

## Overview

The software package HiFiX implements the novel algorithm for **High Fidelity Clustering of Sequences**.

To tackle the challenge of finding proteins families, we model the all-against-all comparison between proteins by a similarity network.

HiFiX combines **network topology** analysis where sequence similarity is seen as a social relationship, **multiple alignment** quality measurement and model **selection theory**.

HiFiX supports **multiprocessing** and is therefore fast enough to be used in practice on large amounts of data.

HiFiX is already included in the experimental pipeline for

[HOGENOM](#) ↗

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## LICENCE

SiLiX is licensed under the  
[General Public License](#)

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## DOWNLOAD

You can download the latest version  
[HERE \(ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/\)](ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/)

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## SYSTEM REQUIREMENTS & DEPENDENCIES

*HiFiX was succesfully tested on Linux (Ubuntu up to 14.04, Debian Wheezy 7.0) and Mac OSX (Darwin 10.5.8)*

*HiFiX does **not work with Python 3.x**, **Python 2.X required Python modules** (already installed by default in Python >=2.7):*

- > NumPy
- > [argparse](#)
- > [subprocess](#)
- > [multiprocessing](#)

**and**

- > [BioPython](#)

(for local install, set the `PYTHONPATH` variable to `/path_to/module`)

**Auxiliary software packages** (installation required)

> [SiLiX \(http://lbbe.univ-lyon1.fr/Download,3009.html?lang=en\)](http://lbbe.univ-lyon1.fr/Download,3009.html?lang=en)

(version >= 1.2.10)

> [MAFFT](#) 

> [HMMER3](#) 

> [Louvain](#) 

: for this program, there is no proper install procedure. First uncompress this

[archive \(ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/Community\\_BGLL\\_CPP/Community\\_BGLL\\_CPP.zip\)](ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/Community_BGLL_CPP/Community_BGLL_CPP.zip)

and go to the *Community\_BGLL\_CPP* directory. Compile with *make* (NB: on MacOS only, create a dummy file with *touch malloc.h*, and compile with *make CFLAGS+=-I.*). Then we suggest three solutions:

- > [RECOMMENDED] copy manually the binaries *community*, *convert* and *hierarchy* in your PATH (in */usr/local/bin* for example)
- > add the */path\_to/Community\_BGLL\_CPP* directory to your PATH (export *PATH=\$PATH:/path\_to/Community\_BGLL\_CPP*)
- > [EASY] pass the */path\_to/Community\_BGLL\_CPP* directory to HiFiX by command line (in this way, the above test procedure will fail... don't panic)

## INSTALLATION

Compilation and installation are compliant with the Python standard procedure

```
tar zxvf hifix-x.x.x.tar.gz
cd hifix-x.x.x
python setup.py test
python setup.py install
```

(for local install, add the flag *--prefix /path\_to/hifix* and set *PYTHONPATH= /path\_to/hifix/lib/python2.x/site-packages*)

## PROGRAMS USE

(see also Tutorial section)

### ➤ THE EASY WAY (most users):

To get information or help:

```
hifix --help
```

The user provides a fasta file FASTAFILE (**\*less than 256 characters per line\*** and no "U" character [to be replaced by "X"]), the result file of

[SiLiX](http://lbbe.univ-lyon1.fr/silix) (<http://lbbe.univ-lyon1.fr/silix>)

clustering FNODESFILE and the network file NETFILE obtained with SiLiX :

```
hifix <FASTAFILE> <NETFILE> <FNODESFILE>
```

If using a multiprocessor machine with NBPROCS cores, it is valuable to specify the option :

```
hifix -t <NBPROCS> ...
```

If you have a /dev/shm directory (shared memory), it is recommended to use it (gains of performance) :

```
hifix -d /dev/shm ...
```

## OUTPUT FORMAT

List of pairs in format "family\_id sequence\_id" where :

- sequence\_id are those of FASTAFILE
- family\_id are build from the prefix of FASTAFILE (prefix.fasta) followed by a unique tag such as
  - "\_i\_j" if family j was deduced from SiLiX pre-family i
  - "\_i" if SiLiX pre-family i was conserved

Exple:

```
seq_1_1 id1  
seq_1_2 id2  
seq_2 id3
```

## CLASSICAL SKETCH

The user provides a fasta file and the result file(s) of a all-against-all BLAST search in tabular format. It is now necessary to use SiLiX as a preliminary step, with `--net` option (see

[Documentation](https://lbbe.univ-lyon1.fr/fr/SiLiX#documentation) (<https://lbbe.univ-lyon1.fr/fr/SiLiX#documentation>)

):

```
silix seq.fasta blastall.out --net > seqSLX.fnodes
```

A file blastall.net has been generated.

NB : if you use the MPI version of SiLiX (with mpirun), you get multiple .net files that you need to concatenate into in single .net file.

The user can now use hifix :

```
hifix seq.fasta blastall.net seqSLX.fnodes > seqHFX.fnodes
```

See also example files in the data/ directory of the package.

## MEMORY USE

URL de la page : <https://lbbe-web.univ-lyon1.fr/fr/Hifix>

Due to mafft-profile requirements, it may be necessary to run HiFiX on computers with more than 2 GB RAM. If SiLiX results displays pre-families larger than 15000 sequences, we recommend using more than 4 GB RAM. Please note that, if HiFiX runs on multiple cores (option -t), the memory requirements are additive with the number of processes.

> **THE HARD WAY** (for very large datasets, if you have cluster or grid facilities, please

[contact us](#)

):

The user must program a pipeline with independent tasks (hifixcore program) distributed and submitted to a scheduler, like this :

```
silix .....
silix-split ....
for all <FASTAFILE> <NETFILE> do
  hifixcore <FASTAFILE> <NETFILE> (job to be submitted)
done
```

## References



HiFiX is developed by :

- > [Laurent Duret \(https://lbbe.univ-lyon1.fr/annuaires-des-membres/duret-laurent\)](https://lbbe.univ-lyon1.fr/annuaires-des-membres/duret-laurent)
- > Daniel Kahn
- > [Vincent Miele \(https://lbbe.univ-lyon1.fr/annuaires-des-membres/miele-vincent\)](https://lbbe.univ-lyon1.fr/annuaires-des-membres/miele-vincent)
- > [Simon Penel \(https://lbbe.univ-lyon1.fr/fr/annuaires-des-membres/penel-simon\)](https://lbbe.univ-lyon1.fr/fr/annuaires-des-membres/penel-simon)

If you use HiFiX in a published work, please cite the following reference :

Miele,V., Penel, S., Daubin,V., Picard,F., Kahn,D. and Duret,L.,  
[High-quality sequence clustering guided by network topology and multiple alignment likelihood](#)  
, **Bioinformatics 2012**

HiFiX is also mentioned in :

Dessimoz,C., Gabaldon,T., Roos, D.S., Sonnhammer,E., Herrero,J. and the Quest for Orthologs Consortium (incl. Miele,V.),  
[Toward Community Standards in the Quest for Orthologs](#)  
, **Bioinformatics 2012**

## Contact



For any bugs, information or feedback, please contact:

[Vincent Miele](#)



## Download

[multidom.fasta](ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/data/) (<ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/data/>)

and

[blastmultidom.out](ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/data/) (<ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/data/>)

- > *.fasta* : sequences in FASTA format (less than 256 character per line and no "U" character [ to be replaced by "X" ])
- > *.out* : BLAST results in tabulated format
- > *.fnodes* : list of pairs in format "family\_id sequence\_id"

## Build pre-families with silix

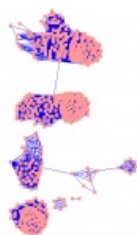
```
silix multidom.fasta blastmultidom.out --net > multidom_SLX.fnodes
```

- > 8 pre-families displayed in *multidom\_SLX.fnodes*



(<https://lbbe.univ-lyon1.fr/fr/media/1171?680/c195cc54ed32417a41416a24f15e0353076b35e0>)

- > *blastmultidom.net* is generated and corresponds to the similarity network represented below



(<https://lbbe.univ-lyon1.fr/fr/media/1172?679/aa4a77abb1a594c3b51c288536c2c34fcd515dfa>)

NB : if you use the MPI version of SiLiX (with mpirun), you get multiple .net files that you need to concatenate into in single .net file.

## Build high-quality families with hifix

```
hifix multidom.fasta blastmultidom.net multidom_SLX.fnodes > multidom_HFX.fnodes
```

- > 9 families displayed in *multidom\_HFX.fnodes*



(<https://lbbe.univ-lyon1.fr/fr/media/1173?681/a772d1e6f424e602b9c68fd35b3757c595ff485a>)

- > if n are processors available, use option

```
-t n
```