# PEAdapterFinder

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# Introduction

PEAdapterFinder is stand for Paired-End Adapter Finder. PEAdapterFinder is capable to identify two consensus adapter sequences from two paired-end FASTQ file as input. Both FASTQ file can be in multi-line FASTQ file or 4-line FASTQ file.

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## Install PEAdapterFinder

1. Download source code from github: _https://github.com/farhanmohdtahir/PEAdapterFinder.git_ (downloaded file will name as PEAdapterFinder-master.zip)

2. Open terminal

3. Go to Downloads directory (or directory which the PEAdapterFinder-master.zip are located)

- Example:
  If Downloads directory is located in path: /export/home/farhan/Downloads
  *cd /export/home/farhan/Downloads*

4. Unzip the PEAdapterFinder-master.zip file

- Example:
  *unzip PEAdapterFinder-master.zip*

5. After unzip, go to the PEAdapterFinder-master directory

- Example:
  *cd /export/home/farhan/Downloads/PEAdapterFinder-master*

6. Make the PEAdapterFinder program by write the following commands:
   *make*

7. Installation complete. You can run PEAdapterFinder as the following tutorial.

## Run PEAdapterFinder

1. Open Terminal

2. Write the command to go to the directory that locate the PEAdapterFinder program

- Example:
  If PEAdapterFinder program is located in path: /export/home/farhan/Downloads/PEAdapterFinder-master:
  *cd /export/home/farhan/Downloads/PEAdapterFinder-master*

3. Write the command to execute PEAdapterFinder program

- Example:
  *./PEAdapterFinder -f1* **file1.fastq** *-f2* **file2.fastq** *[options]*

- -f1 and -f2 are the REQUIRED option for user to insert 2 paired-end FASTQ file
  ***Make Sure both input FASTQ file are presence in the same directory of PEAdapterFinder Program!***

4. Below is the command of the options that can be use:

| Option | Description | Flag |
|---|---|---|
| -f1 | Input File 1. The file must in .fastq OR .fq file format (multi-line OR 4-line FASTQ file). Example: **-f1 *sample1.fastq*** OR **-f1 *sample1.fq*** | **REQUIRED** |
| -f2 | Input File 2. The file must in .fastq OR .fq file format (multi-line OR 4-line FASTQ file). Example: **-f2 *sample2.fastq*** OR **-f2 *sample2.fq*** | **REQUIRED** |
| -seql | Minimum length percentage to get adapter sequence (default = 70, to change use '-seql=') Example: **-seql=80** | OPTIONAL |
| -perc | Minimum match percentage to get adapter sequence (default = 85, to change use '-perc=') Example: **-perc=90** | OPTIONAL |
| -conf | Minimum confidence level of nucleotides (default = 1, to change use '-conf=') Example: **-conf=80** | OPTIONAL |
| -debug | Debug level of programme (default = 0, to change use '-debug=' : 0 - only adapter sequences, 1 - nucleotide count and phred score, 2 - dynamic programming matrix and traceback matrix) Example: **-debug=1** OR **-debug=2** | OPTIONAL |
| – help | To view information about option that can be used | OPTIONAL |

5. Wait for the program to complete it's process for the result of adapter sequence found in both file.