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: Normal Installation)

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: CAN USE IF GIT ALREADY INSTALLED IN THE 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!

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.