Paired-End Adapter Finder

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Contents

Chapter 1

Paired-End Adapter Finder v16

The Paired-End Adapter Finder identify two consensus adapter sequences from Reads 1 and Reads 2 of paired-end sequencing by using the Needleman-Wunsh algorithm to align the two reads and determining which region of the sequence is actually an adapter. The user has to input two fastq format files, corresponding to Read 1 and Read 2, the input file can be 4-line FASTQ file or multi-line FASTQ file, and the result will be the consensus adapter sequences for both the Adapters in Read 1 and Read 2 respectively of the paired-end sequencing.

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Chapter 2

Class Index

2.1. Class List

- Here are the classes, structs, unions and interfaces with brief descriptions:
  - Input
    * The **Input** Class transforms the sequences and format line of input file to be used in finding the Adapter Sequencer . . . .
  - NW
    * The **NW** Class corresponds to the Needleman-Wunsch algorithm which is used to align the two reads . . . .
  - CS
    * The **CS** Class corresponds to the Consensus Sequence which is used obtain the adapter sequences from the two reads . . . .

Chapter 3

Class Documentation

3.1. Input Class Reference

Class transforms the sequences and format line of input file to be used in finding the Adapter Sequencer
#include "Input.h"

- Public Member Functions
  - int complementInput(string&);
  - string reform(string, bool&);

3.2.1. Detailed Description

The Input Class transforms the sequences to be used in the Adapter Sequencer. The Input Class is responsible to reverse complement Read 2 before dynamic programming is done.

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3.2.2. Member Function Documentation

3.2.2.1. int Input::complementInput(string& seq)

Reverse complement the input for sequences from the second input file.

Parameters

Parameter	Description
seq	The sequence to be reversed and complemented

3.2.2.2. string Input::reform(string file, bool &fourline)

Reform multi-line FASTQ file into 4-line FASTQ file and return the name of new file of 4-line FASTQ file after reformation process succeed.

Parameters

Parameter	Description
file	Input file (multi-line FASTQ file)
fourline	Value whether the file is 4-line FASTQ file or multi-line FASTQ file

The documentation for this class was generated from the following file:
- export/home/farhan/PEAdapterFinder/Input.h
- export/home/farhan/PEAdapterFinder/Input.cpp

3.2. NW Class Reference

The NW Class corresponds to the Needleman-Wunsch algorithm which is used to align the two reads. *#include "NW.h"*

- Public Member Functions
  - int nw (string seq_1, string seq_2, string &seq_1_al, string &seq_2_al, int debug)
- Public Attributes
  - int **colmax**
  - int **count**
  - int ** **F**
  - int **Fx**
  - int **Fy**
  - double **percentage**
  - int **rowmax**
  - char ** **traceback**
  - char ** **tracebackscore**
- Private Member Functions
  - void clear()
  - void dpm _init(int **F, char** traceback, int L1, int L2, int d))