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 (Version 1: If git not installed in system)

1. Download source code from github: https://github.com/farhanmohdtahir/PEAdapterFinder.git
   (downloaded file will be named 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 by writing the following command:

   ```
   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 writing the following commands (This will create executable
   PEAdapterFinder program in the directory):

   ```
   make
   ```

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

Install PEAdapterFinder (Version 2: If git already installed in system)

1. Open Terminal

2. Cloning the source code from github by writing the following command:

   ```
   git clone https://github.com/farhanmohdtahir/PEAdapterFinder.git
   ```

3. Go to PEAdapterFinder directory.
   Example:

   ```
   cd PEAdapterFinder
   ```

4. MAKE the PEAdapterFinder program by writing the following commands (This will create executable PEAdapterFinder program in the directory):

   ```
   make
   ```

5. 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 present in the same directory as PEAdapterFinder Program and paired-end to each other!

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.