
IntegronFinder Documentation

Release 2.0

Jean Cury, Bertrand Néron, Eduardo PC Rocha

Jan 17, 2022

CONTENTS

- 1 User Guide 2**
 - 1.1 User Guide 2
- 2 Developer Guide 28**
 - 2.1 Developer Guide 28
- 3 Indices and tables 54**
- Python Module Index 55**
- Index 56**

IntegronFinder is a program that detects integrons in DNA sequences. The program is available on a webserver [Galaxy Pasteur](#), or by command line ([IntegronFinder on github](#)).

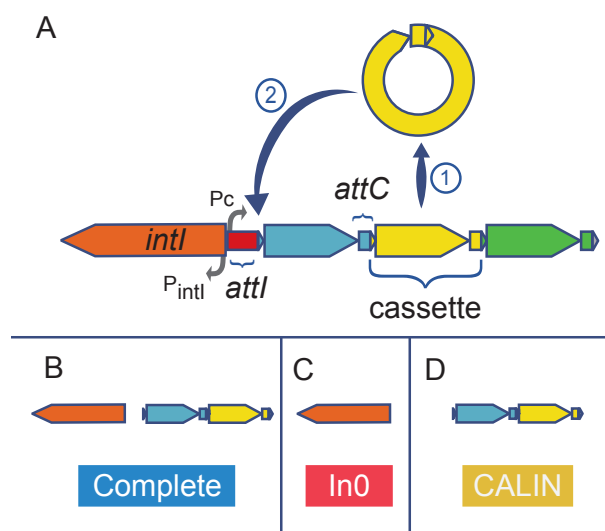
- You already read the [paper](#) and want to install it ? Click [here](#)
- You did not read the paper (yet) but you would like to have rapid introduction to integrons and the program? click [here](#)

USER GUIDE

1.1 User Guide

1.1.1 Introduction

Integrans are major genetic element, notorious for their major implication in the spread of antibiotic resistance genes. More generally, integrans are gene-capturing platform, whose broader evolutionary role remains poorly understood. IntegronFinder is able to detect with high accuracy integran in DNA sequences. It is accurate because it combines the use of HMM profiles for the detection of the essential protein, the site-specific integran integrase, and the use of Covariance Models for the detection of the recombination site, the *attC* site.



How does it work ?

For each sequence in the input file:

- First, IntegronFinder annotates the DNA sequence's CDS with Prodigal.
- Second, IntegronFinder detects independently integran integrase and *attC* recombination sites. The Integrin integrase is detected by using the intersection of two HMM profiles:

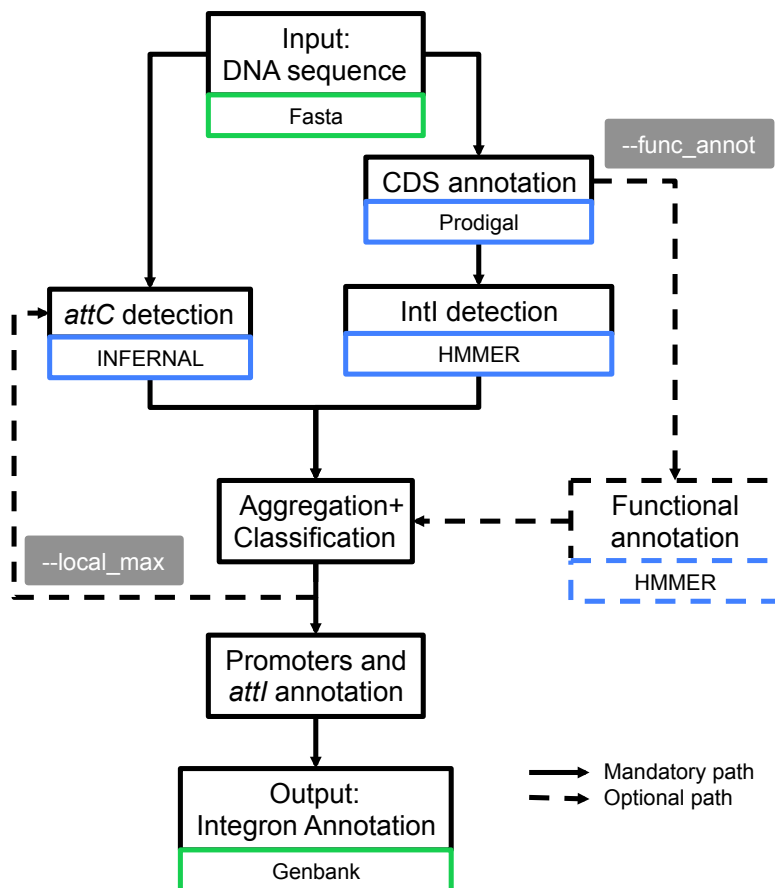
- one specific of tyrosine-recombinase (PF00589)
- one specific of the integron integrase, near the patch III domain of tyrosine recombinases.

The *attC* recombination site is detected with a covariance model (CM), which models the secondary structure in addition to the few conserved sequence positions.

- Third, the results are integrated, and IntegronFinder distinguishes 3 types of elements:
 - **complete integron (panel B above)** Integron with integron integrase nearby *attC* site(s)
 - **In0 element (panel C above)** Integron integrase only, without any *attC* site nearby
 - **CALIN element (panel D above)** Cluster of *attC* sites Lacking INtegrase nearby. A rule of thumb to avoid false positive is to filter out singleton of *attC* site.

IntegronFinder can also annotate gene cassettes (CDS nearby *attC* sites) using Resfams, a database of HMM profiles aiming at annotating antibiotic resistance genes. This database is provided but the user can add any other HMM profiles database of its own interest.

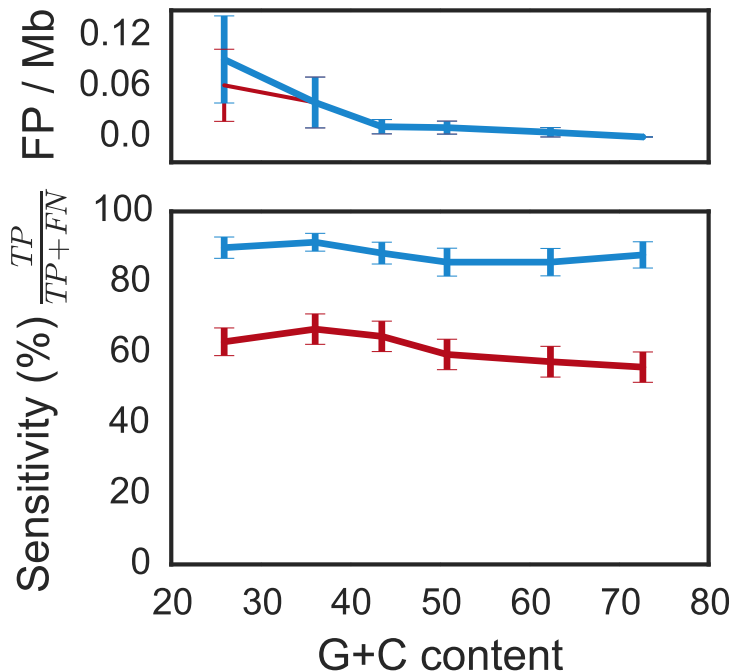
When available, IntegronFinder annotates the promoters and *attI* sites by pattern matching.



Does it work ?

Yes! The estimated sensitivity is 61% on average with the default option and goes up to 88% with the `--local_max` option. The missing *attC* sites are usually at the end of the array. The False positive rate with the `--local_max` option is estimated between 0.03 False Positive per Megabases (FP/Mb) to 0.72 FP/Mb. This leads to a probability of finding 2 consecutive false *attC* sites within 4kb between 4.10^{-6} and 7.10^{-9} . Overall, the probability of finding an integron in a chromosome (including finding a part of it) is more than 95%. Finally, these parameters do not depend on the G+C percent of the given replicon. See the [paper](#) for more information (freely accessible).

	Default	local_max
Sensitivity	61.20%	88.03%
FP rate	0.02 FP/Mb	0.03 FP/Mb
Mean time	2.59 s	86.59 s



The time in the table correspond to the average time per run with a pseudogenome having *attC* sites on a Mac Pro, 2 x 2.4 GHz 6-Core Intel Xeon, 16 Gb RAM, with options `-cpu 20` and `-no-proteins`.

Note: The time does not vary depending of the mode (default or `local_max`), and is about a couple of second, if the replicon does not contain any *attC* site.

1.1.2 Installation

IntegronFinder dependencies

IntegronFinder is built with Python ≥ 3.4 , and a few libraries are needed:

- Python ≥ 3.7
- Pandas (≥ 0.22)
- Numpy ($\geq 1.14.2$)
- Biopython (≥ 1.70)
- Matplotlib ($\geq 2.2.2$)
- colorlog

From version 1.5.1, integron_finder will check and install these libraries for you.

In addition, IntegronFinder has external dependencies, which have to be installed prior the use of the program (click to access the corresponding website).

- [HMMER 3.1b2](#)
- [INFERNAL 1.1.2](#)
- [Prodigal V2.6.2](#)
- [Nextflow](#) (for parallelization)

After installation of these programs, they should be in your `$PATH` (*i.e.* you can type in a terminal `hmmsearch`, `cmsearch`, or `prodigal` and a command not found shall not be displayed). If you have them installed somewhere else, please refer to integron_finder's parameters to give complete path to IntegronFinder.

Installation procedure

Warning: When installing a new version (up to 2.0 included) of IntegronFinder, do not forget to *uninstall* the previous version installed !

Warning: If You upgrading from version prior to 2.0 to 2.0 be careful the python used changed for 3.x. The python 2.7 is not supported anymore. So if you installed `integron_finder` within a virtualenv you need to create a new one based on python3.

From Version 2.0

System wide installation

1. Open a terminal and hit (not recommended):

```
sudo pip install integron_finder
```

Warning: On recent Debian/Ubuntu the `--user` option is forced. So use of `--root` option give an unexpected behavior and you cannot use `--prefix` option at all unless you add option `--system` for instance

```
sudo pip install --system integron_finder
```

or

```
pip install --prefix=/tmp/test_if --system integron_finder
```

2. To get an updated version (no need to uninstall):

```
sudo pip install -U integron_finder
```

User wide installation

1. Open a terminal and hit:

```
pip install --user integron_finder
```

Installation in a virtualenv

The virtual environment ([virtualenv](#)) is a system to isolate a python program from the system and avoid libraries conflict. So you can install a different python or libraries version than your system in each virtualenv. So if you update the system it will not change anything for your program and *vice versa*. If you want to remove the program just remove the virtual environment.

Create a virtual environment:

```
python3 -m venv Integron_Finder
```

or on some systems:

```
virtualenv -p python3 Integron_Finder
```

activate you virtualenv:


```
source Integron_Finder/bin/activate
```

The name of the virtualenv appear in parenthesis at the beginning of the prompt. Then install `integron_finder`:

```
pip install integron_finder
```

To run integron finder, you have to activate (once per session) the virtual environment:

```
source Integron_Finder/bin/activate
```

When you do not need to use `integron_finder` just deactivate the virtual environment. In the active terminal just type:

```
deactivate
```

The `integron_finder` command will disappear from the path. The name of the virtualenv disappear from the prompt.

Conda Package

From 2.0 version, `Integron_Finder` is available as `conda` package. `Integron_finder` is in `bioconda` From 2.0 version, `Integron_Finder` is available as `[conda]`(<https://conda.io/docs/index.html>) package. `Integron_finder` is in `[bioconda]`(<https://bioconda.github.io/>) channel. (The advantage with this solution is that it will install prodigal, hmmer, and infernal too.)

1. install conda
2. Set up channels

```
conda config --add channels defaults
conda config --add channels conda-forge
conda config --add channels bioconda
```

3. install `integron_finder`

```
conda install integron_finder
```

(The advantage with this solution is that it will install prodigal, hmmer, and infernal too.)

From Version 1.5.1 and after

1. Open a terminal and hit:

```
(sudo) pip install integron_finder
```

2. To get an updated version (no need to uninstall):

```
(sudo) pip install -U integron_finder
```

For Version 1.5 and before

1. Download the [latest release](#) that can be installed like this (v1.5)
2. Uncompress it
3. In a shell (*e.g.* a terminal), go to the directory and run:

```
(sudo) python setup.py install
```

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 IntegronFinder in the Python libraries of your system, you can install IntegronFinder in a virtual environment. See [virtualenv](#) or if you're using Canopy, see [Canopy CLI](#)

Warning: The installer does not work with pure setuptools procedure, it does not work in egg. Unless you disable egg by using the `--root` option. `python setup.py install --root /prefix/where/to/install/integron_finder`

Uninstallation procedure

From Version 1.5.1 and after

To uninstall IntegronFinder, run in the following command:

```
(sudo) pip uninstall integron_finder
```

It will uninstall `integron_finder` executable

From Version 1.0 to Version 1.5

Go to the directory from where you installed IntegronFinder (e.g. `Integron_Finder-1.5`), and run:

```
(sudo) python setup.py uninstall
```

How to install Python

The purpose of this section is to provide some help about installing python dependencies for IntegronFinder if you never installed any python package.

As IntegronFinder has not been tested on Windows, we assume Unix-based operating system. For Windows users, the best would be to install a unix virtual machine on your computer.

Usually a python distribution is already installed on your machine. However, if you don't know how to install libraries, we recommend to re-install it from a distribution which contains pre-compiled libraries. There are two main distributions (click to access website):

- [Enthought Canopy](#)
- [Anaconda](#)

Download version 3.x which correspond to your machine, then make sure that python from these distributions is the default one (you can possibly choose that in the preference and/or during installation). Make sure Biopython is installed, otherwise, you will have to install Biopython. `pip` or `conda` are recommended as a python packages installer.

It works as follow:

```
(sudo) pip install Biopython==1.71
```

To install version 1.71 of Biopython (recommended for IntegronFinder).

Note: If you don't manage to install all the packages, try googling the error, or don't hesitate to ask a question on [stackoverflow](#).

1.1.3 What's new ?

In Version 2.0

Here are the major changes between versions 1.x and 2.0. Essentially, it has been designed such as it becomes easier to find integrons with high confidence in huge datasets (but it works also for small datasets).

- IntegronFinder now accepts multifasta files as input.
- Only three files are created by default (see output section for details about the other possible output files):
 - A file with all integrons and their elements detected in all sequences in the input file.
 - A summary file with the number and type of integrons per sequence.
 - A file with standard output
- IntegronFinder can be run in parallel easily with a provided Nextflow script that is (almost) ready to use.
- We diversify the installation methods, so it can be easily deployed on a variety of machine. Notably, we built a singularity container which will allow a smooth installation on clusters.
- CALINs are now reported when they have at least 2 *attC* sites (instead of 1 before). This value can be changed by the user with `-calin-threshold x`
- Promoters and attI sites are not detected by default to increase speed
- It is now easy to obtain multiple alignments of detected attC sites
- Improve the documentation, especially on the developer part so anyone can contribute.
- Add unit (or non regression) tests.

1.1.4 Quick start

We assume here that the program is *installed*.

You can see all available options with:

```
integron_finder -h
```

For impatient

Go to the directory containing your input file(s), or specify the path to that file and call:

```
integron_finder mysequences.fst
```

or:

```
integron_finder path/to/mysequences.fst
```

It will perform a search, and outputs the results in a directory called `Results_Integron_Finder_mysequences`.

Input and Outputs

Inputs

`integron_finder` can take as an input:

- a fasta file
- a multi-fasta file
- many (multi-)fasta files

Outputs

By default, `integron_finder` will output 3 files under `Results_Integron_Finder_mysequences`:

- `mysequences.integrans` : A file with all integrans and their elements detected in all sequences in the input file.
- `mysequences.summary` : A summary file with the number and type of integrans per sequence.
- `integron_finder.out` : A copy standard output. The stdout can be silenced with the argument `--mute`

The amount of log in the standard output can be controlled with `--verbose` for more or `--quiet` for less, and both are cumulative arguments, eg. `-vv` or `-qq`.

Other files can be created on demand:

- `--gbk`: Creates a Genbank files with all the annotations found (present in the `.integrans` file)
- `--pdf`: Creates a simple pdf graphic with complete integrans

- `--split-results`: Creates a `.integrans` a `.summary` file per replicon if the input is a multifasta file.
- `--keep-tmp`: Keep temporary files. See *Keep intermediate files* for more.

For everyone

Note: The different options will be shown separately, but they can be used altogether unless otherwise stated.

Thorough local detection

This option allows a much more sensitive search of *attC* sites. It will be slower if integrons are found, but will be as fast if nothing is detected.

```
integron_finder mysequences.fst --local-max
```

CALIN detection

By default CALIN are reported if they are composed of at least 2 *attC* sites, in order to avoid false positives. This value was chosen as CALIN with 2 *attC* sites were unlikely to be false positive. The probability of a false CALIN with at least 2 *attC* sites within 4kb was estimated between 4.10^{-6} and 7.10^{-9} . However, one can modify this value with the option `-calin-threshold` and use a lower or higher value depending on the risk one is willing to take:

```
integron_finder mysequences.fst --calin-threshold 1
```

Note: If `--local-max` is called, it will run around CALINs with single *attC* sites, even if `--calin-threshold` is 2. The filtering step is done after the search with local max in that case.

Functional annotation

This option allows to annotate cassettes given HMM profiles. As Resfams database is distributed, to annotate antibiotic resistance genes, just use:

```
integron_finder mysequences.fst --func-annot
```

IntegronFinder will look in the directory `Integron_Finder-x.x/data/Functional_annotation` and use all `.hmm` files available to annotate. By default, there is only `Resfams.hmm`, but one can add any other HMM file here. Alternatively, if one wants to use a database which is present elsewhere on the user's computer without copying it into that directory, one can specify the following option

```
integron_finder mysequences.fst --path_func_annot bank_hmm
```

where `bank_hmm` is a file containing one absolute path to a `hmm` file per line, and you can comment out a line

```
~/Downloads/Integron_Finder-x.x/data/Functional_annotation/Resfams.hmm
~/Documents/Data/Pfam-A.hmm
# ~/Documents/Data/Pfam-B.hmm
```

Here, annotation will be made using Pfam-A et Resfams, but not Pfam-B. If a protein is hit by 2 different profiles, the one with the best e-value will be kept.

Search for promoter and *attI* sites

By default `integron_finder` look for *attC* sites and site-specific integron integrase,. If you want to search for known promoters (integrase, Pc-int1 and Pc-int3) and AttI sites in integrons elements you need to add the `--promoter-attI` option on the command line.

Keep intermediate results

Integrons finder needs some intermediate results to run completely. It includes notably the protein file in fasta (`mysequences.prt`), but also the outputs from `hmmer` and `infern`. A folder containing these outputs is generated for each replicon and have name `tmp_<replicon_id>`. This directory is removed at the end. You can keep this directory to analyse further each `integron_finder` steps with the option `--keep-tmp`. Using this argument allows you to rerun `integron_finder` on the same sequences without redetecting proteins and *attC* sites. It is useful if one wants to change clustering parameters, evalues of *attC* sites, or size of them. Note that it won't search for new *attC* sites so it is better to start with relaxed parameters and then rerun `integron_finder` with more strict parameters. See the section [for *integron diggers*](#) for more informations

For each tmp file, there are:

- `<replicon_id>.fst`: a single fasta file with the replicon_name
- `<replicon_id>.prt`: a multifasta file with the sequences of the detected proteins.
- `<replicon_id>_intI_table.res`: hmm result for the intI hmm profile in tabular format
- `<replicon_id>_intI.res`: hmm result for the intI hmm profile
- `<replicon_id>_phage_int_table.res`: hmm result for the tyrosine recombinase hmm profile in tabular format
- `<replicon_id>_phage_int.res`: hmm result for the tyrosine recombinase hmm profile in tabular format
- `<replicon_id>_attc_table.res`: cmsearch result for the attC sites covariance model in tabular format
- `<replicon_id>_attc.res`: significant (according to `evaluate-attc`) attC sites aligned in stockholm format
- `integron_max.pickle`: pickle file so `integron_finder` reuse this instead of re-running the `local_max` part

Topology

By default, IntegronFinder assumes that

- your replicon is considered as **circular** if there is **only one replicon** in the input file.
- your replicons are considered as **linear** if there are **several replicons** in the input file.

However, you can change this default behavior and specify the default topology with options `--circ` or `--lin`:

```
integron_finder --lin mylinearsequence.fst
integron_finder --circ mycircularsequence.fst
```

If you have multiple replicon in the input file with different topologies you can specify a topology for each replicon by providing a topology file. The syntax for the topology file is simple:

- one topology by line
- one line start by the seqid followed by 'circ' or 'lin' for circular or linear topologies.

example:

```
seq_id_1 circ
seq_id_2 lin
```


You can also mix the options `--circ` or `--lin` with option `--topology-file`:

```
integron_finder --circ --topology-file path/to/topofile mysequences.  
→fst
```

In the example above the default topology is set to *circular*. The replicons specified in *topofile* supersede the default topology.

Warning: However, if the replicon is smaller than $4 \times dt$ (where *dt* is the distance threshold, so 4kb by default), the replicon is considered linear to avoid clustering problem. The topology used to searching integron is report in the **.integrans file*

For big data people

Parallelization

The time limiting part are HMMER (search integrase) and INFERNAL (search *attC* sites). So if you have to analyze one or few replicons the user can set the number of CPU used by HMMER and INFERNAL:

```
integron_finder mysequences.fst --cpu 4
```

Default is 1.

If you want to deal with a fasta file with a lot of replicons (from 10 to more than thousand) we provide a workflow to parallelize the execution of the data. This mean that we cut the data input into chunks (by default of one replicon) then execute IntegronFinder in parallel on each replicon (the number of parallel tasks can be limited) then aggregate the results in one global summary. The workflow use the [nextflow](#) framework and can be run on a single machine or a cluster.

First, you have to install [nextflow](#) first, and [integron_finder](#). Then we provide 2 files (you need to download them from the IntegronFinder github repo.)

- *parallel_integron_finder.nf* which is the workflow itself in nextflow syntax
- *nextflow.config* which is a configuration file to execute the workflow.

The workflow file should not be modified. Whereas the profile must be adapted to the local architecture.

The file *nextflow.config* provide for profiles:

- a standard profile for local use
- a cluster profile
- a standard profile using singularity container

- a cluster profile using singularity container

Warning: On Ubuntu Bionic Beaver (18.04) The default java is not suitable to run nextflow
So you have to install another jvm

```
sudo add-apt-repository ppa:webupd8team/java sudo apt-get update sudo apt-get
install oracle-java8-installer
```

for more details see: <https://medium.com/coderscorner/installing-oracle-java-8-in-ubuntu-16-10-845507b13343>

so now install nextflow. If you have capsule error like

```
CAPSULE EXCEPTION: Error resolving dependencies. while processing_
↳ attribute Allow-Snapshots: false (for stack trace, run with -
↳ Dcapsule.log=verbose)
Unable to initialize nextflow environment
```

install nextflow (>=0.29.0) as follow (change the nextflow version with the last release)

```
wget -O nextflow http://www.nextflow.io/releases/v0.30.2/nextflow-0.
↳ 30.2-all
chmod 777 nextflow
```

for more details see: <https://github.com/nextflow-io/nextflow/issues/770#issuecomment-400384617>

How to get parallel_integron_finder

The release contains the workflow *parallel_integron_finder.nf* and the *nextflow.config* at the top level of the archive But If you use pip to install Integron_Finder you have not easily access to them. But they can be downloaded or executed directly by using nextflow.

to download it

```
nextflow pull gem-pasteur/Integron_Finder
```

to get the latest version or use *-r* option to specify a version

```
nextflow pull -r release_2.0 gem-pasteur/Integron_Finder
```

to see what you download

```
nextflow see Integron_Finder
```

to execute it directly

```
nextflow run gem-pasteur/Integron_Finder -profile standard --replicons_
↳all_coli.fst --circ
```

or:

```
nextflow run -r release_2.0 gem-pasteur/Integron_Finder -profile_
↳standard --replicons all_coli.fst --circ
```

standard profile

This profile is used if you want to parallelize IntegronFinder on your machine. You can specify the number of tasks in parallel by setting the queueSize value

```
standard {
    executor {
        name = 'local'
        queueSize = 7
    }
    process{
        executor = 'local'
        $integron_finder{
            errorStrategy = 'ignore'
            cpu=params.cpu
        }
    }
}
```

If you installed IntegronFinder with singularity, just uncomment the container line in the script, and set the proper path to the container.

All options available in non parallel version are also available for the parallel one. except the `--outdir` which is not available and `--replicons` option which is specific to the parallelized version. `--replicons` allows to specify the path of a file containing the replicons.

A typical command line will be:

```
./parallel_integron_finder.nf -profile standard --replicons all_coli.
↳fst --circ
```

Note: Joker as `*` or `?` can be used in path to specify several files as input.

But **do not forget** to protect the wild card from the shell for instance by enclosing your glob pattern with simple quote.

```
nextflow run -profile standard parallel_integron_finder.nf --replicons  
→ 'replicons_dir/*.fst'
```

Two asterisks, i.e. `**`, works like `*` but crosses directory boundaries. Curly brackets specify a collection of sub-patterns.

```
nextflow run -profile standard parallel_integron_finder.nf --replicons  
→ 'data/**/*.fa'  
nextflow run -profile standard parallel_integron_finder.nf --replicons  
→ 'data/**/*.fa'  
nextflow run -profile standard parallel_integron_finder.nf --replicons  
→ 'data/file_{1,2}.fa'
```

The first line will match files ending with the suffix `.fa` in the `data` folder and recursively in all its sub-folders. While the second one only match the files which have the same suffix in any sub-folder in the data path. Finally the last example capture two files: `data/file_1.fa`, `data/file_2.fa`

More than one path or glob pattern can be specified in one time using comma. **Do not** insert spaces surrounding the comma

```
nextflow run -profile standard parallel_integron_finder --replicons  
→ 'some/path/*.fa,other/path/*.fst'
```

The command above will analyze all files ending by `.fa` in `/some/path` with `.fst` extension in `other/path`

For further details see: <https://www.nextflow.io/docs/latest/channel.html#frompath>

Note: The option `-outdir` is not allowed. Because you can specify several replicon files as input, So in this circumstances specify only one name for the output is a none sense.

Note: The options starting with one dash are for nextflow workflow engine, whereas the options starting by two dashes are for `integron_finder` workflow.

Note: Replicons will be considered linear by default (see above), here we use `-circ` to consider replicons circular.

Note: If you specify several input files, the split and merge steps will be parallelized.

If you execute this line, 2 kinds of directories will be created.

- One named *work* containing lot of subdirectories this for all jobs launch by nextflow.
- Directories named *Results_Integron_Finder_XXX* where XXX is the name of the replicon file. So, one directory per replicon file will be created. These directories contain the final results as in non parallel version.

cluster profile

The cluster profile is intended to work on a cluster managed by SLURM. If Your cluster is managed by an other drm change executor name by the right value (see [nextflow supported cluster](#))

You can also managed

- The number of task in parallel with the *executor.queueSize* parameter (here 500). If you remove this line, the system will send in parallel as many jobs as there are replicons in your data set.
- The queue with *process.queue* parameter (here common,dedicated)
- and some options specific to your cluster management systems with *process.clusterOptions* parameter

```
cluster {
  executor {
    name = 'slurm'
    queueSize = 500
  }

  process{
    executor = 'slurm'
    queue= 'common,dedicated'
    clusterOptions = '--qos=fast'
    $integron_finder{
      cpu=params.cpu
    }
  }
}
```

To run the parallel version on cluster, for instance on a cluster managed by slurm, I can launch the main nextflow process in one slot. The parallelization and the submission on the other slots is made by nextflow itself. Below a command line to run *parallel_integron_finder* and use 2 cpus per *integron_finder* task, each *integron_finder* task can be executed on different machines, each *integron_finder* task claim 2 cpus to speed up the attC sites or integrase search:

```
sbatch --qos fast -p common nextflow run parallel_integron_finder.nf -
→profile cluster --replicons all_coli.fst --cpu 2 --local-max --gbk --
→circ
```

The results will be the same as describe in local execution.

singularity profiles

If you use the singularity integron_finder image, use the profile *standard_singularity*. With the command line below nextflow will download parallel_integron_finder from github and download the integron_finder image from the singularity-hub so you haven't to install anything except nextflow and singularity.

```
nextflow run gem-pasteur/Integron_Finder -profile standard_singularity_
↳--replicons all_coli.fst --circ
```

You can also use the integron_finder singularity image on a cluster, for this use the profile *cluster_singularity*.

```
sbatch --qos fast -p common nextflow run gem-pasteur/Integron_
↳Finder:2.0 -profile cluster_singularity --replicons all_coli.fst --
↳cpu 2 --local-max --gbk --circ
```

In the case of your cluster cannot reach the world wide web. you have to download the singularity image

```
singularity pull --name Integron_Finder shub://gem-pasteur/integron_
↳finder:2.0
```

the move the image on your cluster modify the nextflow.config to point on the location of the image, and adapt the cluster options (executor, queue, ...) to your architecture

```
cluster_singularity {
    executor {
        name = 'slurm'
        queueSize = 500
    }

    process {
        container = /path/to/integron_finder
        queue = 'common,dedicated'
        clusterOptions = '--qos=fast'
        withName: integron_finder {
            cpus = params.cpu
        }
    }
    singularity {
        enabled = true
        runOptions = '-B /pasteur'
```

(continues on next page)

(continued from previous page)

```

        autoMounts = false
    }
}
}

```

then run it

```

sbatch --qos fast -p common nextflow run ./parallel_integron_finder.
↪nf -profile cluster_singualrity --replicons all_coli.fst --cpu 2 --
↪local-max --gbk --circ

```

If you want to have more details about the jobs execution you can add some options to generate report:

Execution report

To enable the creation of this report add the `-with-report` command line option when launching the pipeline execution. For example:

```

nextflow run ./parallel_integron_finder.nf -profile standard -with-
↪report [file name] --replicons

```

It creates an HTML execution report: a single document which includes many useful metrics about a workflow execution. For further details see <https://www.nextflow.io/docs/latest/tracing.html#execution-report>

Trace report

In order to create the execution trace file add the `-with-trace` command line option when launching the pipeline execution. For example:

```

nextflow run ./parallel_integron_finder.nf -profile standard -with-
↪trace --replicons

```

It creates an HTML timeline for all processes executed in your pipeline. For further details see <https://www.nextflow.io/docs/latest/tracing.html#timeline-report>

Timeline report

To enable the creation of the timeline report add the `-with-timeline` command line option when launching the pipeline execution. For example:

```
nextflow run ./parallel_integron_finder.nf -profile standard -with-
→timeline [file name] --replicons ...
```

It creates an execution tracing file that contains some useful information about each process executed in your pipeline script, including: submission time, start time, completion time, cpu and memory used. For further details see <https://www.nextflow.io/docs/latest/tracing.html#trace-report>

For integron diggers

Many options are set to prevent false positives. However, one may want higher sensitivity at the expense of having potentially false positives. Ultimately, only experimental experiments will tell whether a given *attC* sites or integrase is functional.

Also, note that because of how `local_max` works (ie. around already detected elements), true *attC* sites may be found thanks to false *attC* sites, because false *attC* sites may trigger `local_max` around them. Hence, one may want to use very relaxed parameters first with the `--keep-tmp` flag to rerun the analysis on the same data while restricting the parameters.

Clustering of elements

attC sites are clustered together if they are on the same strand and if they are less than 4 kb apart (`-dt 4000` by default). To cluster an array of *attC* sites and an integron integrase, they also must be less than 4 kb apart. This value has been empirically estimated and is consistent with previous observations showing that biggest gene cassettes are about 2 kb long. This value of 4 kb can be modified though:

```
integron_finder mysequences.fst --distance-thresh 10000
```

or, equivalently:

```
integron_finder mysequences.fst -dt 10000
```

This sets the threshold for clustering to 10 kb.

Note: The option `--outdir` allows you to chose the location of the Results folder (`Results_Integron_Finder_mysequences`). If this folder already exists, IntegronFinder will not re-run analyses already done, except functional annotation. It allows you to re-run rapidly IntegronFinder with a different `--distance-thresh` value. Functional annotation needs to

re-run each time because depending on the aggregation parameters, the proteins associated with an integron might change.

Integrase

We use two HMM profiles for the detection of the integron integrase. One for tyrosine recombinase and one for a specific part of the integron integrase. To be specific we use the intersection of both hits, but one might want to use the union of both hits (and sees whether it exists cluster of attC sites nearby non integron-integrase...). To do so, use:

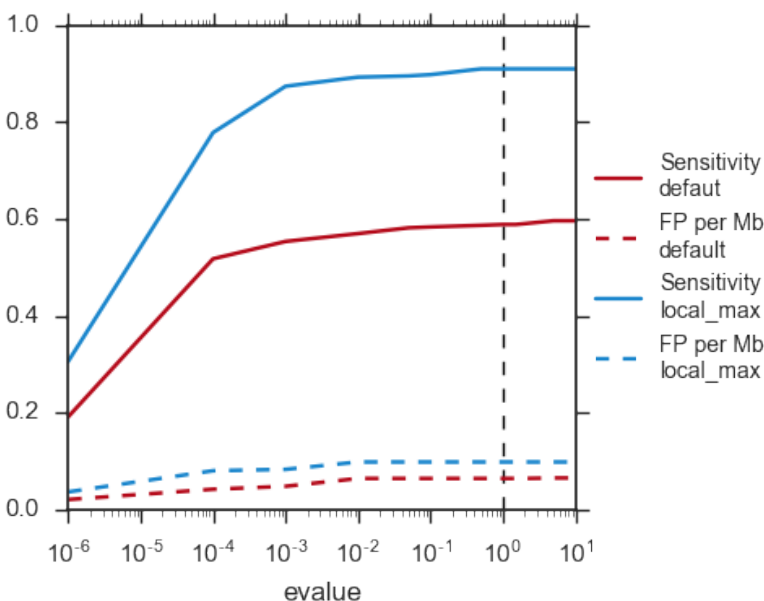
```
integron_finder mysequences.fst --union-integrases
```

attC evalule

The default evalule is 1. Sometimes, degenerated attC sites can have a evalule above 1 and one may want to increase this value to have a better sensitivity.

```
integron_finder mysequences.fst --evalule-attc 5
```

Here is a plot of how the sensitivity and false positive rate evolve as a function of the evalule:



Note: If one wants to have maximum sensitivity, use a high evalule (max is 10), and then integron_finder can be run again on the same data with a lower evalule. It won't work the other way around (starting with low evalule), as attC sites are not searched again.

(continued from previous page)

```
#=GC SS_cons <<<<<<-----<<<-<<<<.....
->.....>>>>>
->>>----->>>>>>
#=GC RF [Rsec]====== [=Lsec]= .....
->.....
->[Lprim]====== [Rprim]
//
```

Which you can manipulate easily with `esl-alimanip` tools provided by `infern` (the following examples should work if your `cmsearch` is in your `PATH`). You can convert the same alignment in dna alphabet (`cmsearch` use RNA alphabet):

```
$ esl-alimanip --dna Results_Integron_Finder_mysequences/tmp_ACBA.0917.
->00019.0001/ACBA.0917.00019.0001_attc.res
# STOCKHOLM 1.0
#=GF AU Infernal 1.1.2

ACBA.0917.00019.0001/315102-315161 GTCTAACAATTC---
->GTTCAAGCCGACGCCGCT-----
->TCGCGGCGCGGCTTAAGTCAAGC---GTTAGAT
#=GR ACBA.0917.00019.0001/315102-315161 PP *****...
->*****
->*****
ACBA.0917.00019.0001/313260-313368 ACCTAACAATTC---
->GTTCAAGCCGAGATCGCTTCGCGGCCGCGGAGTTGTTTCGGAATAATTGTCACAACGCCGCGGCCGCAAAGCGCTCCGGCTT
->---GTTGGGC
#=GR ACBA.0917.00019.0001/313260-313368 PP *****...
->*****
->...*****
ACBA.0917.00019.0001/313837-313906 GCCCAACATGGC---
->GCTCAAGCCGACCGGCCAGCCCT-----
->GCGGGCTGTCCGTCGGCTTAGCTAGGGC---GTTAGAG
#=GR ACBA.0917.00019.0001/313837-313906 PP *****...
->*****
->*****
#=GC SS_cons <<<<<<-----<<<-<<<<.....
->.....>>>>>
->>>----->>>>>>
#=GC RF [Rsec]====== [=Lsec]= .....
->.....
->[Lprim]====== [Rprim]
//
```

You can also convert it to fasta format:

```
$ esl-alimanip --dna --outformat afa Results_Integron_Finder_
→mysequences/tmp_ACBA.0917.00019.0001/ACBA.0917.00019.0001_attc.res
>ACBA.0917.00019.0001/315102-315161
GTCTAACAATTC---GTTCAAGCCGACGCCGCT-----
-----TCGCGGCGCGGCTTAACTCAAGC----GTTAGAT
>ACBA.0917.00019.0001/313260-313368
ACCTAACAATTC---GTTCAAGCCGAGATCGCTTCGCGGCCGCGGAGTTGTTTCGGAAGAAA
TTGTCACAACGCCGCGGCCGCAAAGCGCTCCGGCTTAACTCAGGC----GTTGGGC
>ACBA.0917.00019.0001/313837-313906
GCCCCAATGTC---GCTCAAGCCGACCGCCAGCCCT-----
-----GCGGGCTGTCCGTCGGCTTAGCTAGGGC----GTTAGAG
```

The possible outformat are:

- stockholm
- pfam
- a2m
- psiblast
- afa

1.1.5 web server

Galaxy

You can access IntegronFinder online, on the [Galaxy server of the Pasteur institute](#)

How to use it

Registration on the Galaxy server of the Pasteur institute is not required to use the tool. Yet, if you wish to keep your history, we recommend you to register.

1. Upload your sequence with **Get Data - Upload File** in the menu on the left
2. Select your file in the **Replicon file** list of Integron Finder
3. Select the options you want
4. Click on **Execute**

If you want more options:

3. Select **Show** on advanced parameters
4. Select the options you want

5. Click on **Execute**

You can see the role of the different functions in the [tutorial](#) page.

Results

Once the job is finished, you get your results on right panel. All files contain the log of the run which tells you how many integrons have been found for each types along with the number of *attC* sites per type. There are 4 different outputs created:

- **Raw results archive:** An archive containing all raw results.
- **Integrations annotations:** A tabular file listing all the elements and their characteristics.
- **GenBank:** The GenBank file of the input sequence with the annotation corresponding to the elements found (integrase, *attC*, promoter, attI, etc...).
- **Graphics:** Simple representation of one or more complete integrons found. The representation is very basic and a better representation can be obtained from the GenBank file and a software (eg Geneious) to represent it.

For each of the aforementioned files, you can save them by clicking on the download button.

1.1.6 References

If you use this software, please cite:

- Identification and analysis of integrons and cassette arrays in bacterial genomes Jean Cury; Thomas Jove; Marie Touchon; Bertrand Neron; Eduardo PC Rocha. **Nucleic Acids Research**, 2016; doi: [10.1093/nar/gkw319](https://doi.org/10.1093/nar/gkw319)

Please cite also the following articles:

- Nawrocki, E.P. and Eddy, S.R. (2013) Infernal 1.1: 100-fold faster RNA homology searches. **Bioinformatics**, 29, 2933-2935.
- Eddy, S.R. (2011) Accelerated Profile HMM Searches. **PLoS Comput Biol**, 7, e1002195.
- Hyatt, D., Chen, G.L., Locascio, P.F., Land, M.L., Larimer, F.W. and Hauser, L.J. (2010) Prodigal: prokaryotic gene recognition and translation initiation site identification. **BMC Bioinformatics**, 11, 119.

and if you use ResFams, cite the corresponding articles:

- Gibson, M.K., Forsberg, K.J. and Dantas, G. (2015) Improved annotation of antibiotic resistance determinants reveals microbial resistomes cluster by ecology. **ISME J**, 9, 207-216.

DEVELOPER GUIDE

2.1 Developer Guide

This part is for developers, who want to work on IntegronFinder scripts.

2.1.1 Developer installation

If you are not part of the project, start by forking IntegronFinder repository. For that, sign in to your account on github, and go to https://github.com/gem-pasteur/Integron_Finder. Then, click on 'Fork' (under your account icon). This will create a copy of the repository, but with your username instead of 'gem-pasteur'.

create a virtual environment:

```
virtualenv -p python3 Integron_Finder
```

activate you virtualenv:

```
source Integron_Finder/bin/activate
```

then install integron_finder in developer mode:

```
pip install -e "git+https://github.com/gem-pasteur/Integron_Finder  
→#egg=integron_finder[dev]"
```

or clone your repository manually, then install it

```
mkdir src  
cd src  
git clone https://github.com/gem-pasteur/Integron_Finder  
cd Integron_Finder  
pip install -e ".[dev]"
```

It installs the requirements and create a directory in the virtualenv `src/integron_finder` and create links in the virtualenv. So `integron_finder` is runnable and you can modify the sources and run it again without to reinstall the project.

Note: `[dev]` allow to install extra dependencies to generate documentation, compute test coverage ...

Warning: Debian/Ubuntu distribution `-user` is the default. So the `-prefix` option does not work and the `-root` option has unexpected behavior. Therefore the best solution is to use `-user` or a virtualenv.

2.1.2 Build a new release

1. activate the virtualenv:

```
./Integron_Finder/bin/activate
```

2. Go to the root of the project:

```
cd Integron_Finder/src/Integron_Finder
```

3. Te build the new release:

```
python -m build .
```

it will create a source *tar.gz* distribution and a *wheel*

2.1.3 Send changes to upstream repository

If you want to integrate your code in the upstream (main) repository, you need to create a pull request.

1. Read the [Contibuting guide](#)
2. Create a new branch with `<your branch name>` a descriptive name (e.g. 'adding-xx-feature', 'fixing-typos', etc.), so that others understand what your are working on.
3. Work on it
4. Test that your work does not break the tests. add tests corresponding to your code
5. Push your local branch on your `integron_finder` clone on github

```
git push --set-upstream origin <your branch name>
```

6. ask for pull request

- Go to your forked repository on github https://github.com/<your_login>/Integron_Finder/pulls
- Click on ‘New pull request’
- Choose your repository and the branch on which you did your changes in ‘head fork’ (right-hand side), and choose ‘gem-pasteur/Integron_Finder’ with the branch on which you want to merge (probably master) in ‘base fork’ (left-hand side).
- A green ‘Able to merge’ text should appear if git is able to automatically merge the 2 branches. In that case, click on ‘Create pull request’, write your comments on the changes you made, why etc, and save. We will receive the pull request.

2.1.4 Tests

IntegronFinder is provided with unit tests. You can find them in `tests` directory. You can use them to check that your changes did not break the previous features, and you can update them, and add your own tests for the new features.

Tests are done using unittest.

Running tests

To run the tests `-v` option is to increase the verbosity of the output:

```
python setup.py test
```

or:

```
python tests/run_tests.py -vv
```

or:

```
python tests/run_tests.py -vv tests/test_utils.py
```

to run specific tests.

If you also want to get code coverage (you need to install coverage):

```
coverage run --source integron_finder tests/run_tests.py
```

Add `-vv` to get more details on each test passed/failed. If you want to see the coverage in html output, run (after executing the command above):


```
coverage html
```

The html coverage report will be generated in `coverage_html/index.html`.

Adding tests

If you want to create a new test file, adding a file in tests directory, must start with `test_`. Then, write your TestCase by inherits from `IntegronTest` and your tests using unittest framework (see examples in existing files), and *run them*.

2.1.5 Documentation

Documentation is done using `sphinx`. Source files are located in `doc/sources`. To generate the documentation you just have to run the makefile located in `doc` directory.

```
make html
```

To generate the documentation in *html* format or

```
make latexpdf
```

to generate the documentation in pdf format (for this option you need to have latex installed on your compute)

You can complete them.

2.1.6 Architecture Overview

Project files and directories

Files

COPYING The integron_finder licensing.

COPYRIGHT The integron finder copy rights holders.

MANIFEST.in What must be or should not included in the distribution.

README.md The file to read in first.

requirements.txt The requirements need to use integron_finder.

requirements_dev.txt The extra requirements to develop on integron_finder.

setup.cfg The setup.py configuration file.

setup.py The file to define how to build/install/release/test/... integron finder.

Directories

integron_finder The core of the projects contains integron_finder library The **scripts/finder** contain the main entry point.

tests Contains all needed for tests, the tests themselves, are at the top level and the name must start by test_. The data directory contains all data needed to perform the tests. (see [Tests](#) for further details)

doc Contains the documentation write in sphinx. The **source** directory contains the .rst files, whereas the **build** directory contains the generated documentation. To know how to contribute or generate documentation see [Documentation](#)

Singularity Contains the definition file for singularity container.

data TODO

dist This directory is generated when a distribution is created (python setup.py sdist).

Technical overview

The main entry point is in integron_finder/scripts/finder.py there are 3 functions

`integron_finder.scripts.main()` which is the real main entry point

main call `scripts/finder.parse_args()` which parse the commandline and generate a `config.Config` object. and do a loop over replicon and run `integron_finder.scripts/find_integron_in_one_replicon()`

all results are store in a directory named `Results_Integron_Finder_<replicon_file_name>` this directory is created by `integron_finder.scripts/find_integron_in_one_replicon()` store results in this directory or in a subdirectory call `tmp_<replicon_id>` these subdirectories will be keep only if `--keep-tmp` option is set, otherwise they are removed at the end of the `integron_finder.scripts/find_integron_in_one_replicon()`

when all replicons are computed the main function call `integron_finder.utils.merge_results()` to gather all results files `<replicons_id>.integtrons` and generate a unique file with these information.

to have details on `find_integron_in_one_replicon` works see [Introduction](#)

2.1.7 Integron_finder API Reference

annotation

`integron_finder.annotation.add_feature` (*replicon*, *integron_desc*, *prot_db*,
dist_threshold)

Add integron annotation to the replicon.

Parameters

- **replicon** (a `Bio.Seq.SeqRecord` object.) – The Replicon to annotate
- **integron_desc** (a `pandas.DataFrame`) – integron description
- **prot_db** (a `integron_finder.prot_db.ProteinDB` object.) – the path to the fasta file containing the translation of the replicon.
- **dist_threshold** (*int*) – Two elements are aggregated if they are distant of `dist_threshold` or less.

`integron_finder.annotation.func_annot` (*integrans*, *replicon*, *prot_db*,
hmm_files, *cfg*, *out_dir*='.',
evaluate=10, *coverage*=0.5)

Call hmmer to annotate CDS associated with the integron.

Use NCBIfam-AMRFinder.LIB available here

<https://ftp.ncbi.nlm.nih.gov/hmm/NCBIfam-AMRFinder/>

check for the appropriate version

Parameters

- **integrans** (list of `integron_finder.integron.Integron` objects.) – integrans list to annotate
- **replicon** (`Bio.Seq.SeqRecord` object) – replicon where the integrans were found (genomic fasta file)
- **prot_db** (`integron.prot_db.ProteinDB` object.) – the protein database corresponding to the replicon translation
- **hmm_files** (*List[str]*) – List of path of hmm profiles to use to scan the prot_file
- **cfg** (`integron_finder.config.Config`) – the configuration for this analyse
- **out_dir** (*str*) – the path of the directory where to store the results
- **evaluate** (*float*) –
- **coverage** (*float*) –

Returns

None.

But several files per hmm file are produced.

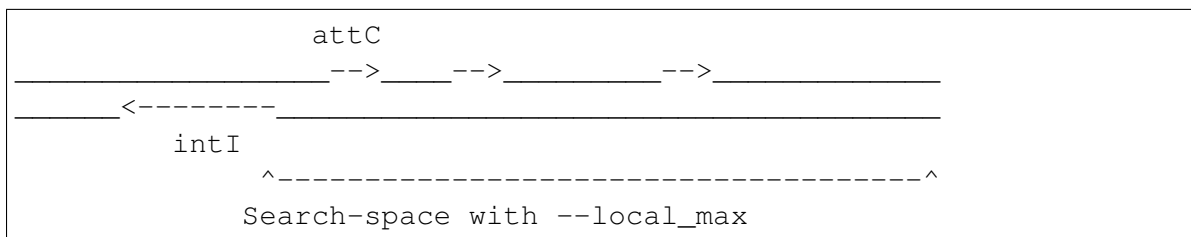
- subseqprot.tmp: fasta file containing a subset of protfile (the proteins belonging to the integron)
- <hmm>_fa.res: an output of the hmm search.
- <hmm>_fa_table.res: an output of the hmm search in tabulated format.

attc

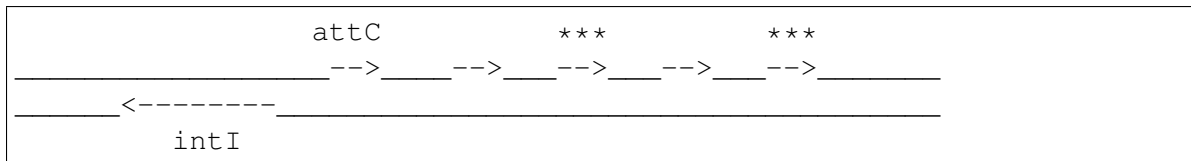
```
integron_finder.attc.find_attc_max(integrans, replicon, distance_threshold, model_attc_path, max_attc_size, min_attc_size, evaluate_attc=1.0, circular=True, out_dir='.', cmsearch_bin='cmsearch', cpu=1)
```

Look for attC site with `cmsearch -max` option which remove all heuristic filters. As this option make the algorithm way slower, we only run it in the region around a hit. We call it `local_max` or `eagle_eyes`.

Default hit



Updated hit



Parameters

- **integrations** (list of `Integron` objects.) – the integrations may contain or not `attC` or `intI`.
- **replicon** (`Bio.Seq.SeqRecord` object.) – replicon where the integrations were found (genomic fasta file).

- **distance_threshold** (*int*) – the maximal distance between 2 elements to aggregate them.
- **evalute_attc** (*float*) – evalute threshold to filter out hits above it.
- **model_attc_path** (*str*) – path to the attc model (Covariance Matrix).
- **max_attc_size** (*int*) – maximum value for the attC size.
- **min_attc_size** (*int*) – minimum value for the attC size.
- **circular** (*bool*) – True if replicon is circular, False otherwise.
- **out_dir** (*str*) – The directory where to write results used indirectly by some called functions as `infernai.local_max()` or `infernai.expand`.
- **cmsearch_bin** (*str*) – The path to the `cmsearch_bin` binary to use
- **cpu** (*int*) – call `local_max` with the right number of cpu

Returns

Return type `pd.DataFrame` object

`integron_finder.attc.search_attc` (*attc_df*, *keep_palindromes*, *dist_threshold*,
replicon_size, *rep_topology*)

Parse the attc data set (sorted along start site) for the given replicon and return list of arrays. One array is composed of attC sites on the same strand and separated by a distance less than `dist_threshold`.

Parameters

- **attc_df** (`pandas.DataFrame`) –
- **keep_palindromes** (*bool*) – True if the palindromes must be kept in attc result, False otherwise
- **dist_threshold** (*int*) – the maximal distance between 2 elements to aggregate them
- **replicon_size** (*int*) – the replicon number of base pair
- **rep_topology** (*str*) – the replicon topology should be ‘lin’ or ‘circ’

Returns a list attC sites found on replicon

Return type list of `pandas.DataFrame` objects

config

class integron_finder.config.**Config**(args)

Config object hold values issue from command lines

__init__(args)

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

__weakref__

list of weak references to the object (if defined)

property default_topology

The default topology available values are: 'circ' for circular or 'lin' for linear.

property func_annot_path

The canonical absolute path to the directory containing file needed for the functional annotation. It does not take in account the argument passed via the command line.

property input_dir

The absolute path to the directory where is located the replicon

property input_seq_path

The absolute path to the input file

property log_level

Returns the level to apply to loggers. $0 \leq \text{level} \leq 50$

Return type int

property model_attc_name

The name of the attc model

property model_attc_path

The absolute path to the attC model file

property model_dir

The absolute path to the directory containing the models

property model_integrase

The absolute path to the integrase model file

property model_len

Returns The length of the attc model (corresponding to CLEN field).

Raises IOError if model_attc_path does match an existing file RuntimeError if the file does not contain CLEN field.

property model_phage_int

The absolute path to the phage-integrase model file

property outdir

The absolute path where to write the results directory

property result_dir

The absolute path to results directory

tmp_dir (*replicon_id*)

The absolute path of the tmp results dir.

hmm

```
integron_finder.hmm.read_hmm(replicon_id, prot_db, infile, cfg, evaluate=1.0,  
                             coverage=0.5)
```

Function that parse hmmer –out output and returns a pandas DataFrame filter output by evaluate and coverage. (Being % of the profile aligned)

Parameters

- **replicon_id** (*str*) – the id of the replicon
- **prot_db** (*integron_finder.prot_db.ProteinDB* object.) – The protein database corresponding to the replicon translation
- **infile** (*str*) – the hmm output (in tabulated format) to parse
- **cfg** (*integron_finder.config.Config* object.) – the config
- **evaluate** (*float*) – filter out hits with evaluate greater tha evaluate.
- **coverage** (*float*) – filter out hits with coverage under coverage (% of the profile aligned)

Returns

data Frame with columns:

”Accession_number”, ”query_name”, ”ID_query”, ”ID_prot”, ”strand”,
”pos_beg”, ”pos_end”, ”evaluate”
each row correspond to a hit.

Return type a `pandas.DataFrame`

```
integron_finder.hmm.scan_hmm_bank(path)
```

Parameters **path** (*str*) –

- if the path is a dir: return all files ending with .hmm in the dir

- if the path is a file: parse the file, each line must be an expression (glob) pointing to hmm files

Returns lists of hmm files to consider for annotation

Return type list of str

Raises **IOError** – if the path does not exists

infernai

```
integron_finder.infernal.expand(replicon, window_beg, win-
                                dow_end, max_elt, circular,
                                dist_threshold, model_attc_path,
                                max_attc_size=200, min_attc_size=40,
                                evaluate_attc=1.0, search_left=False,
                                search_right=False, out_dir='.', cpu=1,
                                cmsearch_bin='cmsearch')
```

for a given element, we can search on the left hand side (if integrase is on the right for instance) or right hand side (opposite situation) or both side (only integrase or only attC sites)

Parameters

- **replicon** (a `Bio.Seq.SeqRecord` object.) – The Replicon to annotate
- **window_beg** (`int`) – start of window to search for attc (position of protein)
- **window_end** (`int`) – end of window to search for attc (position of protein)
- **max_elt** (`pandas.DataFrame` object) – DataFrame with columns:

Accession_number	cm_attC	cm_debut	cm_fin	pos_
↪beg	pos_end	sens	evaluate	

and each row is an occurrence of attc site

- **df_max** (`pandas.DataFrame` object) – DataFrame with columns

Accession_number	cm_attC	cm_debut	cm_fin	pos_
↪beg	pos_end	sens	evaluate	

and each row is an occurrence of attc site

- **circular** (`bool`) – True if replicon topology is circular otherwise False.

- **dist_threshold** (*int*) – Two elements are aggregated if they are distant of dist_threshold [4kb] or less
- **max_attc_size** (*int*) – The maximum value for the attC size
- **min_attc_size** (*int*) – The minimum value for the attC size
- **model_attc_path** (*str*) – the path to the attc model file
- **evaluate_attc** (*float*) – evaluate threshold to filter out hits above it
- **search_left** (*bool*) – trigger the local_max search on the left of the already detected element
- **search_right** (*bool*) – trigger the local_max search on the right of the already detected element
- **out_dir** (*str*) – The path to directory where to write results
- **cpu** (*int*) – the number of cpu use by expand
- **cmsearch_bin** (*str*) – the path to the *cmsearch* binary to use

Returns a copy of max_elt with attC hits

Return type pandas.DataFrame object

```
integron_finder.infernal.find_attc(replicon_path, replicon_id, cm-  
                                  search_path, out_dir, model_attc,  
                                  incE=1.0, cpu=1)
```

Call cmsearch to find attC sites in a single replicon.

Parameters

- **replicon_path** (*str*) – the path of the fasta file representing the replicon to analyse.
- **replicon_id** (*str*) – the id of the replicon to analyse.
- **cmsearch_path** (*str*) – the path to the cmsearch executable.
- **out_dir** (*str*) – the path to the directory where cmsearch outputs will be stored.
- **model_attc** (*str*) – path to the attc model (Covariance Matrix).
- **incE** (*float*) – consider sequences \leq this E-value threshold as significant (to get the alignment with -A)
- **cpu** (*int*) – the number of cpu used by cmsearch.

Returns None, the results are written on the disk.

Raises **RuntimeError** – when cmsearch run failed.

```
integron_finder.infernal.local_max(replicon, window_beg, win-
                                   dow_end, model_attc_path,
                                   strand_search='both',
                                   evaluate_attc=1.0, max_attc_size=200,
                                   min_attc_size=40, cm-
                                   search_bin='cmsearch', out_dir='.',
                                   cpu=1)
```

Parameters

- **replicon** (`Bio.Seq.SeqRecord` object.) – The replicon to analyse
- **window_beg** (`int`) – Start of window to search for attc (position of protein).
- **window_end** (`int`) – End of window to search for attc (position of protein).
- **model_attc_path** (`str`) – The path to the covariance model for attc (eg: attc_4.cm) used by cmsearch to find attC sites
- **strand_search** (`str`) – The strand on which to looking for attc. Available values:
 - 'top': Only search the top (Watson) strand of target sequences.
 - 'bottom': Only search the bottom (Crick) strand of target sequences
 - 'both': search on both strands
- **evaluate_attc** (`float`) – evaluate threshold to filter out hits above it
- **max_attc_size** (`int`) – The maximum value fot the attC size
- **min_attc_size** (`int`) – The minimum value fot the attC size
- **cmsearch_bin** (`str`) – The path to cmsearch
- **out_dir** (`str`) – The path to directory where to write results
- **cpu** (`int`) – The number of cpu used by cmsearch

Returns `DataFrame` with same structure as the `DataFrame` returns by `read_infernal()` where position are converted on position on replicon and attc are filtered by evaluate, min_attc_size, max_attc_size also write a file with intermediate results <replicon_id>_subseq_attc_table_end.res this file store the local_max results before filtering by max_attc_size and min_attc_size

Return type `pandas.DataFrame` object

```
integron_finder.infernal.read_infernal(infile, replicon_id,  
                                       len_model_attc, value=1,  
                                       size_max_attc=200,  
                                       size_min_attc=40)
```

Function that parse cmsearch -tblout output and returns a pandas DataFrame

Parameters

- **infile** (*str*) – the path to the output of cmsearch in tabulated format (-tblout)
- **replicon_id** (*str*) – the id of the replicon are the integrons were found.
- **len_model_attc** (*int*) – the length of the attc model
- **value** (*float*) – evaluate threshold to filter out hits above it
- **size_max_attc** (*int*) – The maximum value for the attC size
- **size_min_attc** (*int*) – The minimum value for the attC size

Returns

table with columns:

”Accession_number”, ”cm_attC”, ”cm_debut”, ”cm_fin”, ”pos_beg”,
”pos_end”, ”sens”, ”value”
and each row is a hit that match the attc covariance model.

Return type pandas.DataFrame object

integrase

```
integron_finder.integrase.find_integrase(replicon_id, prot_file, out_dir,  
                                          cfg)
```

Call Prodigal for Gene annotation and hmmer to find integrase, either with phage_int HMM profile or with intI profile.

Parameters

- **replicon_id** (*str*) – The Replicon identifier to search integrase into
- **prot_file** (*str*) – the path to the fasta file containing the translation of the replicon.
- **out_dir** (*str*) – the relative path to the directory where prodigal outputs will be stored

- **cfg** (a *integron_finder.config.Config* object) – the configuration

Returns None, the results are written on the disk

integron

class *integron_finder.integron.Integron* (*replicon*, *cfg*)

Integron object represents an object composed of an integrase, attC sites and gene cassettes. Each element is characterized by their coordinates in the replicon, the strand (+ or -), the ID of the gene (except attC). The object Integron is also characterized by the ID of the replicon.

__init__ (*replicon*, *cfg*)

Parameters

- **replicon** (a *Bio.Seq.SeqRecord* object) – The replicon where integrons has been found
- **cfg** (a *integron_finder.config.Config* object) – the configuration

__weakref__

list of weak references to the object (if defined)

add_attC (*pos_beg_attC*, *pos_end_attC*, *strand*, *evaluate*, *model*)

Adds attC site to the Integron object.

Parameters

- **pos_beg_attC** (*int*) – the position on the replicon of the beginning attc site
- **pos_end_attC** (*int*) – the position on replicon of the end of the attc site
- **strand** (*int*) – the strand where is found the attc 1 for forward, -1 for reverse
- **evaluate** (*float*) – the evaluate associated to this attc site
- **model** (*str*) – the name of attc model (for instance attc4)

add_attI ()

Looking for AttI sites and add them to this integron.

add_integrase (*pos_beg_int*, *pos_end_int*, *id_int*, *strand_int*, *evaluate*, *model*)

Adds integrases to the integron. Should be called once.

Parameters

- **pos_beg_int** (*int*) – the position on the replicon of the beginning integrase site
- **pos_end_int** (*int*) – the position on replicon of the end of the integrase site
- **id_int** (*str*) – The protein id corresponding to the integrase
- **strand_int** (*int*) – the strand where is found the attc 1 for forward, -1 for reverse
- **eval** (*float*) – the eval associated to this attc site
- **model** (*str*) – the name of integrase model (for instance intersection_tyr_intI)

add_promoter ()

Looks for known promoters if they exists within your integrons element. It takes 1s for about 13kb.

add_proteins (*prot_db*)

Parameters **prot_db** (*integron.prot_db.ProteinDB* object.) – The protein db corresponding to the translation of the replicon

describe ()

Returns

DataFrame describing the integron object The columns are:

”pos_beg”, ”pos_end”, ”strand”, ”eval”, ”type_elt”, ”model”, ”distance_2attC”, ”annotation”, ”considered_topology”

draw_integron (*file=None*)

Represent the different element of the integrons if file is provide save the drawing on the file otherwise display it on screen.

Parameters **file** (*str*) – the path to save the integron schema (in pdf format)

has_attC ()

Returns True if integron has attc sites False otherwise.

has_integrase ()

Returns True if integron has integrase False otherwise.

type ()

Returns

The type of the integrons:

- ’complete’ : Have one integrase and at least one attC

- 'CALIN' : Have at least one attC
- 'In0' : Just an integrase intI

Return type str

```
integron_finder.integron.find_integron(replicon, prot_db, attc_file,  
                                       intI_file, phageI_file, cfg)
```

Function that looks for integrons given rules :

- presence of intI
- presence of attC
- d(intI-attC) <= 4 kb
- d(attC-attC) <= 4 kb

It returns the list of all integrons, be they complete or not. found in attC files + integrases file which are formatted as follow : intI_file : Accession_number ID_prot strand pos_beg pos_end evalua attc_file : Accession_number attC cm_debut cm_fin pos_beg pos_end sens evalua

Parameters

- **replicon** (Bio.Seq.SeqRecord object) – the name of the replicon
- **prot_db** (a *integron_finder.prot_db.ProteinDB* object.) – the protein database corresponding to the replicon translation
- **attc_file** (path to cmsearch output or pd.DataFrame) – the output of cmsearch or the result of parsing of this file by read_infernal
- **intI_file** (*str*) – the output of hmmsearch with the integrase model
- **phageI_file** (*str*) – the output of hmmsearch with the phage model
- **cfg** (a *integron_finder.config.Config* object) – configuration

Returns list of all integrons, be they complete or not

Retype list of *Integron* object

prot_db

The `prot_db` module contains classes to handle protein file and protein description which can be either generate by Prodigal or Provide by Gembase. It also provide an interface to abstract the way to get protein sequences and descriptions

```
class integron_finder.prot_db.GembaseDB(replicon, cfg, gem-  
                                         base_path=None,  
                                         prot_file=None)
```

Implements *ProteinDB* from a Gembase. Managed proteins from Proteins directory corresponding to a replicon/contig

```
__getitem__ (prot_seq_id)
```

Parameters `prot_seq_id` (*str*) – the id of a protein sequence

Returns The Sequence corresponding to the `prot_seq_id`.

Return type `Bio.SeqRecord` object

```
__init__ (replicon, cfg, gembase_path=None, prot_file=None)
```

Parameters

- **replicon** (`Bio.SeqRecord` object with a extra attribute `path`) – The replicon used to create ProteinDB (protein files and extra information)
- **cfg** (`integron_finder.config.Config` object) – The integron_finder configuration
- **prot_file** – The path to a protein file in fasta format which is the translation of the replicon

Warning: The replicon is a modified `Bio.SeqRecord` object. The attribute `path` must be injected in the object This attribute represent the path to a fasta file representing this replicon

```
__iter__ ()
```

Returns a generator which iterate on the protein `seq_id` which constitute the contig.

Return type generator

```
_find_gembase_file_basename (gembase_path, input_seq_path)
```

from the input file name, try to retrieve the basename which is used in gembase This specially useful when IF is run in parallel. The input sequence is split in chunks and treat in parallel. But in this case the name of the chunk does not math neither the `lstinfo`

file nor the protein file. So this method try retrieve the original basenane without extension for instance:

ACBA.0917.00019.fna	=> ACBA.0917.00019
ACBA.0917.00019.0001.fna	=> ACBA.0917.00019
ESCO001.C.00001.C001.fst	=> ESCO001.C.00001.C001
ESCO001.C.00001.C001_chunk_1.fst	=> ESCO001.C.00001.C001

Returns the gemabse basenane corresponding to the input file

Return type string

`_make_protfile()`

Create fasta file with protein corresponding to this sequence, from the corresponding Gembase protfile This step is necessary because in Gembase Draft One nucleic file can contains several contigs, but all proteins are in the same file.

Returns the path of the created protein file

Return type str

`_parse_lst()`

Parse the LSTINFO file and extract information specific to the replicon :return: *class:pandas.DataFrame` object*

`static gembase_complete_parser(lst_path, sequence_id)`

Parameters

- **`lst_path`** (*str*) – the path of of the LSTINFO file Gembase Complet
- **`sequence_id`** (*str*) – the id of the genomic sequence to analyse

Returns the information related to the ‘valid’ CDS corresponding to the `sequence_id`

Return type *class:pandas.DataFrame` object*

`static gembase_draft_parser(lst_path, replicon_id)`

Parameters

- **`lst_path`** (*str*) – the path of of the LSTINFO file from a Gembase Draft
- **`sequence_id`** (*str*) – the id of the genomic sequence to analyse

Returns the information related to the ‘valid’ CDS corresponding to the `sequence_id`

Return type *class:pandas.DataFrame` object*

static `gembase_sniffer` (*lst_path*)

Detect the type of gembase :param str *lst_path*: the path to the LSTINFO file corresponding to the nucleic sequence :returns: either ‘Complet’ or ‘Draft’

get_description (*gene_id*)

Parameters `gene_id` (*str*) – a protein/gene identifier

Returns The description of the protein corresponding to the *gene_id*

Return type *SeqDesc* namedtuple object

Raises

- **IntegronError** – when *gene_id* is not a valid Gembase gene identifier
- **KeyError** – if *gene_id* is not found in GembaseDB instance

class `integron_finder.prot_db.ProdigalDB` (*replicon*, *cfg*,
prot_file=None)

Creates proteins from Replicon/contig using prodigal and provide facilities to access them.

__getitem__ (*prot_seq_id*)

Parameters `prot_seq_id` (*str*) – the id of a protein sequence

Returns The Sequence corresponding to the *prot_seq_id*.

Return type `Bio.SeqRecord` object

__iter__ ()

Returns a generator which iterate on the protein *seq_id* which constitute the contig.

Return type generator

_make_protfile ()

Use *prodigal* to generate proteins corresponding to the replicon

Returns the path of the created protfile

Return type str

get_description (*gene_id*)

Parameters `gene_id` (*str*) – a protein/gene identifier

Returns The description of the protein corresponding to the *gene_id*

Return type *SeqDesc* namedtuple object

Raises

- **IntegronError** – when *gene_id* is not a valid Gembase gene identifier

- **KeyError** – if `gene_id` is not found in ProdigalDB instance

class `integron_finder.prot_db.ProteinDB` (*replicon, cfg, prot_file=None*)

AbstractClass defining the interface for ProteinDB. ProteinDB provide an abstraction and a way to access to proteins corresponding to the replicon/contig CDS.

`__getitem__` (*prot_seq_id*)

Parameters `prot_seq_id` (*str*) – the id of a protein sequence

Returns The Sequence corresponding to the `prot_seq_id`.

Return type `Bio.SeqRecord` object

Raises **KeyError** – when `seq_id` does not match any sequence in DB

`__init__` (*replicon, cfg, prot_file=None*)

Parameters

- **replicon** –
- **cfg** –
- **prot_file** –

`__iter__` ()

Returns a generator which iterate on the protein `seq_id` which constitute the contig.

Return type generator

`__weakref__`

list of weak references to the object (if defined)

`_make_db` ()

Returns an index of the sequence contains in protfile corresponding to the replicon

abstract `_make_protfile` ()

Create fasta file with protein corresponding to the nucleic sequence (replicon)

Returns the path of the created protein file

Return type `str`

abstract `get_description` (*gene_id*)

Parameters `gene_id` (*str*) – a protein/gene identifier

Returns The description of the protein corresponding to the `gene_id`

Return type `SeqDesc` namedtuple object

Raises

- **IntegronError** – when `gene_id` is not a valid Gembase gene identifier
- **KeyError** – if `gene_id` is not found in GembaseDB instance

property `protfile`

Returns The absolute path to the protein file corresponding to contig id

Return type `str`

class `integron_finder.prot_db.SeqDesc` (*id, strand, start, stop*)

__getnewargs__ ()

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

static **__new__** (*_cls, id, strand, start, stop*)

Create new instance of SeqDesc(id, strand, start, stop)

__repr__ ()

Return a nicely formatted representation string

_asdict ()

Return a new dict which maps field names to their values.

classmethod **_make** (*iterable*)

Make a new SeqDesc object from a sequence or iterable

_replace (***kws*)

Return a new SeqDesc object replacing specified fields with new values

id

Alias for field number 0

start

Alias for field number 2

stop

Alias for field number 3

strand

Alias for field number 1

results

The *results* module contains functions to handle the final reports.

- merging results of each sequence
- generate a summary
- or filter the calin

```
integron_finder.results._log = <Logger integron_finder.results (WARNING)>  
    utilities to manage results
```

```
integron_finder.results.filter_calin(result, threshold=2)  
    filter integron report, remove 'CALIN' integron where number of attC sites is lower than  
    threshold.
```

Parameters

- **result** (pandas.DataFrame object) – the output of *integrations_report()*
- **threshold** (int) – the integron CALIN with less attc site than *threshold* are removed

Returns filtered integron report

Return type pandas.DataFrame object

```
integron_finder.results.integrations_report(integrations)
```

Parameters **integrations** (list of *integron_finder.integron.Integron* object.) – list of integrations used to generate a report

Returns a report off all integrations from a replicon

Return type

pandas.DataFrame object. this dataframe have following columns:

"ID_integron", "ID_replicon", "element", "pos_beg", "pos_end", "strand",
"evaluate", "type_elt", "annotation", "model", "type", "default", "distance_2attC", "considered_topology"

```
integron_finder.results.merge_results(*results_file)
```

Parameters **results_file** (str) – The path of the files to merge. The files can be parsed by pandas as DataFrame and have the same columns. It is used to merge the integrations files (.integrations) or summary files (.summary) from different replicons.

Returns all results aggregated in one pandas.DataFrame object. if there is no results to merge, return an empty DataFrame.

Return type a `pandas.DataFrame` object.

`integron_finder.results.summary(result)`

Create a summary of an integron report. Count the number of ‘CALIN’, ‘In0’ or ‘complete’ for each replicon.

Parameters **result** – the integron to summarize

Returns a `pandas.DataFrame` object. with columns ‘ID_replicon’, ‘ID_integron’, ‘complete’, ‘In0’, ‘CALIN’

topology

class `integron_finder.topology.Topology` (*default, topology_file=None*)

Class to parse and handle replicons topologies

`__getitem__` (*replicon_id*)

Parameters **replicon_id** (*str*) – The id of the replicon.

Returns the topology for the replicon corresponding to the `replicon_id`

`__init__` (*default, topology_file=None*)

Parameters

- **default** (*str*) – the default topology
- **topology_file** – the path to the file where topology for replicon are specified

`__weakref__`

list of weak references to the object (if defined)

`_parse` (*topology_file*)

Parse a topology file where topology is specified for replicons on each line a topology is specified for a replicon the syntax of each line is

`replicon_id topology`

the allowed value for topology are ‘circ’, ‘circular’, ‘lin’, ‘linear’

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

`_parse_topology` (*topo*)

Parse a field topology in topology file the authorized values are circular, linear or circ, lin, or in uppercase

Parameters **topo** – the field corresponding to topology in topology file

Returns the topology in “normed” format ‘circ’ or ‘lin’

Return type `str`

utils

class `integron_finder.utils.FastaIterator` (*path*, *replicon_name=None*,
dist_threshold=4000, *alphabet=None*)

Allow to parse over a multi fasta file, and iterate over it

Warning: The sequences order is not guarantee.

`__init__` (*path*, *replicon_name=None*, *dist_threshold=4000*, *alphabet=None*)

Parameters

- **path** (*str*) – The path to the file containing the sequences.
- **alphabet** (*Bio.SeqIUPAC member*) – The authorized alphabet
- **replicon_name** (*str*) – The name of the replicon, if this specify all sequence.name will have this value
- **dist_threshold** (*int*) – The minimum length for a replicon to be considered as circular. Under this threshold even the provided topology is ‘circular’ the computation will be done with a ‘linear’ topology.

`__len__` ()

Returns The number of sequence in the file

`__next__` ()

Returns The next sequence (the order of sequences is not guaranteed).

Return type a `Bio.SeqRecord` object or `None` if the sequence is not compliant with the alphabet.

`__weakref__`

list of weak references to the object (if defined)

`_check_seq_alphabet_compliance` (*seq*)

Parameters **seq** (`Bio.Seq.Seq` instance) – the sequence to check

Returns True if sequence letters are a subset of the alphabet, False otherwise.

`_set_topologies` (*topologies*)

Parameters **topologies** (`integron_finder.Topology` onject) –

Returns

`integron_finder.utils.get_name_from_path` (*path*)

Parameters **path** – The path to extract name for instance the fasta file to the replicon

Returns the name of replicon for instance if path = /path/to/replicon.fasta name = replicon

`integron_finder.utils.log_level(verbose, quiet)`

Returns the level to apply to loggers. $0 \leq \text{level} \leq 50$

Return type int

`integron_finder.utils.make_multi_fasta_reader(alphabet)`

fasta generator maker

Parameters **alphabet** – the alphabet store in the fasta generator closure

Returns generator to iterate on the fasta file in the same order as in fasta file

`integron_finder.utils.model_len(path)`

Parameters **path** (*str*) – the path to the covariance model file

Returns the length of the model

Return type int

`integron_finder.utils.read_multi_prot_fasta(path)`

Parameters **path** – The path to the fasta file.

Returns The sequence parsed.

Return type `Bio.SeqRecord.SeqRecord` object.

INDICES AND TABLES

- genindex
- modindex
- search

PYTHON MODULE INDEX

i

- `integron_finder.annotation`, 33
- `integron_finder.attc`, 34
- `integron_finder.config`, 36
- `integron_finder.hmm`, 37
- `integron_finder.infernal`, 38
- `integron_finder.integrase`, 41
- `integron_finder.integron`, 42
- `integron_finder.prot_db`, 45
- `integron_finder.results`, 50
- `integron_finder.topology`, 51
- `integron_finder.utils`, 52

Symbols

<code>__getitem__()</code>	(<i>integron_finder.prot_db.GembaseDB method</i>), 45	<code>__getitem__()</code>	(<i>integron_finder.prot_db.ProdigalDB method</i>), 47	<code>__getitem__()</code>	(<i>integron_finder.prot_db.ProteinDB method</i>), 48	<code>__getitem__()</code>	(<i>integron_finder.topology.Topology method</i>), 51	<code>__getnewargs__()</code>	(<i>integron_finder.prot_db.SeqDesc method</i>), 49	<code>__init__()</code>	(<i>integron_finder.config.Config method</i>), 36	<code>__init__()</code>	(<i>integron_finder.integron.Integron method</i>), 42	<code>__init__()</code>	(<i>integron_finder.prot_db.GembaseDB method</i>), 45	<code>__init__()</code>	(<i>integron_finder.prot_db.ProteinDB method</i>), 48	<code>__init__()</code>	(<i>integron_finder.topology.Topology method</i>), 51	<code>__init__()</code>	(<i>integron_finder.utils.FastaIterator method</i>), 52	<code>__iter__()</code>	(<i>integron_finder.prot_db.GembaseDB method</i>), 45	<code>__iter__()</code>	(<i>integron_finder.prot_db.ProdigalDB method</i>), 47	<code>__iter__()</code>	(<i>integron_finder.prot_db.ProteinDB method</i>), 48	<code>__len__()</code>	(<i>integron_finder.utils.FastaIterator method</i>), 52	<code>__new__()</code>	(<i>integron_finder.prot_db.SeqDesc static method</i>), 49	<code>__next__()</code>	(<i>integron_finder.utils.FastaIterator method</i>), 52	<code>__repr__()</code>	(<i>integron_finder.prot_db.SeqDesc method</i>), 49	<code>__weakref__</code>	(<i>integron_finder.config.Config attribute</i>), 36	<code>__weakref__</code>	(<i>integron_finder.integron.Integron attribute</i>), 42	<code>__weakref__</code>	(<i>integron_finder.prot_db.ProteinDB attribute</i>), 48	<code>__weakref__</code>	(<i>integron_finder.topology.Topology attribute</i>), 51	<code>__weakref__</code>	(<i>integron_finder.utils.FastaIterator attribute</i>), 52	<code>__asdict__()</code>	(<i>integron_finder.prot_db.SeqDesc method</i>), 49
----------------------------	---	----------------------------	--	----------------------------	---	----------------------------	---	-------------------------------	---	-------------------------	---	-------------------------	---	-------------------------	---	-------------------------	---	-------------------------	---	-------------------------	---	-------------------------	---	-------------------------	--	-------------------------	---	------------------------	---	------------------------	--	-------------------------	---	-------------------------	---	--------------------------	--	--------------------------	--	--------------------------	--	--------------------------	--	--------------------------	--	---------------------------	---

[_check_seq_alphabet_compliance\(\)](#) (*integron_finder.utils.FastaIterator method*), 52
[_find_gembase_file_basename\(\)](#) (*integron_finder.prot_db.GembaseDB method*), 45
[_log](#) (*in module integron_finder.results*), 50
[_make\(\)](#) (*integron_finder.prot_db.SeqDesc class method*), 49
[_make_db\(\)](#) (*integron_finder.prot_db.ProteinDB method*), 48
[_make_protfile\(\)](#) (*integron_finder.prot_db.GembaseDB method*), 46
[_make_protfile\(\)](#) (*integron_finder.prot_db.ProdigalDB method*), 47
[_make_protfile\(\)](#) (*integron_finder.prot_db.ProteinDB method*), 48
[_parse\(\)](#) (*integron_finder.topology.Topology method*), 51
[_parse_lst\(\)](#) (*integron_finder.prot_db.GembaseDB method*), 46
[_parse_topology\(\)](#) (*integron_finder.topology.Topology method*), 51
[_replace\(\)](#) (*integron_finder.prot_db.SeqDesc method*), 49
[_set_topologies\(\)](#) (*integron_finder.utils.FastaIterator method*), 52

A
[add_attC\(\)](#) (*integron_finder.integron.Integron method*), 42
[add_attI\(\)](#) (*integron_finder.integron.Integron method*), 42
[add_feature\(\)](#) (*in module integron_finder.annotation*), 33

[add_integrase\(\)](#) (*integron_finder.integron.Integron method*), 42
[add_promoter\(\)](#) (*integron_finder.integron.Integron method*), 43
[add_proteins\(\)](#) (*integron_finder.integron.Integron method*), 43

C
[Config](#) (*class in integron_finder.config*), 36

D
[default_topology\(\)](#) (*integron_finder.config.Config property*), 36
[describe\(\)](#) (*integron_finder.integron.Integron method*), 43
[draw_integron\(\)](#) (*integron_finder.integron.Integron method*), 43

E
[expand\(\)](#) (*in module integron_finder.infernal*), 38

F
[FastaIterator](#) (*class in integron_finder.utils*), 52
[filter_calin\(\)](#) (*in module integron_finder.results*), 50
[find_attc\(\)](#) (*in module integron_finder.infernal*), 39
[find_attc_max\(\)](#) (*in module integron_finder.attc*), 34
[find_integrase\(\)](#) (*in module integron_finder.integrase*), 41
[find_integron\(\)](#) (*in module integron_finder.integron*), 44
[func_annot\(\)](#) (*in module integron_finder.annotation*), 33
[func_annot_path\(\)](#) (*integron_finder.config.Config property*), 36

G

`gembase_complete_parser()` (*integron_finder.prot_db.GembaseDB static method*), 46

`gembase_draft_parser()` (*integron_finder.prot_db.GembaseDB static method*), 46

`gembase_sniffer()` (*integron_finder.prot_db.GembaseDB static method*), 46

`GembaseDB` (class in *integron_finder.prot_db*), 45

`get_description()` (*integron_finder.prot_db.GembaseDB method*), 47

`get_description()` (*integron_finder.prot_db.ProdigalDB method*), 47

`get_description()` (*integron_finder.prot_db.ProteinDB method*), 48

`get_name_from_path()` (in module *integron_finder.utils*), 52

H

`has_attC()` (*integron_finder.integron.Integron method*), 43

`has_integrase()` (*integron_finder.integron.Integron method*), 43

I

`id` (*integron_finder.prot_db.SeqDesc attribute*), 49

`input_dir()` (*integron_finder.config.Config property*), 36

`input_seq_path()` (*integron_finder.config.Config property*), 36

`Integron` (class in *integron_finder.integron*), 42

`integron_finder.annotation` module, 33

`integron_finder.attc`

module, 34

`integron_finder.config` module, 36

`integron_finder.hmm` module, 37

`integron_finder.infernal` module, 38

`integron_finder.integrase` module, 41

`integron_finder.integron` module, 42

`integron_finder.prot_db` module, 45

`integron_finder.results` module, 50

`integron_finder.topology` module, 51

`integron_finder.utils` module, 52

`integrations_report()` (in module *integron_finder.results*), 50

L

`local_max()` (in module *integron_finder.infernal*), 39

`log_level()` (in module *integron_finder.utils*), 53

`log_level()` (*integron_finder.config.Config property*), 36

M

`make_multi_fasta_reader()` (in module *integron_finder.utils*), 53

`merge_results()` (in module *integron_finder.results*), 50

`model_attc_name()` (*integron_finder.config.Config property*), 36

`model_attc_path()` (*integron_finder.config.Config property*), 36

`model_dir()` (*integron_finder.config.Config property*), 36

`model_integrase()` (*integron_finder.config.Config property*),

36

`model_len()` (in module `integron_finder.utils`), 53

`model_len()` (`integron_finder.config.Config` property), 36

`model_phage_int()` (`integron_finder.config.Config` property), 36

module

- `integron_finder.annotation`, 33
- `integron_finder.attc`, 34
- `integron_finder.config`, 36
- `integron_finder.hmm`, 37
- `integron_finder.infernal`, 38
- `integron_finder.integrase`, 41
- `integron_finder.integron`, 42
- `integron_finder.prot_db`, 45
- `integron_finder.results`, 50
- `integron_finder.topology`, 51
- `integron_finder.utils`, 52

O

`outdir()` (`integron_finder.config.Config` property), 36

P

`ProdigalDB` (class in `integron_finder.prot_db`), 47

`ProteinDB` (class in `integron_finder.prot_db`), 48

`protfile()` (`integron_finder.prot_db.ProteinDB` property), 49

R

`read_hmm()` (in module `integron_finder.hmm`), 37

`read_infernal()` (in module `integron_finder.infernal`), 40

`read_multi_prot_fasta()` (in module `integron_finder.utils`), 53

`result_dir()` (`integron_finder.config.Config` property), 37

S

`scan_hmm_bank()` (in module `integron_finder.hmm`), 37

`search_attc()` (in module `integron_finder.attc`), 35

`SeqDesc` (class in `integron_finder.prot_db`), 49

`start` (`integron_finder.prot_db.SeqDesc` attribute), 49

`stop` (`integron_finder.prot_db.SeqDesc` attribute), 49

`strand` (`integron_finder.prot_db.SeqDesc` attribute), 49

`summary()` (in module `integron_finder.results`), 51

T

`tmp_dir()` (`integron_finder.config.Config` method), 37

`Topology` (class in `integron_finder.topology`), 51

`type()` (`integron_finder.integron.Integron` method), 43