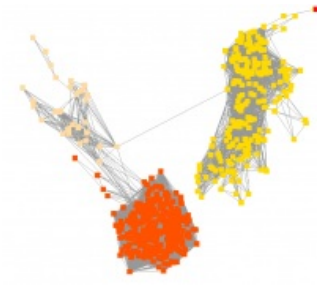
Hifix



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
.

Download

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/)
.

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

  (**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) 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)

Documentation

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
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
) :

```
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

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
- Daniel Kahn
- Vincent Miele
- Simon Penel

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 mentionned 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

Tutorial

Download
multidom.fasta (ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/data/)
and
blastmultidom.out (ftp://pbil.univ-lyon1.fr/pub/logiciel/hifix/data/)

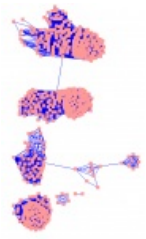
- *.fasta* : sequences in FASTA format (less than 256 character per line and no "U" character [to be replaced by "X"])
- *.out* : BLAST results in tabulated format
- *.fnodes* : list of pairs in format "family_id sequence_id"

Build pre-families with silix

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

- 8 pre-families displayed in *multidom_SLX.fnodes*

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



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*

- if n are processors avalaible, use option

```
-t n
```