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README.md

miteFinder

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Description

We have geneated binary code fro Unix-like, Mac, and Windows users (see in \$miteFinder/bin) Normally, it will works on machines with x86_64.

If it doesn't work, you need to compile the source code for your own.

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Compile

To compile the source code, the latest compilers which supports the standard language C++11, also known as C++0x, is needed. Other older compiler may not support it.

Use the code as the following:

```
cd $miteFinder
```

```
make
```

Then the binary code "miteFidner" will be generated and moved to \$miteFidner/bin.
Finished :)

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Example

```
./bin/miteFinder -input ${your_input_file} -output ${your_output_file}
-pattern_scoring ./profile/pattern_scoring.txt -threshold 0.5
```

Warning: Your input file should be in sequences or genomes in fasta format.

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Result

The description of the MITE is just like this:

```
mite|6|4131|4140|4194|4203|t3|4138|m1|ave_score:0.649614
GTTGCTCACCCCTGCTCTTGAGCCTTTGAAACATCTACACCAATTTTTTATTGTTTTTCAT
CTATCCGTTTAAAGTGGATTAAAATGATGTTTTTTAATTTTTTTTTATTTTTTTGGGCCG
AAAAAACGGACAGCATTGAAAAAAGCCAAGTTTTATTTAATTTAAGAAAAAATAGTCC
AA CCAAATGGTTTAA
```

The 6 means the serial number of chromosome and 4131,4140,4194,4203 is the position of TIR. t3 means the length of TSD is 3. m1 means the TIR is the imperfect inverted repeats and 4138 is the mismatch base. The ave_score:0.649614 is the score of MITE sequence(The more details can be seen in the below citation).

```
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Citation

Hu, Jialu and Zheng, Yan and Shang, Xuequn, "MiteFinderII: a novel tool to identify miniature inverted-repeat transposable elements hidden in eukaryotic genomes", BMC Medical Genomics, 2018, 11(5), 101.

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END

THANKS FOR READING

If you have any questions regarding to the program, please don't hesitate to contact
Releases through email.

No releases published

Packages

No packages published

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Languages

● C++ 96.5% ● Makefile 2.0% ● C 1.1% ● Shell 0.4%