA_t2ss(t2ss, model_A)
modelA_pilO(pilO, model_a, loner=True, inter_gene_max_space=12)
modelB_pilO(pilO, model_b, inter_gene_max_space=5)
```

There is only *one* instance of CoreGene with a given name (model family name, gene name) in one MSF run. But several instance of a ModelGene with the same name may exists. Above, there is 2 <ModelGene> representing *pilO* one in model_a the second in model_b with different properties.

Exchangeable inherits from ModelGene. Then a gene in some model is seen as a Gene, in some other models as an Exchangeable. But there only one instance of the corresponding CoreGene.:

```
core_sctn = gene_bank(("TXSS", "sctN"))
core_sctn_flg = gene_bank(("TXSS", "sctN_FLG"))
model_sctn = ModelGene(core_sctn, model_a)
ex_sctn_flg = Exchangeable(core_stn_flg, model_sctn)
model_sctn.add_exchangeable(ex_sctn_flg)

model_sctn_flg = ModelGene(core_sctn_flg, model_b)
```

which means that in model_a the gene *sctn* can be functionally replaced by *sctn_flg*. In Model_a it appear as an alternative to sctn but in model_B it appear as sctn_flg itself. In one MacSyFinder run several instances of ModelGene and/or Exchangeable with the same name may coexists . But in A whole macsyfinder run there is only one instance core_sctn_flg and core_sctn.

GeneBank

class macsypy.gene.**GeneBank**
Store all Gene objects. Ensure that genes are instanciated only once.

__contains__(*gene*)
Implement the membership test operator
Parameters **gene** (*macsypy.gene.CoreGene* object) – the gene to test
Returns True if the gene is in, False otherwise
Return type boolean

__getitem__(*key*)
Parameters **key** (*tuple (string, string)*) – The key to retrieve a gene. The key is composed of the name of models family and the gene name. for instance CRISPR-Cas/cas9_TypeIIB ('CRISPR-Cas' , 'cas9_TypeIIB') or TXSS/T6SS_tssH ('TXSS', 'T6SS_tssH')
Returns return the Gene corresponding to the key.
Return type *macsypy.gene.CoreGene* object
Raises **KeyError** – if the key does not exist in GeneBank.

__init__()
Initialize self. See help(type(self)) for accurate signature.

__iter__()
Return an iterator object on the genes contained in the bank

__weakref__
list of weak references to the object (if defined)

add_new_gene(*model_location*, *name*, *profile_factory*)
Create a gene and store it in the bank. If the same gene (same name) is add twice, it is created only the first time.
Parameters
- **model_location** (macsypy.registry.ModelLocation object) – the location where the model family can be found.
- **name** (*str*) – the name of the gene to add
- **profile_factory** (profile.ProfileFactory object.) – The Profile factory

Gene

There is two classes to modelize a gene: *macsypy.gene.CoreGene* and *macsypy.gene.ModelGene*. The CoreGene are created using the *macsypy.gene.GeneBank* factory and there is only one instance of a CoreGene with a given name. Whereas several ModelGene with the same name can appear in different model and can have differents properties, *loner* in one model and not in an other, have different *inter_gene_max_space* ... The ModelGene is attached to the model and is composed of a CoreGene.

Note: The *macsypy.hit.Hit* object are link to a CoreGene, whereas the *macsypy.hit.ValidHit* *ref_gene* attribute reference a *macsypy.gene.ModelGene*

CoreGene

class macsypy.gene.**CoreGene**(*model_location*, *name*, *profile_factory*)

Modelize gene attach to a profile. It can be only one instance with the the same name (familly name, gene name)

__hash__()

Return hash(self).

__init__(*model_location*, *name*, *profile_factory*)

Initialize self. See help(type(self)) for accurate signature.

__weakref__

list of weak references to the object (if defined)

property model_family_name

The name of the model family for instance 'CRISPRCas' or 'TXSS'

property name

The name of the gene a hmm profile with the same name must exists.

property profile

The HMM protein Profile corresponding to this gene *macsypy.profile.Profile* object

ModelGene

class macsypy.gene.**ModelGene**(*gene*, *model*, *loner=False*, *multi_system=False*, *inter_gene_max_space=None*)

Handle Gene describe in a Model

__hash__()

Return hash(self).

__init__(*gene*, *model*, *loner=False*, *multi_system=False*, *inter_gene_max_space=None*)

Handle gene described in a Model

Parameters

- **gene** (a *macsypy.gene.CoreGene* object.) – a gene link to a profile
- **model** (*macsypy.model.Model* object.) – the model that owns this Gene
- **loner** (*boolean.*) – True if the Gene can be isolated on the genome (with no contiguous genes), False otherwise.
- **multi_system** (*boolean.*) – True if this Gene can belong to different occurrences of this System.
- **inter_gene_max_space** (*integer*) – the maximum space between this Gene and another gene of the System.

__str__()

Print the name of the gene and of its exchangeable genes.

__weakref__

list of weak references to the object (if defined)

add_exchangeable(*exchangeable*)

Add a exchangeable gene to this Gene

Parameters **exchangeable** (*macsypy.gene.Exchangeable* object) – the exchangeable to add

alternate_of()

Returns the gene to which this one is an exchangeable to (reference gene), or itself if it is a first level gene.

Return type *macsypy.gene.ModelGene* object

property exchangeables

Returns the list of genes which can replace this one without any effect on the model

Return type list of *macsypy.gene.ModelGene* objects

property inter_gene_max_space

Returns The maximum distance allowed between this gene and another gene for them to be considered co-localized. If the value is not set at the Gene level, return the value set at the System level.

Return type integer.

is_accessory(*model*)

Returns True if the gene is within the *accessory* genes of the model, False otherwise.

Parameters **model** (*macsypy.model.Model* object.) – the query of the test

Return type boolean.

property is_exchangeable

Returns True if this gene is describe in the model as an exchangeable. False if ot is describe as first level gene.

is_forbidden(*model*)

Returns True if the gene is within the *forbidden* genes of the model, False otherwise.

Parameters **model** (*macsypy.model.Model* object.) – the query of the test

Return type boolean.

is_mandatory(*model*)

Returns True if the gene is within the *mandatory* genes of the model, False otherwise.

Parameters **model** (*macsypy.model.Model* object.) – the query of the test

Return type boolean.

property loner

Returns True if the gene can be isolated on the genome, False otherwise

Return type boolean

property model

Returns the Model that owns this Gene

Return type *macsypy.model.Model* object

property multi_system

Returns True if this Gene can belong to different occurrences of **the model** (and can be used for multiple System assessments), False otherwise.

Return type boolean.

Exchangeable

class macsypy.gene.**Exchangeable**(*c_gene*, *gene_ref*)

Handle Exchangeables. Exchangeable are ModelGene which can replaced functionally an other ModelGene. Biologically it can be Homolog or Analog

__init__(*c_gene*, *gene_ref*)

Parameters

- **c_gene** (*macsypy.gene.CoreGene* object.) – the gene
- **gene_ref** (*macsypy.gene.ModelGene* object.) – the gene to which the current can replace it.

add_exchangeable(*exchangeable*)

This method should never be called, it's a security to avoid to add exchangeable to an exchangeable.

Parameters **exchangeable** (*macsypy.gene.Exchangeable*) –

Raises ***MacsypyError*** –

alternate_of()

Returns the gene to which this one is an exchangeable to (reference gene)

Return type *macsypy.gene.ModelGene* object

property is_exchangeable

Returns True

GeneStatus

class macsypy.gene.**GeneStatus**(*value*)

Handle status of Gene GeneStatus can take 4 value:

- MANDATORY
- ACCESSORY
- FORBIDDEN
- NEUTRAL

profile

The *Profile object* is used for the search of the gene with Hmmer. A *"Profile"* must match a HMM protein profile file, which name is based on the profile name. For instance, the *gspG* gene has the corresponding "gspG.hmm" profile file provided at a dedicated location.

ProfileFactory

class macsypy.profile.**ProfileFactory**(*cfg*)

Build and store all Profile objects. Profiles must not be instanciated directly. The profile_factory must be used. The profile_factory ensures there is only one instance of profile for a given name. To get a profile, use the method get_profile. If the profile is already cached, this instance is returned. Otherwise a new profile is built, stored in the profile_factory and then returned.

__init__(*cfg*)

Initialize self. See help(type(self)) for accurate signature.

__weakref__

list of weak references to the object (if defined)

get_profile(*gene*, *model_location*)

Parameters

- **gene** (macsypy.gene.Gene or macsypy.gene.Homolog or macsypy.gene.Analog object) – the gene associated to this profile
- **model_location** (*macsypy.registries.ModelLocation* object.) – The where to get the profile

Returns the profile corresponding to the name. If the profile already exists, return it. Otherwise build it, store it and return it.

Return type *macsypy.profile.Profile* object

Profile

class macsypy.profile.**Profile**(*gene*, *cfg*, *path*)

Handle a HMM protein profile

__init__(*gene*, *cfg*, *path*)

Parameters

- **gene** (macsypy.secretion.Gene object) – the gene corresponding to this profile
- **cfg** (*macsypy.config.Config* object) – the configuration
- **path** (*string*) – the path to the hmm profile.

__len__()

Returns the length of the HMM protein profile

Return type int

__str__()

Print the name of the corresponding gene and the path to the HMM profile.

__weakref__

list of weak references to the object (if defined)

_profile_features()

Parse the HMM profile to extract the length and the presence of GA bit threshold

Returns the lentgh, presence of ga bit threshold

Return type tuple(int length, bool ga_threshold)

execute()

Launch the Hmmer search (hmmsearch executable) with this profile

Returns an object storing information on the results of the HMM search (HMMReport)

Return type *macsypy.report.HMMReport* object

hit

A Hit is created when *hmmsearch* find similarities between a profile and protein of the input dataset

hit

class macsypy.hit.**Hit**(*gene*, *hit_id*, *hit_seq_length*, *replicon_name*, *position_hit*, *i_eval*, *score*, *profile_coverage*, *sequence_coverage*, *begin_match*, *end_match*)

Handle the hits filtered from the Hmmer search. The hits are instanciated by `HMMReport.extract()` method

__eq__(*other*)

Return True if two hits are totally equivalent, False otherwise.

Parameters **other** (`macsypy.report.Hit` object) – the hit to compare to the current object

Returns the result of the comparison

Return type boolean

__gt__(*other*)

compare two Hits. If the sequence identifier is the same, do the comparison on the score. Otherwise, do it on alphabetical comparison of the sequence identifier.

Parameters **other** (`macsypy.report.Hit` object) – the hit to compare to the current object

Returns True if self is > other, False otherwise

__hash__()

To be hashable, it's needed to be put in a set or used as dict key

__init__(*gene*, *hit_id*, *hit_seq_length*, *replicon_name*, *position_hit*, *i_eval*, *score*, *profile_coverage*, *sequence_coverage*, *begin_match*, *end_match*)

Parameters

- **gene** (*macsypy.gene.CoreGene* object) – the gene corresponding to this profile
- **hit_id** (*str*) – the identifier of the hit
- **hit_seq_length** (*int*) – the length of the hit sequence
- **replicon_name** (*str*) – the name of the replicon
- **position_hit** (*int*) – the rank of the sequence matched in the input dataset file
- **i_eval** (*float*) – the best-domain evalue (i-evalue, "independent evalue")
- **score** (*float*) – the score of the hit
- **profile_coverage** (*float*) – percentage of the profile that matches the hit sequence
- **sequence_coverage** (*float*) – percentage of the hit sequence that matches the profile
- **begin_match** (*int*) – where the hit with the profile starts in the sequence
- **end_match** (*int*) – where the hit with the profile ends in the sequence

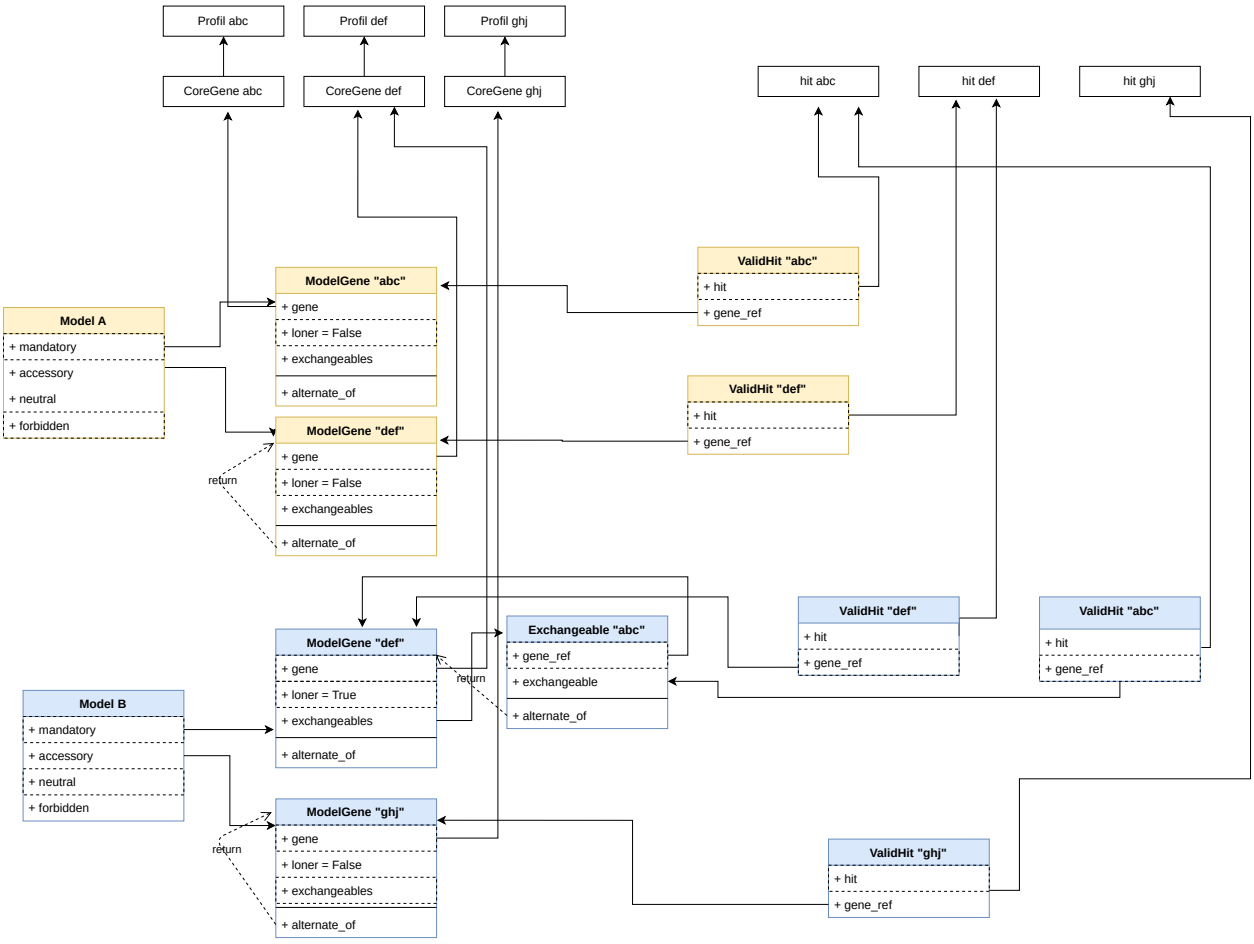


Fig. 2: A diagram showing the interaction between CoreGene, ModelGene, Model, HIt, ValidHit interactions The diagram above represents the models, genes and hit generated from the definitions below.

```
<model name="A" inter_gene_max_space="2">
    <gene name="abc" presence="mandatory"/>
    <gene name="def" presence="accessory"/>
</model>

<model name="B" inter_gene_max_space="5">
    <gene name="def" presence="mandatory"/>
        <exchangeables>
            <gene name="abc"/>
        </exchangeables>
    <gene name="ghj" presence="accessory"
</model>
```

__lt__(*other*)
Compare two Hits. If the sequence identifier is the same, do the comparison on the score. Otherwise, do it on alphabetical comparison of the sequence identifier.

Parameters **other** (`macsypy.report.Hit` object) – the hit to compare to the current object

Returns True if self is < other, False otherwise

__str__()

Returns Useful information on the Hit: regarding Hmmer statistics, and sequence information

Return type str

__weakref__
list of weak references to the object (if defined)

get_position()

Returns the position of the hit (rank in the input dataset file)

Return type integer

class macsypy.hit.**HitWeight**(*itself: float = 1*, *exchangeable: float = 0.8*, *mandatory: float = 1*, *accessory: float = 0.5*, *neutral: float = 0*, *loner_multi_system: float = 0.7*)
The weight to compute the cluster and system score see user documentation macsyfinder functionning for further details by default

- itself = 1
- exchangeable = 0.8
- mandatory = 1
- accessory = 0.5
- neutral = 0
- loner_multi_system = 0.7

__weakref__
list of weak references to the object (if defined)

class macsypy.hit.**ValidHit**(*hit*, *gene_ref*, *gene_status*)
Encapsulates a `macsypy.report.Hit` This class stores a Hit that has been attributed to a putative system. Thus, it also stores:

- the system,
- the status of the gene in this system, ('mandatory', 'accessory', ...
- the gene in the model for which it's an occurrence

__eq__(*other*)
Return self==value.

__gt__(*other*)
Return self>value.

__init__(*hit*, *gene_ref*, *gene_status*)

Parameters

- **hit** (*macsypy.hit.Hit* object) – a match between a hmm profile and a replicon

- **gene_ref** (*macsypy.gene.ModelGene* object) – The ModelGene link to this hit The ModeleGene have the same name than the CoreGene But one hit can be link to several ModelGene (several Model) To know for what gene this hit play role use the *macsypy.gene.ModelGene.alternate_of()*

```
hit.gene_ref.alternate_of()
```

- **gene_status** (*macsypy.gene.GeneStatus* object) –

__lt__(*other*)
Return self<value.

__weakref__
list of weak references to the object (if defined)

macsypy.hit.**get_best_hits**(*hits*, *key='score'*)
If several hits match the same protein, keep only the best match based either on

- score
- i_evalue
- profile_coverage

Parameters

- **hits** ([*macsypy.hit.Hit* object, ...]) – the hits to filter, all hits must match the same protein.
- **key** (*str*) – The criterion used to select the best hit 'score', i_evalue', 'profile_coverage'

Returns the list of the best hits

Return type [*macsypy.hit.Hit* object, ...]

cluster

A cluster is an ordered set of hits related to a model which satisfy the model distance constraints.

cluster

class macsypy.cluster.**Cluster**(*hits*, *model*, *hit_wheights*)
Handle hits relative to a model which collocates

__contains__(*v_hit*)

Parameters **v_hit** (*macsypy.hit.ValidHit* object) – The hit to test

Returns True if the hit is in the cluster hits, False otherwise

__init__(*hits*, *model*, *hit_wheights*)

Parameters

- **hits** ([*macsypy.hit.Hit* | *macsypy.hit.ValidHit*, ...]) – the hits constituting this cluster
- **model** (*macsypy.model.Model*) – the model associated to this cluster

__str__()

Returns a string representation of this cluster

__weakref__
list of weak references to the object (if defined)

_check_replicon_consistency()

Raise MacsypyError if all hits of a cluster are NOT related to the same replicon

fulfilled_function(*gene*)

Parameters **gene** (macsypy.gene.Gene object) – The gene which must be tested.

Returns True if the cluster contains one hit which fulfill the function corresponding to the gene (the gene hitself or an exchageable)

merge(*cluster*, *before=False*)
merge the cluster in this one. (do it in place)

Parameters

- **cluster** (*macsypy.cluster.Cluster* object) –
- **before** (*bool*) – If False the hits of the cluster will be add at the end of this one, Otherwise the cluster hits will be inserted before the hits of this one.

Returns None

Raises ***MacsypyError*** – if the two clusters have not the same model

macsypy.cluster.**build_clusters**(*hits*, *rep_info*, *model*, *hit_weights*)
From a list of filtered hits, and replicon information (topology, length), build all lists of hits that satisfied the constraints:

- max_gene_inter_space
- loner
- multi_system

If Yes create a cluster A cluster contains at least two hits separated by less or equal than max_gene_inter_space Except for loner genes which are allowed to be alone in a cluster

Parameters

- **hits** (list of *macsypy.hit.Hit* objects) – list of filtered hits
- **rep_info** (macsypy.Indexes.RepliconInfo object) – the replicon to analyse
- **model** (*macsypy.model.Model* object) – the model to study

Returns list of clusters

Return type List of *Cluster* objects

macsypy.cluster.**filter_loners**(*cluster*, *loners*)
filter loners to remove those which are already in the cluster

Parameters

- **cluster** (*macsypy.cluster.Cluster* object) – The cluster
- **loners** (*list of cluster [Cluster, ..]*) – the clusters constituted by one loner to filter

Returns list of loners which are not already in the cluster

Return type [Clsuter, ..]

macsypy.cluster.**get_loners**(*hits*, *model*, *hit_weights*)
Create a list of Clusters each cluster is build with one hit matching a loner

Parameters

- **hits** – The list of hits to filter
- **model** (*macsypy.model.Model* object) – the model which will used to build the clusters

Returns The list of cluster which each element is build at least with one loner

Return type [*Cluster*, ..]

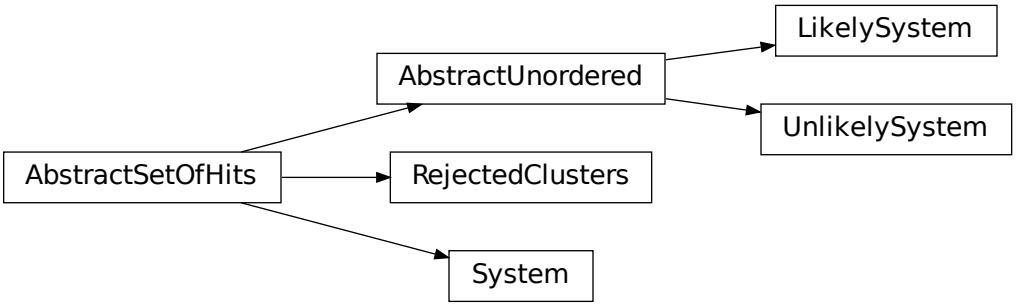
system

This module classes and functions which a given set of hits and a model compute if this set satisfy the model or not

The object which check the compliance of hits to a model is MatchMaker which have 2 sub-classes for ordered and unordered replicons

MatchMaker.match method link hit to a model (*macsypy.hit.ValidHit*) and then check if these valid hit satisfy the quorum constraints defined in the model. According this it instanciate a *macsypy.system.System* or *macsypy.system.RejectedClusters* for ordered replicons or *macsypy.system.LikelySystem* or *macsypy.system.UnlikelySystem* for unordered replicons

below the inheritance diagram:



Warning: The abstract class *macsypy.system.AbstractSetOfHits* is controlled by the metaclass *macsypy.system.MetaSetOfHits* which inject on the fly several private attributes and public properties (see more in *macsypy.system.MetaSetOfHits* documentation)

System

class macsypy.system.**AbstractSetOfHits**(**args*, ***kwargs*)
Is the mother class of System, RejectedCluster, LikelySystems UnlikelySystem, ...

__init__(*model*, *replicon_name*)
Initialize self. See help(type(self)) for accurate signature.

__weakref__
list of weak references to the object (if defined)

count()
fill structures one for supported status mandatory, accessory, ... each structure count how many hit for each gene of the model mandatory_occ = { gene_name : [ValidHit, ...] :return: None

property position

Returns The position of the first and last hit, excluded the hit coding for loners. If the system is composed only by loners, used loners to compute position

Return type tuple (start: int, end:int)

property replicon_name

Returns The name of the replicon

Return type str

property wholeness

Returns a score indicating the genes ratio of the model which have at least one hit ('neutral' genes do not count)

Return type float

class macsypy.system.**AbstractUnordered**(**args*, ***kwargs*)
Technical abstract class to factorize code share between LikelySystem and UnlikelySystem

__init__(*model*, *mandatory_hits*, *accessory_hits*, *neutral_hits*, *forbidden_hits*)
Initialize self. See help(type(self)) for accurate signature.

property accessory_hits

Returns The list of accesory hits

Return type list of *macsypy.hit.ValidHit* objects

property allowed_hits

Returns The list of allowed (mandatory, accessory, neutral) hits

Return type list of *macsypy.hit.ValidHit* objects

property forbidden_hits

Returns The list of forbidden hits

Return type list of *macsypy.hit.ValidHit* objects

property hits

Returns The list of all hits sorted by their position

Return type list of *macsypy.hit.ValidHit* objects

property mandatory_hits

Returns The list of mandatory hits

Return type list of *macsypy.hit.ValidHit* objects

property neutral_hits

Returns The list of neutral hits

Return type list of *macsypy.hit.ValidHit* objects

class macsypy.system.**ClusterSystemTracker**(*systems*)
track in which system is implied each cluster

__init__(*systems*)
Initialize self. See help(type(self)) for accurate signature.

__weakref__
list of weak references to the object (if defined)

class macsypy.system.**HitSystemTracker**(*systems*)
track in which system is implied each hit

__init__(*systems*)
Initialize self. See help(type(self)) for accurate signature.

__weakref__
list of weak references to the object (if defined)

class macsypy.system.**LikelySystem**(**args*, ***kwargs*)
" Handle components that fill the quorum requirements defined in model. with no idea about genetic organization (gene cluster) so we cannot take in account forbidden genes

__str__()

Returns a string representation of this LikelySystem

class macsypy.system.**MatchMaker**(*model*)
Is an abstract class for (Odered/Unordered)MatchMaker the *match* class method must be implemented in concrete classes

__init__(*model*)
Initialize self. See help(type(self)) for accurate signature.

__weakref__
list of weak references to the object (if defined)

_create_exchangeable_map(*genes*)
create a map between an exchangeable (formly homolog or analog) gene name and it's gene reference

Parameters **genes** (list of *macsypy.gene.ModelGene* objects) – The genes to get the exchangeable genes

Return type a dict with keys are the exchangeable gene_name and the value the reference gene name

present_genes()

Returns the lists of genes name in model which are present replicon (included exchangeable)

Return type tuple of 4 lists for mandatory, accessory, neutral and forbidden ([str gene_name, ..], [str gene_name], [str gene_name], [str gene_name])

sort_hits_by_status(*hits*)
sort *macsypy.hit.Hit* according the the status of the gene the hit code for.

Parameters **hits** – list of *macsypy.hit.Hit* object

Returns the valid hits according their status

Return type

a tuple of 4 lists

- *macsypy.hit.ValidHit* for MANDATORY genes
- *macsypy.hit.ValidHit* for ACCESSORY genes
- *macsypy.hit.ValidHit* for NEUTRAL genes
- *macsypy.hit.ValidHit* for FORBIDDEN genes

class macsypy.system.**MetaSetOfHits**(*name*, *bases*, *namespace*, ***kwargs*)

This metaclass control the AbstractSetOfHits class creation. In this metaclass we inject on the fly several attributes and properties two private attributes and one public property corresponding to each value of _supported_status class attribute defined in the concrete classes. for instance for System class

- **the attributes**
  - self._mandatory
  - self._mandatory_occ
  - self._accessory
  - self._accessory_occ
  - self._neutral
  - self._neutral_occ
- **and the properties**
  - mandatory
  - accessory
  - neutral

are automatically injected

The value for attributes _<*status*>_*occ* are filled by the *count* method which is defined in AbstractSetOfHits

__call__(**args*, ***kwargs*)

Call self as a function.

getter_maker()

Create a property which allow to access to the gene corresponding of the cat of the model

Parameters **cat** (*str*) – the type of gene category to which we create the getter

Returns unbound method

class macsypy.system.**OrderedMatchMaker**(*model*, *redundancy_penalty*)

check if a set of hits match the quorum for ordered replicons (ordered_replicon or gembase)

__init__(*model*, *redundancy_penalty*)

Initialize self. See help(type(self)) for accurate signature.

match(*clusters*)

Check a set of clusters fill model constraints. If yes create a *macsypy.system.System* otherwise create a macsypy.cluster.RejectedClusters.

Parameters **clusters** (list of *macsypy.cluster.Cluster* objects) – The list of cluster to check if fit the model

Returns either a System or a RejectedClusters

Return type *macsypy.system.System* or macsypy.cluster.RejectedClusters object

class macsypy.system.**RejectedClusters**(**args*, ***kwargs*)

Handle a set of clusters which has been rejected during the `macsypy.system.match()` step This clusters (can be one) does not fill the requirements or contains forbidden genes.

__init__(*model*, *clusters*, *reasons*)

Parameters

- **model** (*macsypy.model.Model* object) –
- **clusters** (list of *macsypy.cluster.Cluster* objects) – list of clusters. These Clusters should be created with *macsypy.cluster.Cluster* of *macsypy.hit.ValidHit* objects
- **reason** (*list of string*) – the reason why these clusters have been rejected

__str__()

Returns a string representation of this RejectedCluster

property hits

Returns The list of all hits that compose this system

Return type [macsypy.hit.ValidHits, ...]

class macsypy.system.**System**(**args*, ***kwargs*)

Modelize as system. a system is an occurrence of a given model on a replicon.

__init__(*model*, *clusters*, *redundancy_penalty=1.5*)

Parameters

- **model** (*macsypy.model.Model* object) – The model which has ben used to build this system
- **clusters** (list of *macsypy.cluster.Cluster* objects) – The list of cluster that form this system

property hits

Returns The list of all hits that compose this system

Return type [macsypy.hit.ValidHits, ...]

is_compatible(*other*)

Parameters **other** (*macsypy.system.System* object) – the other systems to test compatibility

Returns

True if other system is compatible with this one. False otherwise. Two systems are compatible if they do not share *macsypy.hit.Hit* except hit corresponding to a multi_system gene in the model.

Note: This method is used to compute the best combination of systems.

---

property loci

Returns The number of loci of this system (loners are not considered)

Return type int > 0

property multi_loci

Returns True if the systems is multi_loci. False otherwise

Return type bool

occurrence()

sometimes several systems collocates so they form only one cluster so macsyfinder build only one system the occurrence is an indicator of how many systems are it's based on the number of occurrence of each mandatory genes The multi_system genes are not take in account.

Returns a predict number of biologic systems

property score

Returns a score take in account * if a hit match for the gene or it is an exchangeable gene * if a hit is duplicated and already present in the system or the cluster * if a hit match for mandatory/accessory gene of the model

Return type float

class macsypy.system.**UnlikelySystem**(**args*, ***kwargs*)

Handle components that not fill the quorum requirements defined in model.

__init__(*model*, *mandatory_hits*, *accessory_hits*, *neutral_hits*, *forbidden_hits*, *reasons*)

Parameters

- **model** (*macsypy.model.Model* object) – The model which has ben used to build this system
- **allowed_hits** (list of *macsypy.hit.ValidHit* objects) – The list of hits that form this potential system this hits status must be MANDATORY, ACCESSORY or NEUTRAL
- **forbidden_hits** (list of *macsypy.hit.ValidHit* objects) – The list of hits that are forbidden
- **reasons** (*List of str*) – the reasons why this set of hits has been rejected

__str__()

Returns a string representation of this UnlikelySystem

property reasons

Returns The reasons why it probably not a system

Return type list of string

class macsypy.system.**UnorderedMatchMaker**(*model*)

report

A *"HMMReport"* object represents the results of a Hmmer program search on a dataset with a hidden Markov model protein profile (see *this section*). This object has methods to extract and filter Hmmer raw outputs (see *generated output files*), and then build Hits relevant for system detection. For matches selected with the filtering parameters, *"Hit"* objects (`macsypy.HMMReport.Hit`) are built.

HMMReport API reference

class macsypy.report.**HMMReport**(*gene*, *hmmer_output*, *cfg*)

Handle the results from the HMM search. Extract a synthetic report from the raw hmmer output, after having applied a hit filtering. This class is an **abstract class**. There are two implementations of this abstract class depending on whether the input sequence dataset is "ordered" ("gembase" or "ordered_replicon" db_type) or not ("unordered" db_type).

__init__(*gene*, *hmmer_output*, *cfg*)

Parameters

- **gene** (*macsypy.gene.CoreGene* object) – the gene corresponding to the profile search reported here
- **hmmer_output** (*string*) – The path to the raw Hmmer output file
- **cfg** (*macsypy.config.Config* object) – the configuration object

__str__()

Returns string representation of this report

Return type str

__weakref__

list of weak references to the object (if defined)

_build_my_db(*hmm_output*)

Build the keys of a dictionary object to store sequence identifiers of hits.

Parameters **hmm_output** (*string*) – the path to the hmmsearch output to parse.

Returns a dictionary containing a key for each sequence id of the hits

Return type dict

_fill_my_db(*macsyfinder_idx*, *db*)

Fill the dictionary with information on the matched sequences

Parameters

- **macsyfinder_idx** (*string*) – the path the macsyfinder index corresponding to the dataset
- **db** (*dict*) – the database containing all sequence id of the hits.

_hit_start(*line*)

Parameters **line** (*string*) – the line to parse

Returns True if it's the beginning of a new hit in Hmmer raw output files. False otherwise

Return type boolean.

_parse_hmm_body(*hit_id*, *gene_profile_lg*, *seq_lg*, *coverage_threshold*, *replicon_name*, *position_hit*, *i_evalue_sel*, *b_grp*)

Parse the raw Hmmer output to extract the hits, and filter them with threshold criteria selected ("coverage_profile" and "i_evalue_select" command-line parameters)

Parameters

- **hit_id** (*str*) – the sequence identifier
- **gene_profile_lg** (*int*) – the length of the profile matched
- **coverage_threshold** (*float*) – the minimal coverage of the profile to be reached in the Hmmer alignment for hit selection.
- **replicon_name** (*str*) – the identifier of the replicon
- **position_hit** (*int*) – the rank of the sequence matched in the input dataset file
- **i_evalue_sel** (*float*) – the maximal i-evalue (independent evalue) for hit selection
- **b_grp** (*list of list of strings*) – the Hmmer output lines to deal with (grouped by hit)

Paramint seq_lg the length of the sequence

Returns a sequence of hits

Return type list of `macsypy.report.Hit` objects

_parse_hmm_header(*h_grp*)

Parameters **h_grp** (*sequence of string (<itertools._grouper object at 0x7ff9912e3b50>)*) – the sequence of string return by groupby function representing the header of a hit

Returns the sequence identifier from a set of lines that corresponds to a single hit

Return type string

best_hit()

Return the best hit among multiple hits

abstract extract()

Parse the raw Hmmer output file and produce a new synthetic report file by applying a filter on hits. Contain selected and sorted hits (**this abstract method is implemented in inherited classes**)

save_extract()

Write the string representation of the extract report in a file. The name of this file is the concatenation of the gene name and of the "res_extract_suffix" from the config object

GeneralHMMReport API reference

class macsypy.report.**GeneralHMMReport**(*gene*, *hmmer_output*, *cfg*)

Handle HMM report. Extract a synthetic report from the raw hmmer output. Dedicated to any type of 'unordered' datasets.

extract()

Parse the output file of hmmer compute from an unordered genes base and produced a new synthetic report file.

OrderedHMMReport

class macsypy.report.**OrderedHMMReport**(*gene*, *hmmer_output*, *cfg*)

Handle HMM report. Extract a synthetic report from the raw hmmer output. Dedicated to 'ordered_replicon' datasets.

extract()

Parse the output file of Hmmer obtained from a search in an ordered set of sequences and produce a new synthetic report file.

GembaseHMMReport

class macsypy.report.**GembaseHMMReport**(*gene*, *hmmer_output*, *cfg*)

Handle HMM report. Extract a synthetic report from the raw hmmer output. Dedicated to 'gembase' format datasets.

extract()

Parse the output file of Hmmer obtained from a search in a 'gembase' set of sequences and produce a new synthetic report file.

... MacSyFinder - Detection of macromolecular systems in protein datasets using systems modelling and similarity search. Authors: Sophie Abby, Bertrand Néron Copyright © 2014-2020 Institut Pasteur (Paris), and CNRS. See the COPYRIGHT file for details MacsyFinder is distributed under the terms of the GNU General Public License (GPLv3). See the COPYING file for details.

search_genes

manage the paralelization of code which execute *in fine hmmsearch* to find the genes constituting the models in the input dataset.

search_genes

macsypy.search_genes.**search_genes**(*genes*, *cfg*)

For each gene of the list, use the corresponding profile to perform an Hmmer search, and parse the output to generate a HMMReport that is saved in a file after Hit filtering. These tasks are performed in parallel using threads. The number of workers can be limited by worker_nb directive in the config object or in the command-line with the "-w" option.

Parameters

- **genes** (list of *macsypy.gene.CoreGene* objects) – the genes to search in the input sequence dataset
- **cfg** (*macsypy.config.Config* object) – the configuration object

solution

MacSyFinder find lot of potential systems for the same model, all these systems are saved in "all_systems.xxx" files. This module allow to explore among of all systems which combination seems to be more probable.

Solution

macsypy.solution.**find_best_solutions**(*systems*)
Among the systems choose the combination of systems which does not share *macsypy.hit.Hit* and maximize the sum of systems scores

Parameters **systems** (list of *macsypy.system.System* object) – the systems to analyse

Returns the list of list of systems which represent one best solution and the it's score

Return type tuple of 2 elements ([[*macsypy.system.System*, ...], [*macsypy.system.System*, ...]], float score) The inner list represent a best solution

serialization

This module is a technical module where we can find the different way to serialize the results:

- the Systems found
- The best solutions (best combination of systems)
- The rejected clusters

class macsypy.serialization.**SystemSerializer**
handle the different way to serialize a system

__weakref__
list of weak references to the object (if defined)

class macsypy.serialization.**TsvSolutionSerializer**
Handle Solution (list of Systems) serialization in tsv format

__init__()
Constructor

__weakref__
list of weak references to the object (if defined)

serialize(*solution*, *sol_id*, *hit_system_tracker*)

Parameters

- **solution** (list of *macsypy.system.System* object) – the solution to serialize
- **hit_system_tracker** (*macsypy.system.HitSystemTracker* object) –

Returns a serialisation of this solution (a list of systems) in tabulated separated value format each line represent a hit and have the same structure as system serialization *macsypy.serialization.TsvSystemSerializer.serialize()* but with an extra column sol_id which is a technical id to identified the different solutions.

class macsypy.serialization.**TsvSystemSerializer**
Handle System serialization in tsv format

serialize(*system*, *hit_system_tracker*)

Returns

a serialisation of this system in tabulated separated value format each line represent a hit and have the following structure:

replicon\thit_id\tgene_name\thit_pos\tmodel_fqn\tsys_id\tsys_loci\tsys_wholeness\tsys_score \tsys_occ\thit_gene_ref.alternate_of\thit_status\thit_seq_len\thit_i_eval\thit_score\thit_profile_cov \thit_seq_cov\tit_begin_match\thit_end_match

Return type str

class macsypy.serialization.**TxtSystemSerializer**

Handle System serialization in text

serialize(*system*, *hit_system_tracker*)

Returns a string representation of system readable by human

Database

The "database" object handles the indexes of the sequence dataset in fasta format, and other useful information on the input dataset.

MacSyFinder needs to have the length of each sequence and its position in the database to compute some statistics on Hmmer hits. Additionally, for ordered datasets (db_type = 'gembase' or 'ordered_replicon'), MacSyFinder builds an internal "database" from these indexes to store information about replicons, their begin and end positions, and their topology.

The begin and end positions of each replicon are computed from the sequence file, and the topology from the parsing of the topology file (–topology-file, see *Topology files*).

Thus it also builds an index (with .idx suffix) that is stored in the same directory as the sequence dataset. If this file is found in the same folder than the input dataset, MacSyFinder will use it. Otherwise, it will build it.

The user can force MacSyFinder to rebuild these indexes with the "–idx" option on the command-line.

database

class macsypy.database.**Indexes**(*cfg*)

Handle the indexes for macsyfinder:

- find the indexes required by macsyfinder to compute some scores, or build them.

__init__(*cfg*)

The constructor retrieves the file of indexes in the case they are not present or the user asked for build indexes (–idx) Launch the indexes building.

Parameters **cfg** (*macsypy.config.Config* object) – the configuration

__weakref__

list of weak references to the object (if defined)

_build_my_indexes()

Build macsyfinder indexes. These indexes are stored in a file.

The file format is the following:

- one entry per line, with each line having this format:
- sequence id;sequence length;sequence rank

build(*force=False*)
Build the indexes from the sequence data set in fasta format

Parameters **force** (*boolean*) – If True, force the index building even if the index files are present in the sequence data set folder

find_my_indexes()

Returns the file of macsyfinder indexes if it exists in the dataset folder, None otherwise.

Return type string

class macsypy.database.**RepliconDB**(*cfg*)
Stores information (topology, min, max, [genes]) for all replicons in the sequence_db the Replicon object must be instantiated only for sequence_db of type 'gembase' or 'ordered_replicon'

__contains__(*replicon_name*)

Parameters **replicon_name** (*string*) – the name of the replicon

Returns True if replicon_name is in the repliconDB, false otherwise.

Return type boolean

__getitem__(*replicon_name*)

Parameters **replicon_name** (*string*) – the name of the replicon to get information on

Returns the RepliconInfo for the provided replicon_name

Return type *RepliconInfo* object

Raise KeyError if replicon_name is not in repliconDB

__init__(*cfg*)

Parameters **cfg** (*macsypy.config.Config* object) – The configuration object

Note: This class can be instanciated only if the db_type is 'gembase' or 'ordered_replicon'

__weakref__
list of weak references to the object (if defined)

_fill_gembase_min_max(*topology*, *default_topology*)
For each replicon_name of a gembase dataset, it fills the internal dictionary with a namedtuple RepliconInfo

Parameters

- **topology** (*dict*) – the topologies for each replicon (parsed from the file specified with the option –topology-file)
- **default_topology** (*string*) – the topology provided by the config.replicon_topology

_fill_ordered_min_max(*default_topology=None*)
For the replicon_name of the ordered_replicon sequence base, fill the internal dict with RepliconInfo

Parameters **default_topology** (*string*) – the topology provided by config.replicon_topology

_fill_topology()
Fill the internal dictionary with min and max positions for each replicon_name of the sequence_db

get(*replicon_name*, *default=None*)

Parameters

- **replicon_name** (*string*) – the name of the replicon to get informations
- **default** (*any*) – the value to return if the replicon_name is not in the RepliconDB

Returns the RepliconInfo for replicon_name if replicon_name is in the repliconDB, else default. If default is not given, it is set to None, so that this method never raises a KeyError.

Return type *RepliconInfo* object

items()

Returns a copy of the RepliconDB as a list of (replicon_name, RepliconInfo) pairs

iteritems()

Returns an iterator over the RepliconDB as a list (replicon_name, RepliconInfo) pairs

replicon_infos()

Returns a copy of the RepliconDB as list of replicons info

Return type RepliconInfo instance

replicon_names()

Returns a copy of the RepliconDB as a list of replicon_names

class macsypy.database.**RepliconInfo**(*topology*, *min*, *max*, *genes*)

__getnewargs__()
Return self as a plain tuple. Used by copy and pickle.

static __new__(*_cls*, *topology*, *min*, *max*, *genes*)
Create new instance of RepliconInfo(topology, min, max, genes)

__repr__()
Return a nicely formatted representation string

_asdict()
Return a new OrderedDict which maps field names to their values.

classmethod _make(*iterable*)
Make a new RepliconInfo object from a sequence or iterable

_replace(***kwds*)
Return a new RepliconInfo object replacing specified fields with new values

property genes
Alias for field number 3

property max
Alias for field number 2

property min
Alias for field number 1

property topology
Alias for field number 0

macsypy.database.**fasta_iter**(*fasta_file*)

Parameters **fasta_file** (*file object*) – the file containing all input sequences in fasta format.

Author http://biostar.stackexchange.com/users/36/brentp

Returns for a given fasta file, it returns an iterator which yields tuples (string id, string comment, int sequence length)

Return type iterator

errors

The errors specific to macsyfinder and macsydata

error

exception macsypy.error.**MacsyDataLimitError**
Raised when the maximum number of github api call is reached

exception macsypy.error.**MacsydataError**
Raised when error is encounter during model package handling

exception macsypy.error.**MacsypyError**
The base class for MacSyFinder specific exceptions.

__weakref__
list of weak references to the object (if defined)

exception macsypy.error.**ModelInconsistencyError**
Raised when a definition model is not consistent.

exception macsypy.error.**OptionError**
Raised when command line option is not set properly

exception macsypy.error.**SystemDetectionError**
Raised when the detection of systems from Hits encountered a problem.

utils

Here some useful functions in the rest of macsyfinder code

utils API reference

macsypy.utils.**get_def_to_detect**(*models*, *model_registry*)

Parameters

- **models** (*list of tuple with the following structure: [('model_1', ('def1, def2, ..)), ('model_2', ('def1', ..)), ..]*) – the list of models to detect as returned by config.models.
- **model_registry** (*macsypy.registries.ModelRegistry* object.) – the models registry for this run.

Returns the definitions to parse

Return type list of *macsypy.registries.DefinitionLocation* objects

Raises **ValueError** – if a model name provided in models is not in model_registry.

package

Allow to handles model package either on localhost or from a remote location. the model packages can be stored in github organization to be downloaded and installed locally. The classes below are used by *macsydata*, which is the entry point to manipulate models package.

ModelIndex

class macsypy.package.**AbstractModelIndex**(**args*, ***kwargs*)
This the base class for ModelIndex. This class cannot be implemented, it must be subclassed

__init__(*cache: str = ''*)

static __new__(*cls*, **args*, ***kwargs*)
Create and return a new object. See help(type) for accurate signature.

__weakref__
list of weak references to the object (if defined)

unarchive_package(*path: str*) → str
Unarchive and uncompress a package under <*remote cache*>/<*organization name*>/<*package name*>/<*vers*>/<*package name*>

Parameters **path** (*str*) –

Returns The path to the package

class macsypy.package.**LocalModelIndex**(**args*, ***kwargs*)
It allow to manage installation from a local package (tarball)

__init__(*cache=None*) → None

class macsypy.package.**RemoteModelIndex**(**args*, ***kwargs*)
This class allow to interact with ModelIndex on github

__init__(*org: str = 'macsy-models'*, *cache=None*) → None

Parameters **org** – The name of the organization on github where are stored the models

_url_json(*url: str*) → Dict
Get the url, deserialize the data as json

Parameters **url** (*str*) – the url to download

Returns the json corresponding to the response url

download(*pack_name: str*, *vers: str*, *dest: str = None*) → str
Download a package from a github repos and save it as <remote cache>/<organization name>/<package name>/<vers>.tar.gz

Parameters

- **pack_name** (*str*) – the name of the package to download
- **vers** (*str*) – the version of the package to download
- **dest** (*str*) – The path to the directory where save the package This directory must exists If dest is None, the macsyfinder cache will be used

Returns The package archive path.

get_metadata(*pack_name: str*, *vers: str = 'latest'*) → Dict
Fetch the metadata_path from a remote package

Parameters

- **pack_name** (*str*) – The package name
- **vers** (*str*) – The package version

Returns the metadata_path corresponding to this package/version

Return type dictionary corresponding of the yaml parsing of the metadata_path file.

list_package_vers(*pack_name: str*) → List[str]
List all available versions from github model repos for a given package

Parameters **pack_name** (*str*) – the name of the package

Returns the list of the versions

list_packages() → List[str]
list all model packages available on a model repos :return: The list of package names.

remote_exists() → bool
check if the remote exists and is an organization :return: True if the Remote url point to a github Organization, False otherwise

Package

class macsypy.package.**Package**(*path: str*)
This class Modelize a package of Models a package is a directory with the name of the models family it must contains at least - a subdirectory definitions - a subdirectory profiles - a file metadata.yml it is also recomanded to add a file for licensing and copyright and a README. for further explanation see TODO

__init__(*path: str*) → None

Parameters **path** (*str*) – The of the package root directory

__weakref__
list of weak references to the object (if defined)

_check_metadata() → Tuple[List[str], List[str]]
Check the QA of package metadata_path

Returns errors and warnings

Return type tuple of 2 lists ([str error_1, ..], [str warning_1, ..])

_check_model_consistency() → Tuple[List, List]
check if each xml seems well write, each genes have an associated profile, etc :return:

_check_structure() → Tuple[List[str], List[str]]
Check the QA structure of the package

Returns errors and warnings

Return type tuple of 2 lists ([str error_1, ..], [str warning_1, ..])

_find_readme() → Optional[str]
find the README file

Returns The path to the README file or None if there is no file.

_load_metadata() → Dict
Open the metadata_path file and de-serialize it's content :return:

check() → Tuple[List[str], List[str]]
Check the QA of this package

help() → str
return the content of the README file

info() → str

Returns some information about the package

property metadata

Returns The parsed metadata as a dict

CHAPTER

THREE

INDICES AND TABLES

- genindex
- modindex
- search

PYTHON MODULE INDEX

m

INDEX

Symbols

A

B

C

D

E

F

G

H

I

J

L

M

N

O

P

R

S

T

U

V

W