

libMems

About libMems

libMems is a freely available software development library to support DNA string matching and comparative genomics. Among other things, libMems implements an algorithm to perform approximate multi-MUM and multi-MEM identification. The algorithm uses spaced seed patterns in conjunction with a seed-and-extend style hashing method to identify matches. The method is efficient, requiring a maximum of only 16 bytes per base of the largest input sequence, and this data can be stored externally (i.e. on disk) to further reduce memory requirements.

Documentation

API documentation for the latest libMems is automatically generated nightly from our source code repository and available here: <http://gel.ahabs.wisc.edu/apidocs/libMems>

Source code repository

We maintain a subversion based source code repository for libMems as part of the Mauve sourceforge project. The latest source code can be obtained with the following subversion command:

```
svn co https://mauve.svn.sourceforge.net/svnroot/mauve/libMems/trunk libMems
```

The source code repository can also be [browsed online](#).

Download

The latest source code snapshot of libMems is available from:

<http://gel.ahabs.wisc.edu/mauve/source/snapshots/libmems-snapshot.tar.gz>

As this is a nightly snapshot it contains all the latest developments, including works in progress, and we can not guarantee that it will compile, much less actually work. Tested libMems releases are generally made in conjunction with releases of the Mauve genome alignment software. Source code can be found in the versioned mauve release folders here:

<http://gel.ahabs.wisc.edu/mauve/source>