

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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 - Jan 2017

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)