Manual of ABCmutate

Instructions to download

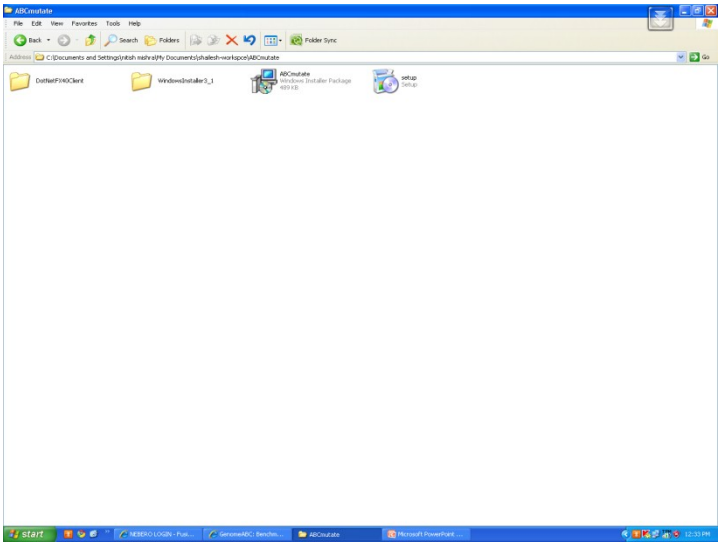
[1] **Unzip the software package and follow the instructions.**

[2] **Download the software and install the setup.**

[3] **Minimum requirement of this software is service pack 3 on windows machines.**

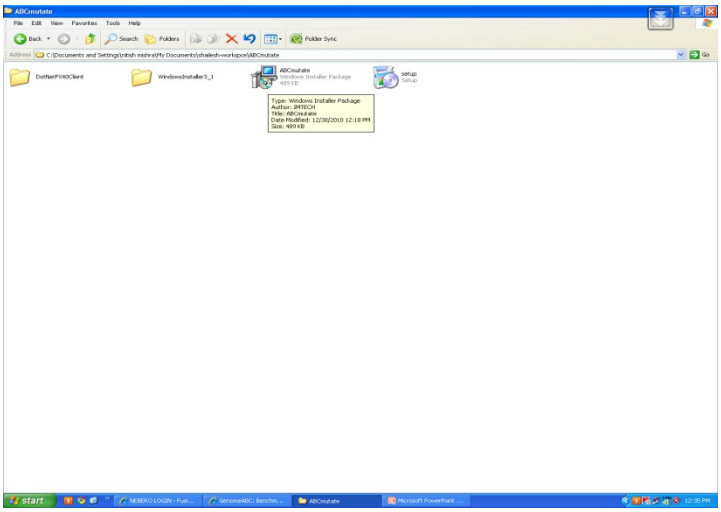
Step 1

Unzip the software package.



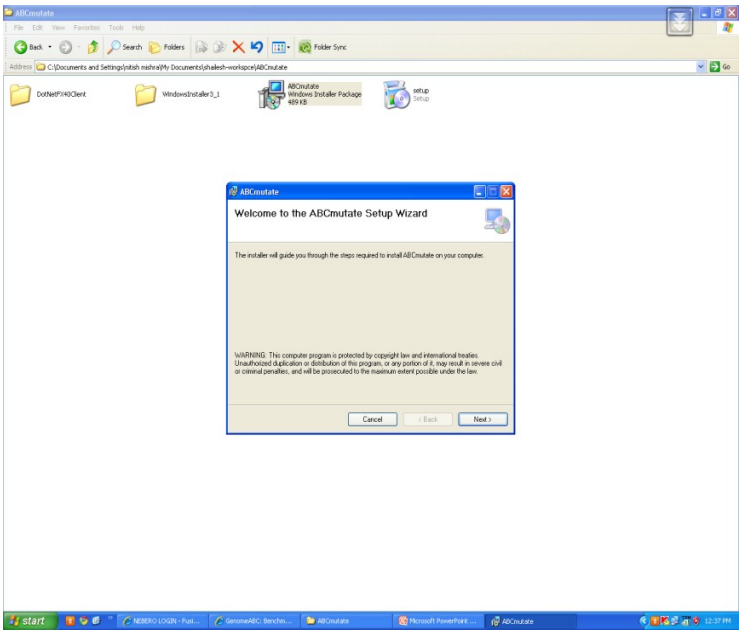
Step 2

Install the ABCmutae software.



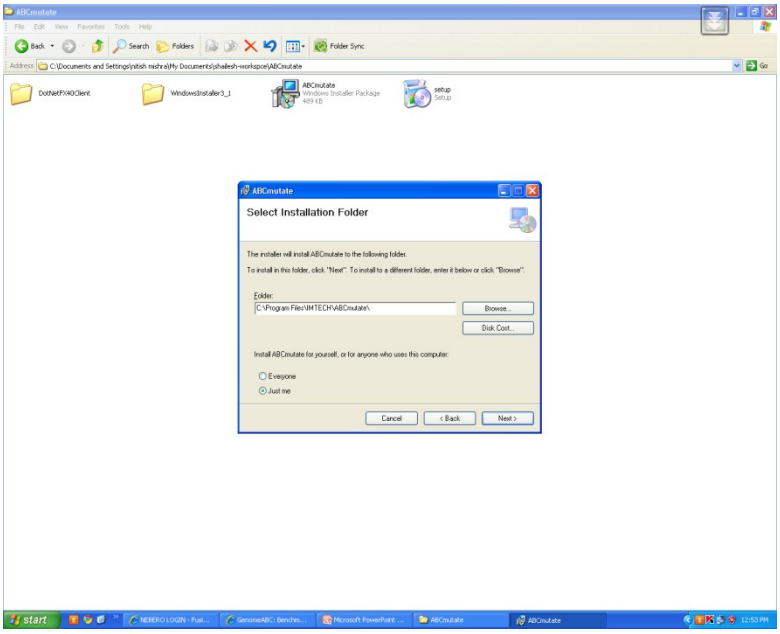
Step 3

Click next.



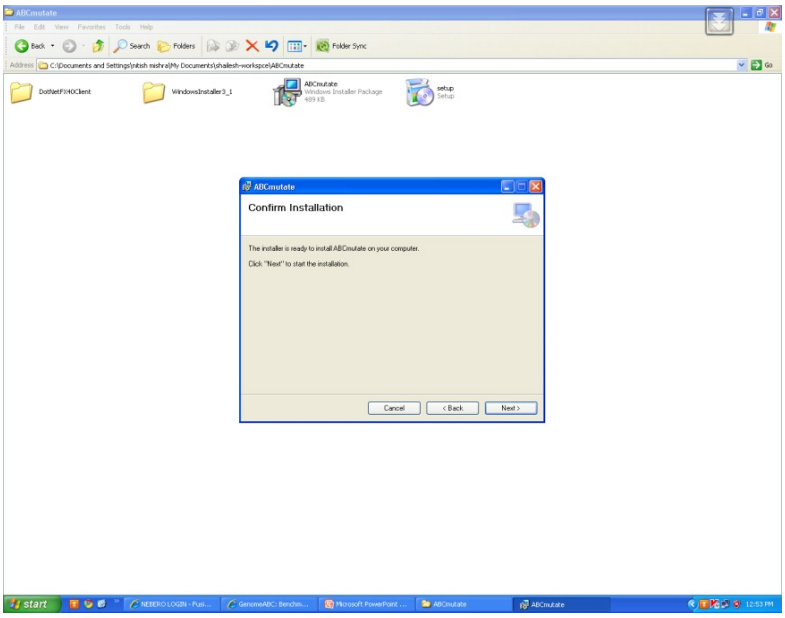
Step 4

Give the location to download the software.

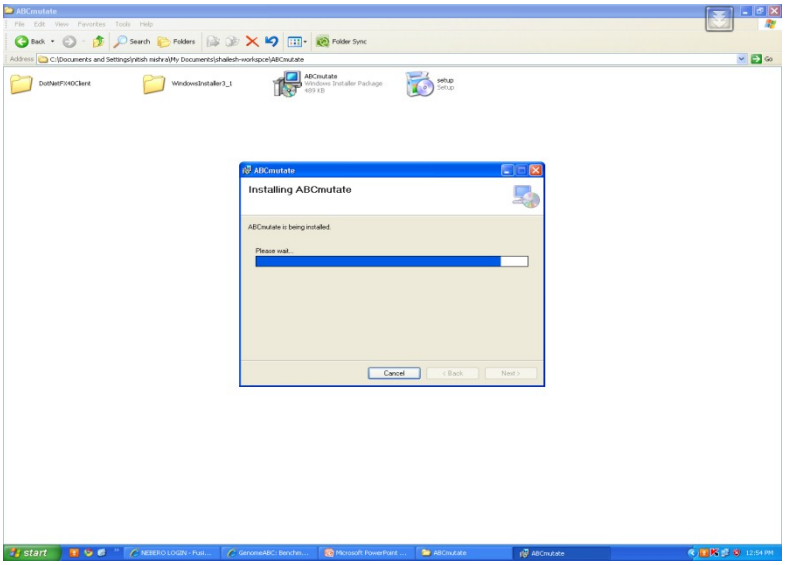


Step 5

Conform to install.

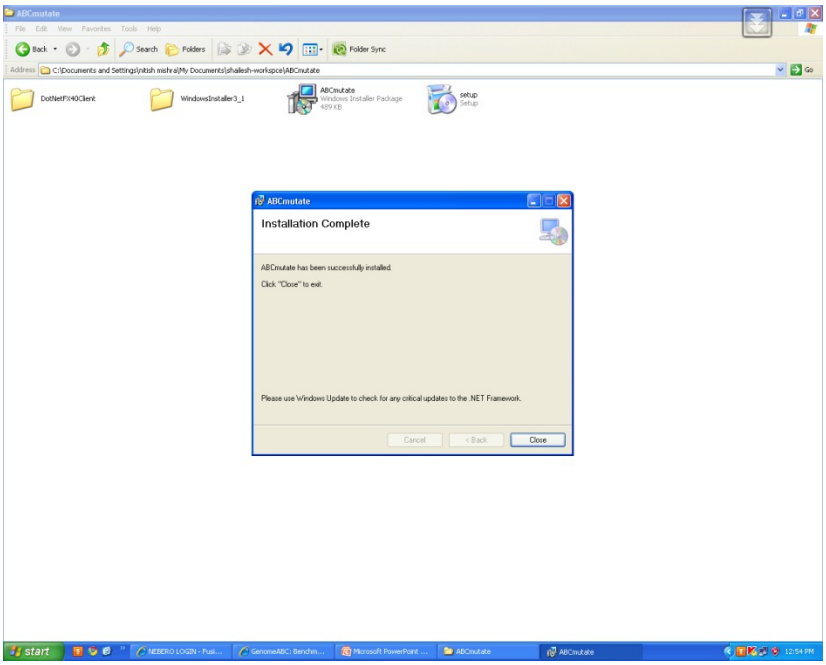


Step 6



Step 7

Click close at last.



About ABCmutate

This software allows user to mutate a genome, where desired number of nucleotides are mutated. It allows user to specify % number of nucleotide to be mutated in genome. This software also generates simulated short reads for mutated genomes. This dataset (short reads and mutated genome) is important for evaluating an assembler when similar genome is available. Single end or paired end Solexa type reads can be generated after the random mutation. For generation of reads, this software use the same strategy as adopted in the Solexa technology. Reads generated, does not contain the errors like vector sequence contamination which is usually present in the data generated by the sequencing machines. Purpose of generating mutation in the genome is that, the data generated in form of reads can be comparable with real data generated by the sequencing machine as the sequencing machine usually generate reads with several errors like contamination of vector sequences. Genome and sequencing reads generated from that will be used for the benchmarking of genome assemblers. Reads can be assembled into complete genome by these genome assemblers and then the assembled genome can be aligned to the reference genome (created by this software) with the help of BLAT (Kent, 2002).

Parameters required

Parameters required for the creation of mutated genome.

1. File of genome: - Input file should be provided to mutate that genome and further generation of reads from this.

2. Mutation value (%):- This is the percentage mutation value by which the given genome will be mutated.
Example:-If you want to mutate the given genome to 20%, then provide the value 20 in the desired field.

Parameters required for the generation of reads.

1. Coverage value: - This is the value of coverage of sequencing.
Example: - If you want to sequence the genome at 40X coverage then provide the value 40 in the box. Coverage value should not be zero.

2. Insert length: - Insert length is the length of that randomly generated fragment from which the reads are generated. This type of fragments is generated in the Solexa technology. Insert length should be less than the size of genome and greater than the read size.
Example:-If you want insert length of 400 then provide value 400 in the corresponding box.

3. Read length: - Read length is length of reads that you have to generate. Read length should not be greater that insert length as the reads it are generated by the sequencing of one end of random fragments generated of that insert length. Reads can be single end or paired end.

Example:-If you want to generate reads of 36 nucleotides, then give the value 36 in the corresponding box.

Results

Results will be stored in files. You have to provide the location and name of result files. After completion of running, a success massage will appear.