Version 2

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Multitrim V.2

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1 *Works for me* This protocol is published without a DOI.

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ABSTRACT

Multitrim is an Illumina short read trimming pipeline which facilitates effectively and easily trimming either single end or paired end FASTQ data. Multitrim achieves high quality trimming results by automating the detection of Illumina adapter sequences and sequentially applying two independent read trimming tools with complimentary properties. The script additionally produces quality assessment reports for both the input reads and the post-trim reads, creates consistent naming conventions for results, and compresses the trimmed reads to save on space.

EXTERNAL LINK

https://github.com/KGerhardt/multitrim

ATTACHMENTS

Multitrim How-To.pdf

EXTERNAL LINK

https://github.com/KGerhardt/multitrim

PROTOCOL CITATION

Kenji Gerhardt, Kostas Konstantinidis 2020. Multitrim. **protocols.io**
https://protocols.io/view/multitrim-bnsnmede
Version created by Kenji Gerhardt

EXTERNAL LINK

https://github.com/KGerhardt/multitrim

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trimming, read trimming, short read trimming

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Multitrim How-To.pdf

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1 All contents of this protocol are best viewed in either the attached manual **Multitrim_User_Manual.pdf** , or by going to the Multitrim user manual google doc. You can also follow the instructions on this page to achieve the same results.

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2 Install the correct version of Anaconda or Miniconda for Python 3.6+ for your system, if it is not already present.

Note: Miniconda will take up less space on your computer, and is the recommended method of preparing your computer to run Multitrim, but Anaconda will
Step 2 includes a Step case.
Windows OS
Mac OS
Linux

step case

Windows OS

If you are using Windows, please install Ubuntu for Windows, then follow all Linux instructions for installing Multitrim from the Ubuntu terminal. You can open the Ubuntu terminal by typing "Ubuntu" in the search bar after installing it.

3 Copy and paste the following lines of code in your system's terminal to download and install Multitrim and its dependencies:

```
curl https://raw.githubusercontent.com/KGerhardt/multitrim/master/multitrim.yml > multitrim.yml
conda env create -f multitrim.yml
```

4 Activate the Multitrim environment by entering the following line of code:

```
conda activate multitrim
```

5 Test if the installation worked by simply typing "multitrim" in your terminal. Usage instructions will appear if multitrim installed successfully.

6 Example usage

Single end:

```
multitrim -u unpaired_reads.fastq.qz -o output_directory --max
```

Paired end:

```
multitrim -1 forward_reads.fastq.gz -2 reverse_reads.fastq.gz --o output_directory --max
```