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Deconvolute_staggered

Compiling and Boost libraries

This program requires the C++ Boost libraries to be installed on the server. Compiling with q++ (all on one line)

g++ Deconvolute_staggered.cpp Engine.cpp DataStore.cpp -I <path to boost installation> -L <path to boost libraries> -Iboost_iostreams -o Deconvolute_staggered.exe 2> errors.txt

Any errors in the compiling will be saved to the errors.txt file. If this file has zero size the build as worked. If not look in the file and resolve the first error and then rebuild until it works.

Command line arguments

Parameter on command line: Read one filename with path, Read two filename with path, Primer file with path, Index file with path, Path to folder to save data in, Minimum PCR length, Maximum PCR length.

Example primer file

GGATTGCGCTGTTATCC AGACGAGAAGACCCTAT

These sequences can contain degenerate bases: S, W, R or Y.

Example index file

AACTGTAG

ACACTAAG

ACAGGCGC

ACTCGTGT

AGTACTCC

ATTGTGAA

CAATTAAC

CATAGAGT

CCATTCGA

CCTTCACC

GACGTCTT

GCCACAGG

GTCTACAC

GTGAATAT

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GTGTCGGA

TAAGGTCA

TGCGAGAC

TGGCCGGT

TTCCTGTT

TTGCCTAG

These sequences can only contain standard bases: A, C, G or T.

Library production

The Sequence is PCR amplified with the primers of interest and the product cleaned up to remove primer dimer and primers. The amplicon is then used to make a whole genome library with a kit like the NEB NextUltra

Example of reads with Primers

Sequence	Comment
1)	
ATGGGGACTCGTGTGGATTGCGCTGTTATCCCTAGGGTA	Start of read with forward primer
GGATTGCGCTGTTATCC	Target primer sequence which is 14 to 17 bp from start
ACTCGTGT	Index sequence which before the target sequence
NNNNN	Unique id and stagger to create difference offset to aid base calling
2)	
ATTCGTACACTAAGAGACGAGAAGACCCTATGGAGCTTT	Start of read with reverse prime
AGACGAGAAGACCCTAT	
ACACTAAG	
NNNNN	
3)	
TTCAGTCCAATTAACGGATTGCGCTGTTATCCCTAGGGT	Start of read with forward primer with 7Ns
GGATTGCGCTGTTATCC	
CAATTAAC	

NNNNNN