MacSyFinder v2: Improved modelling and search engine to identify molecular systems in genomes

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ABSTRACT

Complex cellular functions are usually encoded by a set of genes in one or a few organized genetic loci in microbial genomes. MacSyFinder uses these properties to model and then annotate cellular functions in microbial genomes. This is done by integrating the identification of each individual gene at the level of the molecular system. We hereby present a major release of MacSyFinder (Macromolecular System Finder), MacSyFinder version 2 (v2). This new version is coded in Python 3 (>= 3.7). The code was improved and rationalized to facilitate future maintainability. Several new features were added to allow more flexible modelling of the systems. We introduce a more intuitive and comprehensive search engine to identify all the best candidate systems and sub-optimal ones that respect the models' constraints. We also introduce the novel *macsydata* companion tool that enables the easy installation and broad distribution of the models developed for MacSyFinder (macsy-models) from GitHub repositories. Finally, we have updated, improved, and made available MacSyFinder popular models for this novel version: TXSScan to identify protein secretion systems, TFFscan to identify type IV filaments, CONJscan to identify conjugative systems, and CasFinder to identify CRISPR associated proteins.

INTRODUCTION

Microbial nanomachines and pathways (hereafter called “systems”) can be very complex and involve many proteins (hereafter called “components”). In the genomes of Bacteria and Archaea, the components of these systems are often encoded in a highly organized way, involving one or a few operons with functionally related genes. For example, loci encoding the peptides of a protein complex or the enzymes of a metabolic pathway have specific genetic organizations that tend to be remarkably conserved (Dandekar et al., 1998; Teichmann and Babu, 2002). Neighbouring operons in genomes are also often functionally related (Huynen et al., 2000). This means that gene co-localization can be used to infer gene functions and improve homology inference, *e.g.,* when sequence similarity is low. Co-localization also facilitates the distinction between functionally diverging homologs (Abby and Rocha, 2012). The hypothesis is that the member of the protein family that co-localizes with the rest of the system's genes is the one performing the function of interest. Conversely, many cellular processes require an ensemble of coherent components. In such cases, a function can only be identified when the repertoire of genes is analyzed at the system-level. For example, a minimum set of components is necessary for the functioning of a protein secretion system.

In 2014, we published the “Macromolecular System Finder” (MacSyFinder v1) program for the functional annotation of cellular machineries and metabolic pathways in microbial genomes (Abby et al., 2014). It makes a system-level annotation that takes advantage of the typical functional organization of microbial genomes (co-localization) and the requirement of a core set of protein components to perform the function (quorum). MacSyFinder consists of a generic modelling framework and a search engine to screen genomes for candidate systems. The modelling framework enables the user to define models for the systems of interest, including the components' identity, category, and genetic organization. MacSyFinder v1 has three categories of components: mandatory, accessory, and forbidden. Parameters of gene co-localization describe the genomic architecture of the system at the level of each component or of the entire system. Each component corresponds to one HMM (hidden Markov model) profile to enable sequence similarity search with HMMER (Eddy, 2011) and different components (and thus profiles) can be defined as exchangeable if they have the same role in the system. The search engine screens a database of genomes for potential systems using HMM profile searches and the clustering of co-localized hits along the genome that match the systems’ model.

MacSyFinder has been used with success to annotate a variety of microbial machineries and pathways, including protein secretion systems (Abby et al., 2016), CRISPR-Cas systems (Abby et al., 2014; Couvin et al., 2018) and other prokaryotic defence systems (Tesson et al., 2022), capsular loci (Rendueles et al., 2017), DNA conjugation systems (Cury et al., 2020), the butyrate production pathway (Sharp and Foster, 2022), methanogenic and methylotrophic metabolisms (Adam et al., 2019; Chibani et al., 2022) , cell division machineries (Pende et al., 2021) and outer membrane protein clusters (Taib et al., 2020). It has enabled wide-scale genomic analyses of biologically relevant systems and was integrated into the popular MicroScope genome annotation pipeline and in the reference CRISPRCasFinder program (Couvin et al., 2018; Vallenet et al., 2020). Yet it has several limitations. In

terms of software engineering, it is coded in the now obsolete Python v2.7, lacks tools to improve its future development and maintenance, and some parts of the program are not efficient. In terms of modelling, it cannot use component-specific filtering criteria to annotate the genes. Furthermore, it lacks a way to annotate genes of interest that are neutral concerning the systems' assessment. More importantly, the greedy search engine is not optimal and has complex, sometimes counter-intuitive behaviours.

We hereby present a major release of MacSyFinder, MacSyFinder version 2 (v2) coded in Python 3 (>= 3.7). In addition, we have updated and improved the most popular MacSyFinder models to the novel version to make them readily usable.

MATERIALS AND METHODS

- **Input & Output files**

MacSyFinder v2, like v1, gets as input files the models of the systems to search and a multi-protein fasta file (Figure 1). When the proteins are ordered in the file as in the replicon, one can use the most powerful search mode – "ordered_replicon" – to study the genetic organization. Otherwise, the search mode "unordered" must be used. The significant modifications in v2 concern the organization of the input systems' models ("macsy-model" packages, see below) and the output files. The latter were adapted to reflect the new MacSyFinder search engine results. In addition, various easy-to-parse text tabulated files are now proposed, including the raw and filtered results of the components' similarity search with HMMER, the component-wise description of the possible systems, the systems constituting the best solutions, and the component-wise description of rejected candidates. For more details, one can consult MacSyFinder's comprehensive documentation, including the User Guide, the Modeller Guide, and the Developer Guide, created with Sphinx and available at: https://macsyfinder.readthedocs.io/.

- **Formalizing macsy-model packages**

MacSyFinder v1 required two directories containing one or several systems' models ("definitions" folder) and the corresponding HMM profiles ("profiles" folder). These files were passed to the command line as mandatory parameters and were distributed as standalone archives. Unfortunately, these have the inconvenience of being poorly versionable or traceable. To improve the reproducibility of analyses with MacSyFinder v2, we increased the traceability of the models and facilitated their retrieval and installation by formalizing a package structure that we call "macsy-model" package (see Fig. S1).
A macsy-model package must have two directories: "definitions" and "profiles". The "definitions" directory contains all model definitions written in the MacSyFinder-specific XML grammar (one file per model definition). This directory can include several sub-directories and levels (Fig. S1). The "profiles" directory contains all HMM protein profiles appearing in the definitions. In addition, a new file, "*metadata.yml"*, was introduced to store necessary metadata such as the package name, version, description, citation, distribution license, and the contacts of its author(s)/maintainer(s). Some facultative but recommended files can be added: LICENSE/copying, Contributing, README.md, and model_conf.xml. The README file should explain how to use the models and can be displayed using the command *macsydata help* (see below). The file *model_conf.xml* allows the modeller to set package-specific configurations such as score configuration options (see paragraph on scoring) or criteria to filter the hits when searching the components (profile coverage threshold, usage of GA scores with HMMER…). The user can easily supersede these recommended values using the command line and configuration files.

- **Grammar update for the modelling framework**

The models of MacSyFinder are written using a dedicated XML grammar with a

hierarchy that fits the hierarchical nature of the biological systems to model: systems' models are made of gene components (Fig. 3, Supplementary Table 1). The two main objects in the hierarchy of a system's model are thus the "model" (replacing the "system" keyword in v1) at the top level and the "gene" at the lower level. In addition, a feature "vers" was added at the model level to indicate the version of the grammar: "vers=2.0" matches MacSyFinder v2.

We simplified the XML grammar to ensure better readability and easier maintenance of the models (Fig. 3, Supplementary Table 1). Relative to the first version, some keywords were removed or merged into novel ones. This is the case of the keywords "homologs" and "analogs" that were replaced by the new keyword "exchangeables" to indicate that some components can be "exchanged" by others (*i.e.,* fill the same role in systems). The gene attribute "exchangeable" was thus removed as not needed anymore. The "system_ref" keyword was also removed.

When designing a system's model or investigating the distribution of genes within genomic occurrences of a system, one may want to annotate genes that are not important to the identification/discrimination of the system. We introduced a new type of component called "neutral". It adds to the pre-existing mandatory, accessory, and forbidden components, except that this new type is not used to score the systems or assess their quorum (minimal number of components required in a system). Neutral components are identified using HMM protein profiles and placed into clusters like the other components. Hence, even if they do not contribute to the scoring of systems, they can "connect" or "extend" clusters of mandatory and accessory components. Details, examples, and a tutorial concerning the XML grammar v2 are available in MacSyFinder's documentation, which now includes a novel section called the "Modeller Guide" to explain how to build novel models of systems. We also provide some of the most popular models translated with improvements for MacSyFinder v2 (Table 1). They are readily usable and installable through the *macsydata* program (see Results section).

- **<u>Enabling component-wise filtering by setting up GA scores</u>**

The search for components can now use the "GA" (Gathering) scores of the HMM profiles. This allows using component-wise criteria for hit filtering instead of having the same criteria for all components (as in v1 of MacSyFinder). If a GA score is present in the HMM profile file, the system calls HMMER using the option "--cut_ga", which supersedes the i-evalue and profile coverage default values otherwise used in the absence of GA scores. It is possible to deactivate the GA scores using the new option "--no-cut-ga" (False by default). The rules for the filtering of the components can be specified (by decreasing order of priority): in the command line, in the model configuration file of the system ("model_conf.xml"), or using the HMM protein profile GA scores (or the "i-evalue" and "profile coverage" if GA scores not provided).

Many of the HMM protein profiles used in MacSyFinder models are from PFAM or TIGRFam (Sonnhammer et al., 1997; Haft et al., 2003) and already include GA thresholds. To enable users to efficiently use the profiles previously developed for MacSyFinder v1 models, we computed the GA scores for CasFinder, TXSScan, CONJScan, and TFFscan profiles (see Table 1). To this end, we annotated with the corresponding models the completely assembled genomes of 21105 bacterial and

archaeal strains retrieved from the non-redundant NCBI RefSeq database (as of March, 2021). We analysed the distribution of the scores for the hits for the different genes found in the detected systems, and attributed as GA score the minimal score observed to the corresponding profile.

In total, 1000 HMM profiles from the four packages are available with GA scores. They thus now offer the possibility for component-wise filtering with HMMER, ensuring optimal usage of the 104 macsy-models hereby updated for this new version of MacSyFinder.

- **Sharing and handling macsy-models with the *macsydata* command and the "MacSy Models" organization**

The novel tool "*macsydata*" was created to make macsy-model packages easily traceable, versionable, shareable, and automatically installable. It was designed to be as light as possible for the modellers and was inspired by the packaging workflows found in some Linux distributions such as Gentoo (https://www.gentoo.org). In addition, the *macsydata* API was inspired by *pip,* which is familiar to most Python users. *macsydata* implements common sub-commands such as *search, install*, *upgrade*, *uninstall*, and *help* (see Table 2*)*. We also implemented some specific useful sub-commands for MacSyFinder, such as *cite* to display how to cite the macsy-model package and *definition* to show a set of models' definitions in XML format.

The "MacSy Models" Github organization was designed to serve as an umbrella organization to host any macsy-model package. It allows the modeller to distribute their packages to all MacSyFinder v2 users efficiently. First, the modeller creates a *git* repository. Then, the quality of the package (package structure, model definitions syntax, the coherence between definitions and profiles) can be checked using the *macsydata check* command on the directory containing the entire file architecture of a macsy-model package (Fig. S1). Finally, when everything is up to standards, the modeller has just to tag the repository and push it under the Github organization "MacSy Models". This action allows the model package to be visible from the *macsydata search* tool and thus findable and accessible for remote installation to all MacSyFinder users. *macsydata* uses the Github Rest API to search and download the packages. Of note, *macsydata* can also install macsy-model packages from a tarball archive, given it respects the above-described file architecture.

- **The macsyprofile companion tool**

The novel tool "*macsyprofile*" of the MacSyFinder suite allows filtering and extracting HMMER hits with settings different from those used during the run. This allows retrieving relevant hits not initially included in predicted systems, e.g., to understand why they were "missed". This could be particularly useful to assist the design of the profiles and the systems' models or to search for atypical versions of the systems (see details in the online documentation).

- **Code implementation, dependencies, and availability**

The code was carried under Python 3 (>=3.7). Many unit and functional tests were implemented to reach a coverage of the code of 97%. The program requires the HMMER suite (>=3.1b2) for the search of components and several well-established

and stable Python libraries to facilitate models' packaging (*pyyaml*, *packaging*), deal with output files (*colorlog*, *pandas*), and search for the best solution (*NetworkX*, see below).
The code and macsy-model packages are available on Github under the GPL v3 license: https://github.com/gem-pasteur/macsyfinder and https://github.com/macsy-models. In addition, a pypi package, a conda package and a Docker container were created to enable the easy deployment of the MacSyFinder suite.

THE MACSYFINDER V2 SEARCH ENGINE

An overview of the new search engine is provided in Figure 1. The first steps of MacSyFinder v2 search engine remain mostly unchanged relative to v1. First, it uses HMMER to search for occurrences of the non-redundant components listed in the models in the input genome(s). The best hits are assigned to the corresponding components, and are filtered by profile coverage (>50% by default) and i-evalue (<0.001 by default) when no GA score is available for the profiles.

- **System-wise creation of candidate systems**

In version 2, the systems are searched one by one: the identified components have their hits filtered by type of system, and clusters of components are built from components respecting the co-localization criteria ("inter-gene-max-space" parameter) (Fig. 1). Candidate systems are built using the clusters of components and the components authorized to be outside of clusters ("loner" components). For "single-locus" systems, combinations of individual clusters with loner components not yet represented in the cluster are examined as candidate systems. For systems allowed to be encoded by multiple loci, all possible combinations of identified clusters and loner components (not found in clusters) are assessed as candidate systems. The eligible systems are the candidate systems that respect the systems' model in terms of the minimal quorum criteria for all components and the mandatory ones. The other systems are rejected for now and kept aside. In the case where "multi-system" genes are part of the systems' model, the list of the corresponding components will be collected from the eligible systems and combinatorically added to the set of rejected candidates to be assessed for the formation of new eligible systems.

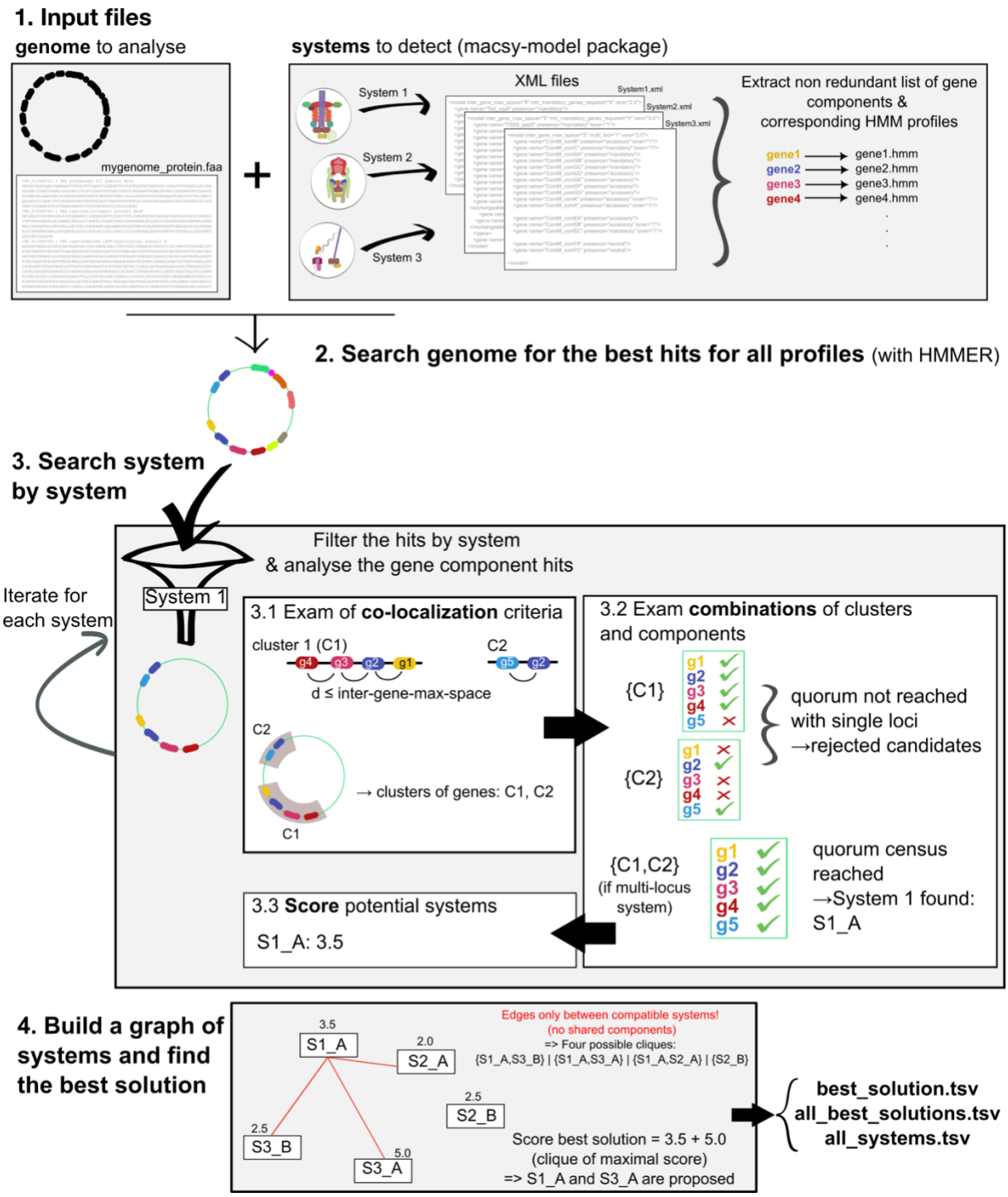


Figure 1. Overview of the major steps of MacSyFinder v2.
(1) The user gives as input the genome(s) to analyse under the form of a multi-protein fasta file (order respecting that of the genes on genome if possible) and a macsy-model package with the systems to detect. Then the search engine establishes the non-redundant list of corresponding components. (2) The components are then searched with HMMER (hmmsearch using GA scores when available). The proteins with the best hits are filtered by i-evalue and profile coverage (if no GA score was available). (3) A system-by-system search is then performed. The hits corresponding to a first system are selected ("g1" as hit for gene 1), and clusters of components are formed by

gathering the hits respecting the maximal inter-gene-max-space (3.1). Components allowed to be “out-of-clusters” are also collected (loners and multi-systems). Then the possible combinations of clusters and “out-of-clusters” components are computed, and the program tests if they respect the quorum for the system (3.2). Finally, all candidate systems are scored (3.3). Step (3) is re-iterated for each system to be detected. Once all systems are examined, the best solution is searched using a graph-based approach. Step (4) A graph connecting all compatible candidate systems (i.e., systems with no shared components) is built, each node having the score of the corresponding system. The best solution is defined as the set of compatible systems obtaining the highest cumulative score. This corresponds to the clique of maximal score. Diverse output files are provided to the user, including one with the composition of (one of) the best solution, a file with all equivalent best solutions (if several reach the highest score), and one with all eligible candidate systems whether they are part of the best solution or not. Drawings of systems at Step (1) are derived from (Denise et al., 2019).

- **<u>Introducing a scoring scheme for candidate systems</u>**

Candidate systems that respect the quorum and co-localization conditions imposed by a system’s model are designated as eligible systems and are assigned a score (Fig. 2A). The core of the system score is the sum of three terms: the sum of the scores of the *n* Clusters, the sum of the scores of the *o* out-of-cluster components (loner or multi-system, see below), plus a penalty P_{system} for the redundancy within the system.

$$S_{System} = \sum_{i=0}^{n} S_{Cluster\ i} + \sum_{i=0}^{o} S_{out-of-clust\ i} + P_{System}$$

Multiple occurrences of a component within the same cluster are counted as a single occurrence of the component. The score of each cluster is a function of the number of mandatory (*m)* and accessory components (*a*), and of the number of exchangeable mandatory (*xm*) and exchangeable accessory (*xa*) components it contains. These values are weighted to give more importance to mandatory components: $w_{mandatory} = 1$, $w_{accessory} = 0.5$, and $w_{neutral} = 0$ (Fig. 2A). Moreover, to give more value to the originally listed gene than to the listed “exchangeables”, a factor $f_{exchang} = 0.8$ is applied to the scores when an exchangeable gene fulfils the function. The score $S_{Cluster}$ is then given by:

$$S_{Cluster} = m \times w_{mandatory} + f_{exchang}.xm \times w_{mandatory} + a \times w_{accessory} + f_{exchang}.xa \times w_{accessory}$$

The score of the genes found outside of a system’s cluster is computed like the score of the components found in clusters *“s_c”* (see above), except that a factor $f_{out\text{-}of\text{-}clust}$ = 0.7 is applied. Here, s_c can represent any of the component-specific parts of the $S_{Cluster}$ sum presented above, depending on the mandatory, accessory, and/or exchangeable status of the out-of-cluster component:

$$S_{out-of-clust} = f_{out-of-clust}.s_c$$

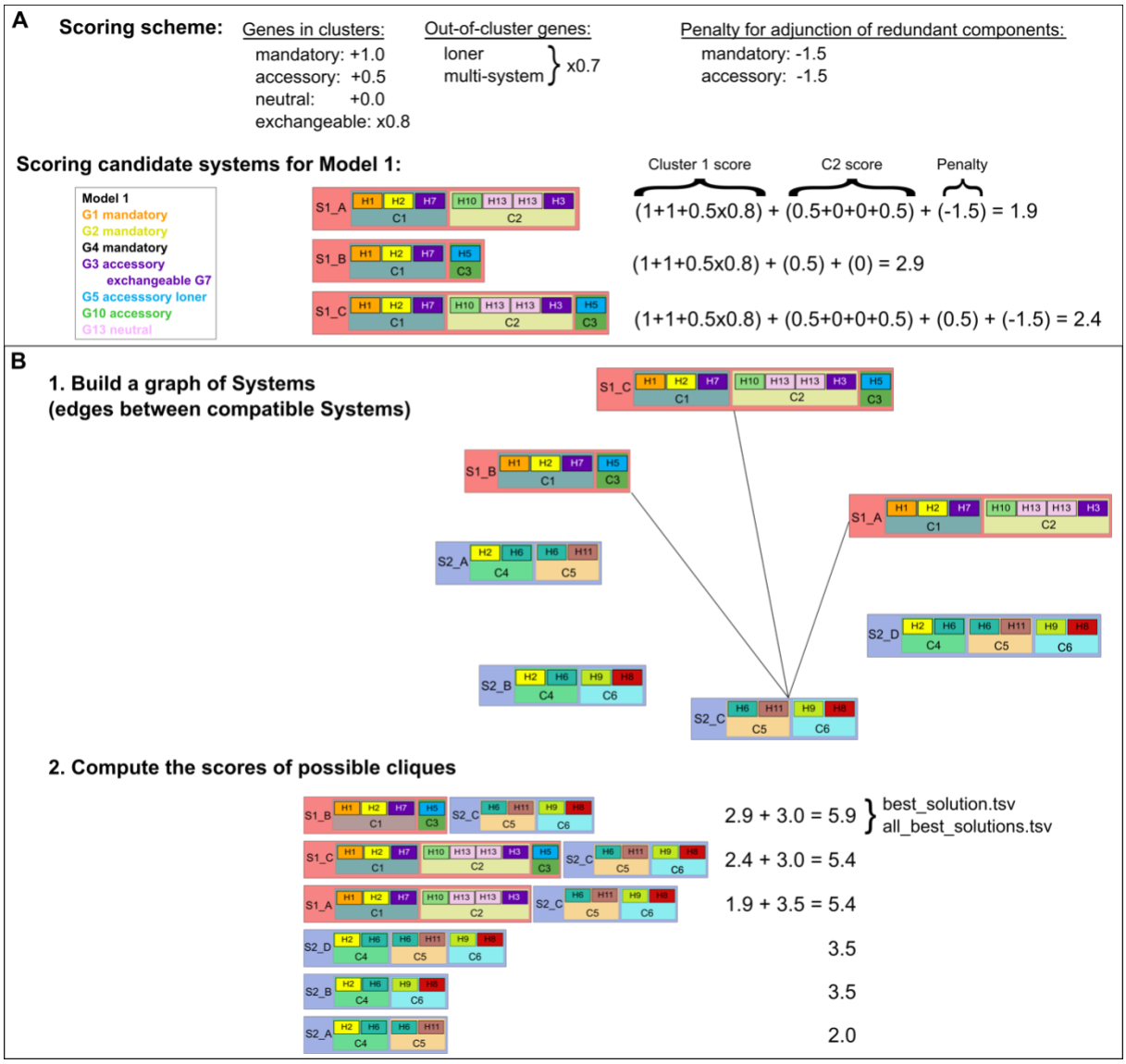
A component is deemed redundant only if found in more than one cluster. The penalty part of a score thus penalizes candidate systems with *r* redundant mandatory or accessory components, where *r* thus corresponds to the number of clusters with the component minus one. We define P_{System} ($p_{redundant}$ = -1.5 by default):

$$P_{System} = \sum_{i=0}^{r} p_{redundant}$$

The default values of the different score parts are indicative and allow MacSyFinder to behave as expected in the cases we have tested. The users can fully parameterize the weights, factors, and penalties. The modeller of a system can also ship, with a macsy-model package, its recommended values for the weights of the scoring system using the optional "*model_conf.xml*" file.

- **<u>Combinatorial exploration of solutions</u>**

Once all models were searched and their occurrences were assigned scores (see above), a combinatorial examination of the possible sets of compatible systems is performed (Fig. 1 and 2B). Two systems are deemed compatible if they are made of distinct gene components. Thus, unless specified using the "multi_system" or "multi_model" features, a component cannot be involved in several systems. A MacSyFinder search solution is defined as a set of compatible systems. The search for the best solution corresponds to the well-known weighted maximum clique search problem (Brandes and Erlebach, 2005). The program builds a graph connecting all pairs of compatible systems, each node representing a system whose weight corresponds to its score. The goal is to identify a set of systems that are all compatible with each other, meaning that they are all inter-connected in a sub-graph. This is the definition of a "clique". The best solution is the clique harboring the highest cumulated systems' score, the score of a solution being the sum of the systems' scores composing it. The "find_cliques" function proposed in the NetworkX Python library is used to find the set of maximal cliques that correspond to the best possible solutions in terms of cumulated nodes' weights of the cliques (Hagberg et al., 2008). This may result in several solutions with the maximal score, in which case they are all provided to the user (file "all_best_solutions.tsv"). The best solution, or one among the best, is given in the dedicated output file "best_solution.tsv".



<u>Figure 2.</u> Scoring scheme and combinatorial search of MacSyFinder v2 search engine. A. The scoring scheme is summarized, and then illustrated by an example for a hypothetical Model1. “H1” stands for a hit for gene 1 “G1” in the genome. **B**. Step (1). The graph of candidate systems is drawn by connecting all compatible systems, i.e. those with non-overlapping hits (unless authorized by the multi-model or multi-system feature). Step (2). The clique of maximal cumulated score (best solution) is searched, with the score being defined as the sum of the systems’ scores that are part of the clique. The results are stored in the files “best_solution.tsv” and “all_best_solutions.tsv”, and all candidate systems are stored in “all_systems.tsv”.

RESULTS & DISCUSSION

I/ Grammar changes and macsy-model file architecture enable better, simpler, and more intuitive systems' modelling and sharing

Version 1 of MacSyFinder lacked a dedicated file architecture to share MacSyFinder's systems' models. We now define a structured file architecture for the novel "macsy-model packages" (see Materials and Methods and Fig. S1). In particular, there now may be several levels of sub-directories for the "definitions" folder. This enables running *macsyfinder* with only a pre-defined subset of models and establishing a hierarchy of models in a biologically relevant manner. The introduction of this file architecture thus satisfies two main objectives: it allows the file architecture of the macsy-model packages to reflect the biological specificities of the systems while enabling automated handling of the macsy-model packages for easier distribution and installation via the *macsydata* tool. Several popular MacSyFinder models from v1 were carried under MacSyFinder v2 grammar and file architecture. They are now available at the "MacSy Models" Github organization for automated installation with MacSyFinder v2 using the *macsydata* tool (discussed in detail below, see also Materials and Methods, Table 1 and Table 2). The creation of the "MacSy Models" organization enables the macsy-model packages to be versioned for better reproducibility. This organization also constitutes the first step towards unifying a MacSyFinder modeller community.

Table 1. Overview of MacSyFinder v2 macsy-model packages available at the "MacSy models" organization https://github.com/macsy-models

Model repository	Version tag	Original reference	Systems detected	Nb models	Nb profiles	Remark
CasFinder	3.1.0	(Abby et al., 2014; Couvin et al., 2018)	CRISPR-Cas systems (Cas clusters detection, annotation, and classification)	44	535	This new version: - provides the possibility to detect more subtypes than the previous ones - greatly improves the detection of tandem systems - improves the detection of degenerated and atypical systems - can now be ran at once for the three levels of classification - GA scores added to HMM profiles
CONJscan	2.0.1	(Cury et al., 2017)	Conjugative, mobilizable and decayed conjugative systems	34	124	This new version: - allows the detection of decayed conjugative systems - provides models adapted to the detection in chromosomes or plasmids - contains tailored thresholds for each type of MPF - GA scores added to HMM profiles
TFFscan	1.0.0	(Denise et al.,	Systems members	7	169	As in the original paper, but

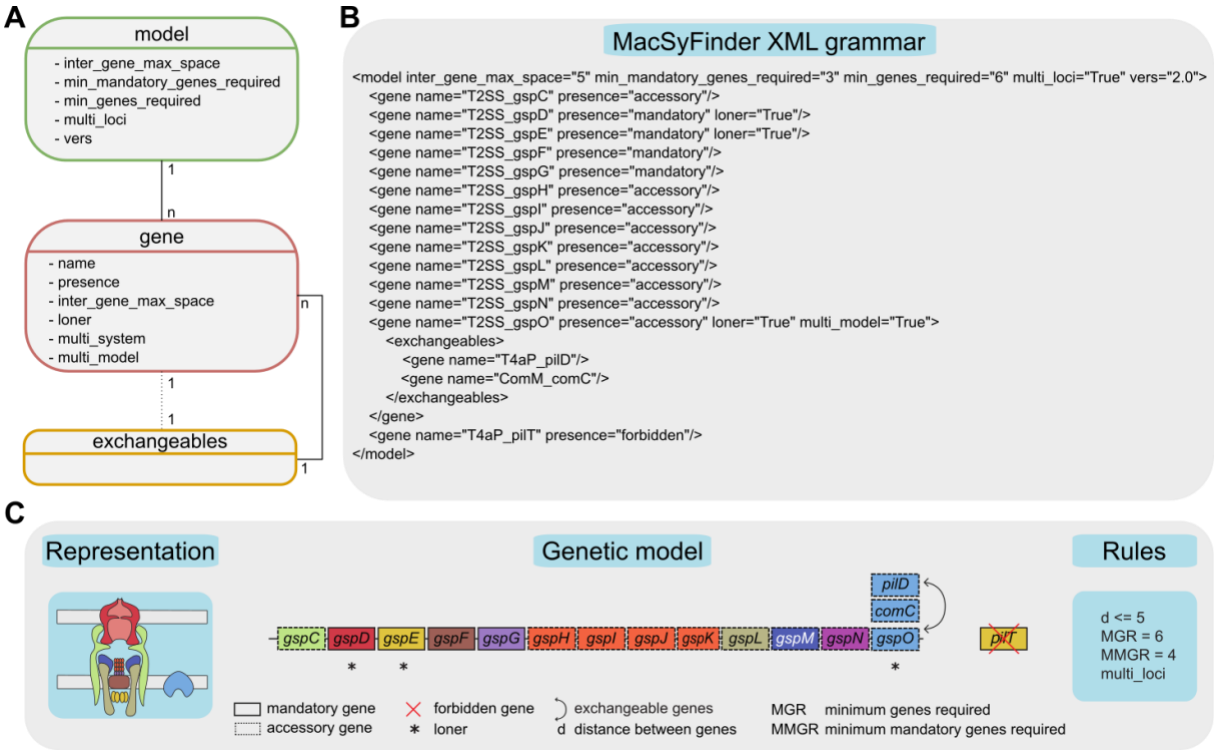
		2019)	of the type IV filament super-family			with GA scores added to HMM profiles
TXSScan	1.0.0	(Abby et al., 2016)	Protein secretion systems and related appendages	22	205	As in the original paper, but with GA scores added to HMM profiles
TXSScan	1.1.0	(Abby et al., 2016; Denise et al., 2019)	Protein secretion systems and related appendages, including members of the type IV filament super-family	26	341	Merger of TFF-SF v1.0 and TXSScan v1.0: - TFF-SF models from Denise et al. replace older model versions from TXSScan version 1.0 (Abby et al.) for the T2SS, Tad and T4aP systems. Models added: ComM, T4bP and Archaeal_T4P. - Hierarchy of models by domain of life, and then by membrane type to allow to search only the relevant models.

Table 2. The *macsydata* companion tool to handle macsy-model packages

macsydata **command**	**Description**	**Examples**
available	List all macsy-model packages available at the default or specified organization	*macsydata available*
list	List installed packages	*macsydata list*
check	Allows to check the sanity and consistency of a macsy-model package before diffusion	*macsydata check*
install / uninstall	Automatically retrieve and install (uninstall) the designated package	*macsydata install* TFF-SF
cite	Displays the citation information stored in the metadata.yml file of the package	*macsydata cite* TFF-SF
definition	Displays the definition(s) (XML file) of the specified model(s). It can be a directory containing several models to display.	*macsydata definition* TXSS T1SS *macsydata definition* TXSS/archaeal *macsydata definition* –models-dir my-models System1
search	Search for the models based on their names, or based on string searches in the models' description	*macsydata search* TXSS *macsydata search* -s Secretion
macsydata <subcommand> --help	List the help message for the specified sub-command	*macsydata search* --help

To illustrate the interest of the novel file architecture, we carried under the v2 grammar and assembled into a new version of "TXSScan" (v1.1.0) the models for the type IV filament super-family ("TFF-SF") and for the protein secretion systems (former "TXSScan", v1.0.0) that we had previously developed for MacSyFinder v1 (Abby et al., 2016; Denise et al., 2019). These systems represent a coherent set of bacterial appendages dedicated to motility and secretion that share evolutionary relations (see

(Denise et al., 2020) for a review). We organized the models into sub-directories with respect to relevant biological criteria (Fig. S1). The models' sub-directories were split by domains of life (archaea versus bacteria) and then by membrane type (monoderm bacteria versus diderm bacteria). This new architecture enables the search for all models at once, or only the domain-specific ones or those specific to a given bacterial membrane type. This allows more targeted and less costly searches for biological systems. Of note, the XML grammar simplifications introduced in v2 enabled the production of much more compact, readable, and simple models (Fig. 3). For example, the definition of the type III secretion system (T3SS) now consists of 20 lines for 15 listed components, whereas the v1 version counted 52 lines. v2 versions of the popular TXSScan and TFF-SF models are also available as originally published (Abby et al., 2016; Denise et al., 2019) (v1.0.0 versions of TXSScan and TFFscan respectively, Table 1). Yet the new search engine has a different behaviour than v1; it will produce different results in some cases (see below and Fig. 4).



<u>Figure 3.</u> Description of the hierarchical grammar used in MacSyFinder models and example of the T2SS model.

A. The “model” is the root element of the XML document according to the grammar. It represents the system to model and contains at least one element “gene”. The “gene” element describes the components constituting a system. It may contain one element “exchangeables”. The dashed line between “gene” and “exchangeables” illustrate the fact that a gene does not necessary contain an “exchangeables” element. The “exchangeables” element contains a set of genes (one at least) that can replace functionally the parent “gene” in the system quorum. The one-to-many relationships between the different elements is represented by lines connecting the boxes, with the cardinality of the relationship appearing next to the element. The diverse possible features of each element are represented in the corresponding boxes. **B.** XML

grammar of the T2SS from TXSScan v1.1.0 (and TFFscan v1.0.0) (Abby et al., 2016; Denise et al., 2019). **C.** A schematic representation of the T2SS machinery spanning the membranes of a diderm bacterium is displayed on the left. The genetic model corresponding to the T2SS model in panel B is illustrated in the central part, with gene boxes filled with the colour of the corresponding proteins on the T2SS schema. The quorum and co-localization rules to fulfil the T2SS model are described on the right. Gene components' names were abbreviated in the genetic model compared to the names in the XML model. The C panel was derived from (Denise et al., 2019).

II/ A new system modelling and search engine for a more relevant exploration of possible systems

MacSyFinder v1 had a greedy search engine with sub-optimal and sometimes unexpected behaviours, especially in complex cases such as co-localized systems or those with multiple occurrences in a genome. The novel v2 search engine explores the space of possible solutions more thoroughly. It provides optimal solutions with an explicit scoring system favouring complete but concise systems (Fig. 1). A fundamental improvement is that the systems are now searched one by one: the identified components are filtered by type of system and assembled in clusters if relevant (Fig. 1). The new search engine can thus resolve more complex case scenarios than the previous one (see below and Fig. 4). Using a system-by-system approach also prevents the spurious elimination of relevant candidate systems, e.g., when a component from another system is within a cluster of the candidate system. This was a cause for the elimination of certain valid systems in v1 (see below and Fig. 4).

The combinatorial exam of sets of components and clusters to build up candidate systems (see Materials and Methods) allows to deal with more complex cases, e.g. the occurrence of multiple scattered systems (see below and Fig. 4 for an example). However, the combinatorial exploration may be computationally costly, especially when there are many occurrences of clusters and components. This cost is partly relieved by filtering the components using the GA scores (or other criteria), because this effectively removes many false positives and leaves fewer components and clusters to consider. Yet when testing the new search engine, we were sometimes confronted to cases of genomes with dozens of hits for "out-of-cluster" components (loner or multi_system components). The analysis of all combinations of such components can be extremely costly. To make these cases manageable, MacSyFinder v2 uses a heuristic that considers several occurrences of the same "out-of-cluster" component as a single component when forming combinations of potential systems. This "representative" is selected as the best matching component (best HMMER score). The other "out-of-cluster" components detected are kept and listed separately in dedicated files (best_solution_loners.tsv and best_solution_multisystems.tsv). This makes the combinatorial exploration of solutions manageable in most if not all the cases. If this is not the case, we advise the users to revise their system's modelling strategy and/or HMM profiles specificity (e.g., increase the GA score thresholds). Finally, the graph-based search for the best solution (see Materials and Methods and Fig. 2B) also provides sub-optimal solutions that may be of interest to the user in some situations (system variants discovery, detection of degraded systems, etc.).

We illustrate and discuss in the following sections the advantage of MacSyFinder v2

over v1 for the search of molecular systems. For this, we present its application to three types of systems: the CRISPR-Cas system (CasFinder package), the conjugative systems (CONJscan package), and the type IV filament super-family (TFFscan and TXSScan packages).

III/ Application of MacSyFinder v2 to CasFinder

CRISPR-Cas systems are adaptive immune systems that protect bacteria and archaea from invasive agents (phages, plasmids…) (Hampton et al., 2020). A typical CRISPR-Cas system consists of a CRISPR array and adjacent cluster of *cas* (CRISPR associated) genes that form one or more operons of 1 to 13 genes (Fig. 4A) (Makarova et al., 2020). As CRISPR arrays do not code for proteins, this part of the system is not identified by MacSyFinder. The *cas* genes clusters are very diverse and are currently classified into two classes, six types (I-VI) and more than 30 subtypes based on their composition in *cas* genes (Makarova et al., 2020). We have previously developed a package of models called CasFinder dedicated to the detection of CRISPR-Cas systems using MacSyFinder v1 (Abby et al., 2014; Couvin et al., 2018). We hereby propose an updated and improved version of CasFinder that benefits from the new features of MacSyFinder v2.

The graph-based approach improves tandem systems detection

CRISPR-Cas systems can be subdivided into three distinct, though partially overlapping, functional modules. Some of these, e.g., the adaptation module mainly composed of Cas1, Cas2, and Cas4 proteins, may be very similar between subtypes or even types, making the detection of tandem systems particularly challenging. With the v2 new search engine, all systems are searched one by one. The best possible combination of systems is retrieved using a graph-based approach, which significantly improves the identification of tandem systems. This improvement is even more important when the number of tandem systems exceeds two, as MacSyFinder v1 could not handle these rare complex situations at the subtype level (Fig. 4B).

The “Multi_model” component feature enables tandem, overlapping systems detection

Most CRISPR-Cas systems have an adaptation module when they are alone. But, when they are in tandem, it is not uncommon to find that only one module is present for both systems (Bernheim et al., 2019). This complicates its detection, especially when it is located between tandem systems. In v1, the adaptation module was assigned to one of the two systems at the risk of missing the second one if the latter turned out to be too small (i.e., with a minimum number of required genes lower than the defined threshold). In v2, thanks to the new “multi_model” gene feature, it is possible to allow a component to be present in different models. Thus, by defining the proteins involved in the adaptation module as “multi_model”, they are assigned to the two overlapping systems (Fig. 4C).

The new search engine and scoring system allow searching for different levels of classification simultaneously

Some Cas subtypes are extremely similar in terms of gene content and require very precise decision rules to distinguish them. However, the more precise these rules are, the higher the risk is of missing systems. To overcome this difficulty, we have previously

defined different sets of models providing detection at three levels of classification, from the most permissive to the most specific one: (1) a general model (called CAS_cluster) allowing the identification of any cluster of *cas* genes, (2) a set of models for detection at the type level, (3) and finally a set of models for detection at the subtype level. MacSyFinder v1 analyzed the models one by one in a pre-defined order and selected the first model whose rules were satisfied. Using all three sets of models simultaneously meant that not all possibilities were explored. Thanks to the new v2 search engine and scoring system, all models can now be analyzed at once. Therefore, it is possible that the same cluster is detected at several classification levels (Fig. 4A). The choice of the best solution presented to the user among these different assignments is based on the score of each candidate, then on their wholeness (proportion of genes found over the number of listed ones, or over “max_nb_genes” if defined in the model). Here, the subtype level models have been defined with a “max_nb_genes” parameter lower than for the models higher in the classification. Thus, for a given system that will obtain the same score from several classification levels, the most specific one will obtain the higher system’s wholeness, ensuring the most specific annotation is proposed as the best solution. We thus favoured annotation at the subtype level as being by far the most informative. Still, when the subtype-level search fails, the program allows the detection of atypical or degenerated clusters via the models at the other levels (type-level or general case).

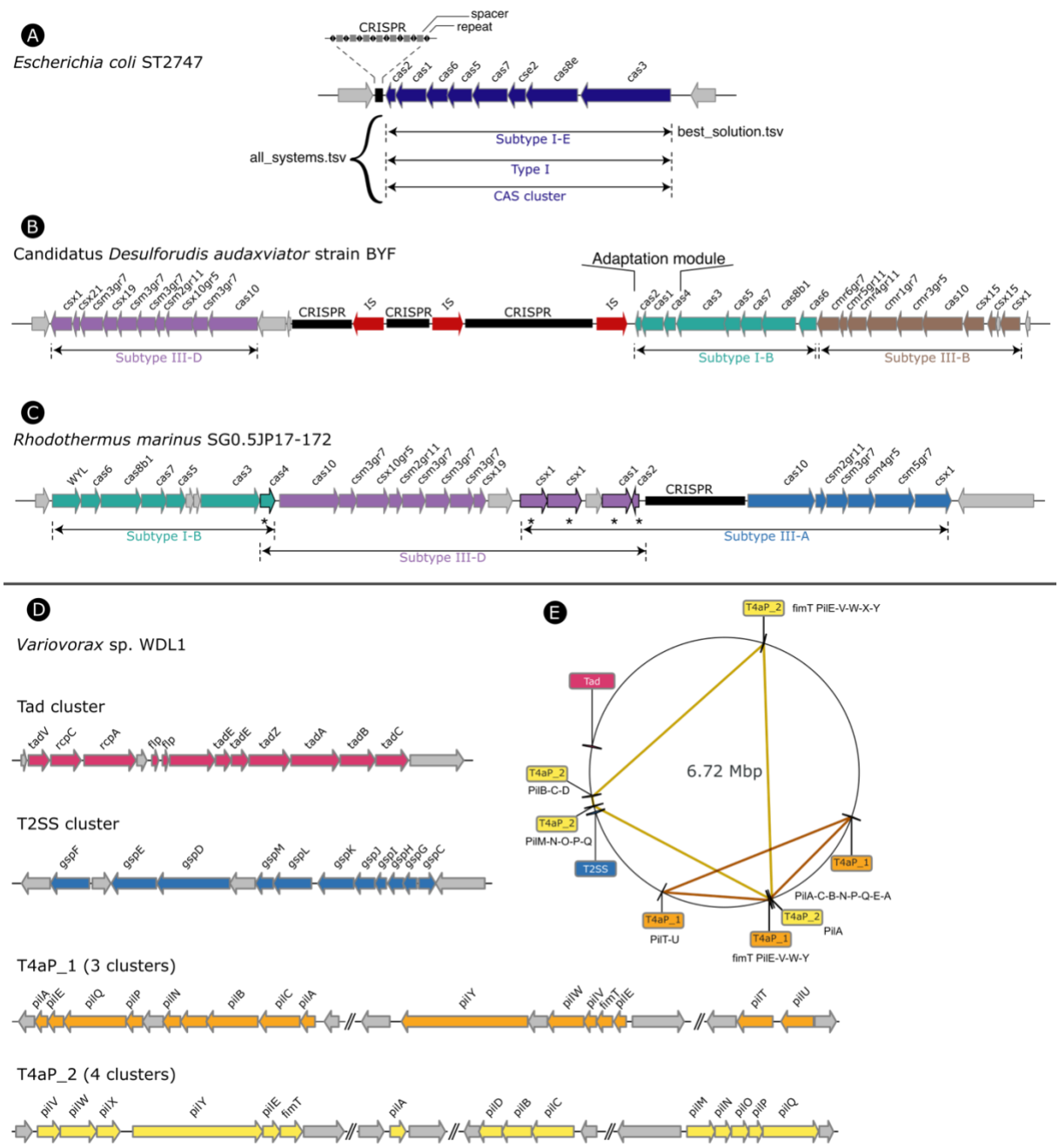


Figure 4. Application of MacSyFinder v2 to CasFinder (v3.1.0) and TFFscan (v1.0.0). (A) CRISPR-Cas system has two parts: a CRISPR array and a cluster of *cas* genes. The new MacSyFinder search engine simultaneously annotates Cas clusters at 3 levels of classification from the most accurate (i.e. the subtype level) to the most permissive. When possible, it favours as the best solution the annotation at the subtype level but allows to recover atypical or degenerated systems with the 2 other levels of classification. **(B)** The combinatorial approach for the search of the best solution improves the detection of tandem systems. All models are tested and challenged, then the best combination of systems is determined. Here, it reveals the presence of 3 systems of different subtype in tandem (one color per subtype). **(C)** The new search engine avoids overlap between different candidate systems to determine the best solution(s), unless specified in the model with the multi_system or multi_model features. As illustrated, the adaptation module (cas1, cas2 and cas4) has been defined

as “multi_model” (indicated by a star*) in some subtype models and can thus be assigned to 2 systems in tandem, which improves their identification. Without this feature newly implemented in v2, one of the two systems would be lost. **(D)** Several members of the Type IV filament super-family (TFF-SF) could be found in the genome of *Variovorax* sp. WDL1. The new search engine enables the annotation of two distinct T4aP in the same genome. Here we can observe that the two detected T4aP are gathering clusters of different and complementary gene composition, underlying their coherence. The two strokes between each gene cluster signifies that the clusters are not close to each other on the chromosome. **(E)** The location of the T4aP gene clusters is displayed along the circular chromosome. A polygon connects the different parts of a same system with colors matching that of the systems in panel D. In all panels, genes are represented by arrows, their length indicates the gene length, and their direction indicates the gene orientation.

IV/ Application of MacSyFinder v2 to TXSScan and CONJscan

The new search engine and scoring system allow the retrieval of various occurrences of Type IV pili encoded at multiple loci.

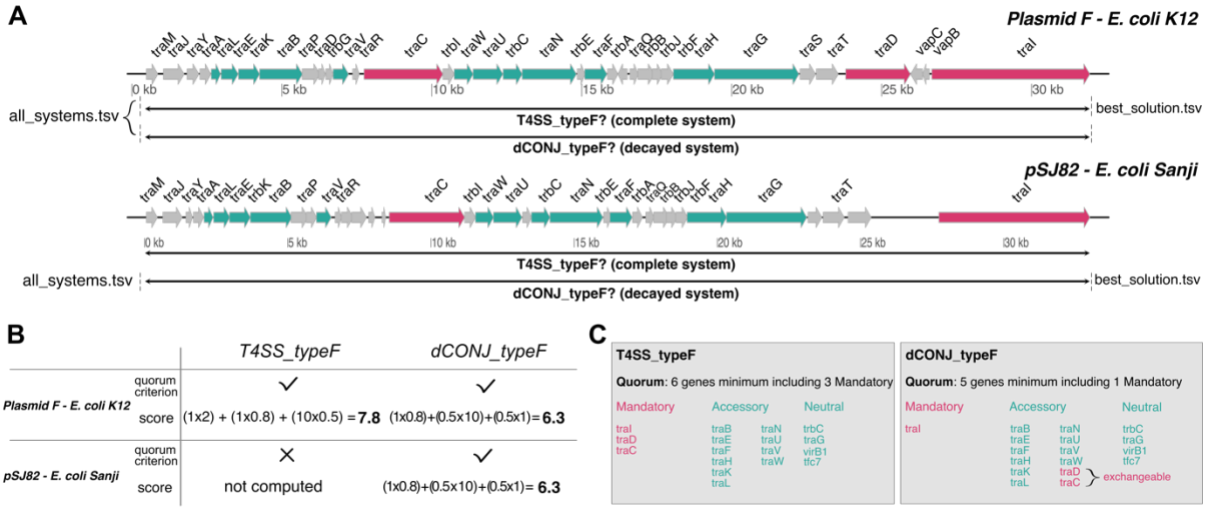
The type IV filaments super-family (TFF-SF) is a family of homologous machineries involved in bacterial and archaeal motility (e. g., the type IVa pilus “T4aP” and archaeal flagellum), toxin secretion (e.g., type II secretion systems, T2SS) or exogenous DNA acquisition (e. g., competence apparatus, Com) (Pelicic, 2008). Some members of the TFF-SF have their genes scattered across the genome (e.g., T4aP and some T2SS), and some genomes may harbour several scattered occurrences of the same system (Denise et al., 2019). In this case, it is not trivial to identify and discriminate the occurrences of the different systems. The search engine of MacSyFinder v 1 collected occurrences of the same system as one large system containing multiple copies of several genes. The new v2 search engine examines and then scores all possible combinations of gene clusters and (authorized) out-of-cluster genes eligible as systems. The scoring of these candidate systems penalizes the presence of the same gene in several gene clusters. This approach favours solutions presenting complete yet concise systems. For example, it allows the separation of two different multi-loci T4aP found in the same genome (Fig. 4D-E).

The new scoring scheme allows to distinguish putatively degenerate conjugative elements from the others.

Integrative conjugative elements and conjugative plasmids are very abundant mobile genetic elements that can transfer themselves from one bacterium to another. To do so, they encode a conjugative system that includes a relaxase (MOB) and a mating pair formation (MPF) machinery responsible for pilus biogenesis and mating junctions (de la Cruz et al., 2010). The known relaxases are currently searched using 11 HMM profiles, and the MPFs are classified into eight different types (FA, FATA, B, C, F, G, I, and T). Together, they make for eight models of T4SS (Guglielmini et al., 2013). MPFs include numerous genes, between eight to several dozens. However, the conserved set of genes seen as mandatory is much smaller (relaxase, VirB4, coupling protein), and the other conserved components oscillate between seven and 27. From wet-lab experiments to pandemic studies or phylogenetic analyses, discriminating between complete transferrable elements and incomplete, potentially immobile conjugative elements, is crucial. We have recently shown that degenerate conjugative

elements are not rare (Coluzzi et al., 2022). Hence, it would be important to have an easy way to identify complete and incomplete systems. To tackle this problem, we developed macsy-models taking advantage of the new scoring scheme implemented in v2.

All systems can be tested and challenged at once in the new version. The selection of the best solution among different candidate systems is based on the score of each candidate. Using this new feature, we created models designed to compete with each other (Fig. 5). For each conjugative system, one model was designed to detect complete systems, while the other was designed to detect both complete and incomplete systems. Used independently, the complete model would only detect complete systems, and the incomplete model would indiscriminately detect complete and incomplete systems. However, when used together in competition, the scoring system attributes actual complete systems to the complete model while incomplete systems are only detected by the "incomplete" model (Fig. 5).



<u>Figure 5.</u> Application of MacSyFinder v2 to distinguish complete and incomplete conjugative systems on bacterial plasmids with CONJscan v2.0.1. A. Representation of a complete conjugative system (top) and a decayed conjugative system (bottom). Arrows represent the predicted genes of the plasmids and their orientation. Mandatory and accessory components of the systems are represented in fuchsia and cyan respectively. **B.** Description of the score for the complete MPF_F (T4SS_TypeF) model and "decayed" MPF_F model (dCONJ_typeF) when computed by the scoring scheme of MacSyFinder v2 (detailed in Fig. 2A). CONJScan plasmids' models were used all at once with the "all" option. **C:** Difference between the complete and decayed models for the MPF_F. Both models list the same components, but the required quorum of mandatory genes and total genes required are different. The model designed to detect complete systems (T4SS_typeF) requires 3 mandatory genes and 6 genes minimum, while the "decayed" model (dCONJ_typeF) was designed to require only 1 mandatory gene and the other mandatory genes were set as "accessory" and exchangeable between each other. Thus, we ensure that if the quorum is reached for a complete system, the score of the "complete" model is always higher than the score of the "decayed" model.

CONCLUSION

MacSyFinder leverages the power of comparative genomics for accurate system-level annotation of microbial genomes. MacSyFinder version 2 enables more relevant and comprehensive system modelling and search capacities. The variety of the applications illustrated here and elsewhere demonstrates the potential of MacSyFinder to annotate many other cellular functions, including biosynthetic gene clusters, metabolic and signalling pathways. The *macsydata* tool and "MacSy Models" Github organization allow systems' modellers to easily share their macsy-model packages. We hope this will increase the visibility of their contribution and enhance the development of novel models for other molecular systems.

DATA AVAILABILITY

MacSyFinder source code and the hereby presented macsy-model packages are available at the following Github repositories: https://github.com/gem-pasteur/macsyfinder and https://github.com/macsy-models.

AUTHORS' CONTRIBUTIONS

BN, EPCR and SSA designed the new version of MacSyFinder. BN conceived the software architecture and design, the test design, and performed the implementation. RD, CC, MT, EPCR and SSA tested MacSyFinder. RD, CC, MT and SSA updated and distributed the presented macsy-model packages on the dedicated repository. RD, CC and MT analysed the results of MacSyFinder detection and implemented GA scores within HMM profiles of the presented macsy-model packages. EPCR and SSA wrote the first versions of the manuscript, and all authors contributed to and approved the final versions of the manuscript.

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