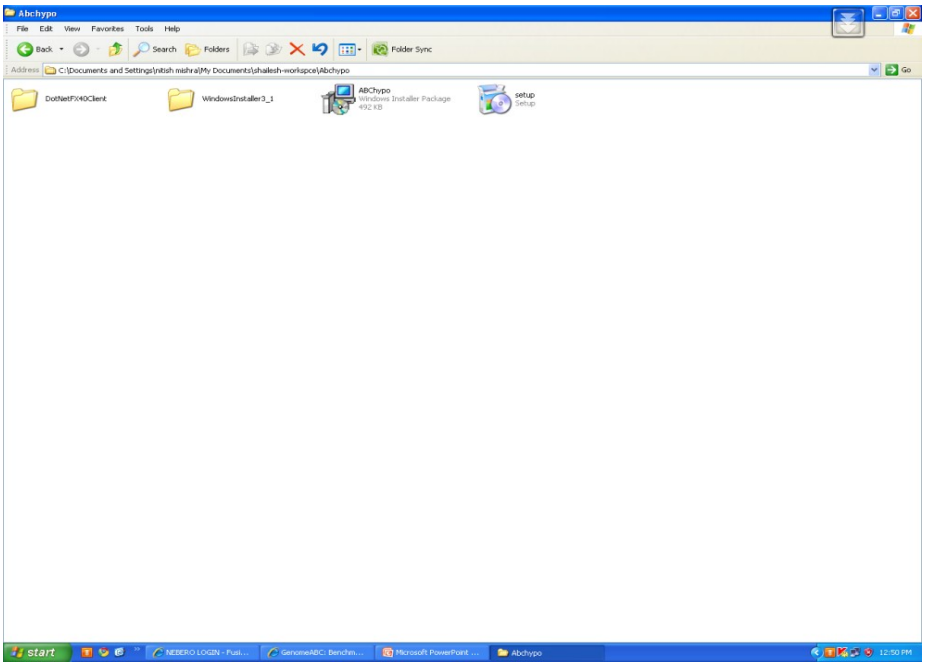
Manual of ABChypo

Instructions to download

- **Unzip the software package.**
- **Download the software and install the setup.**
- **Minimum requirement of this software is service pack 3 on windows machine.**

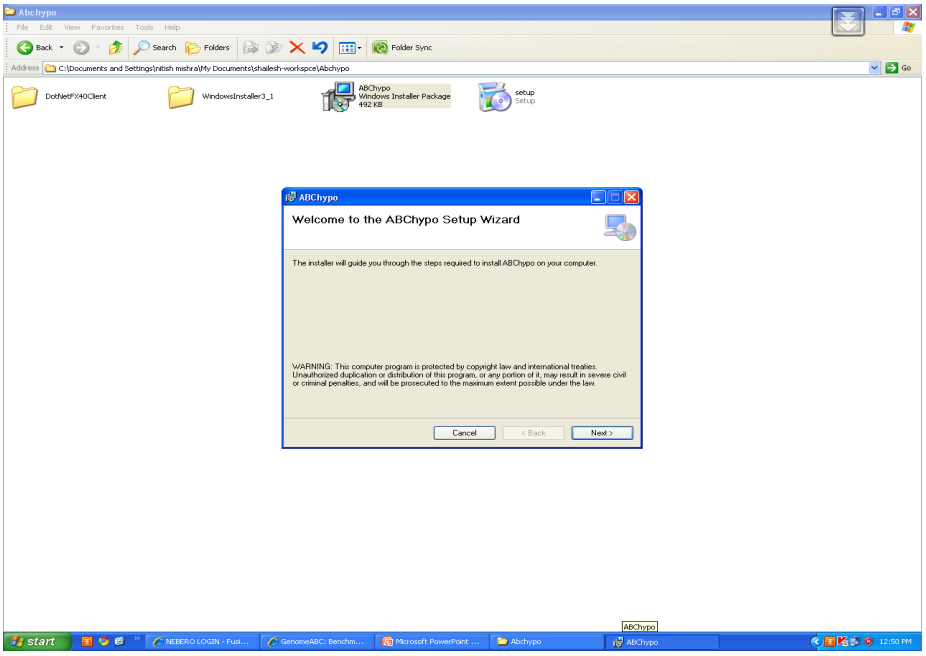
Step 1

Unzip the software package.



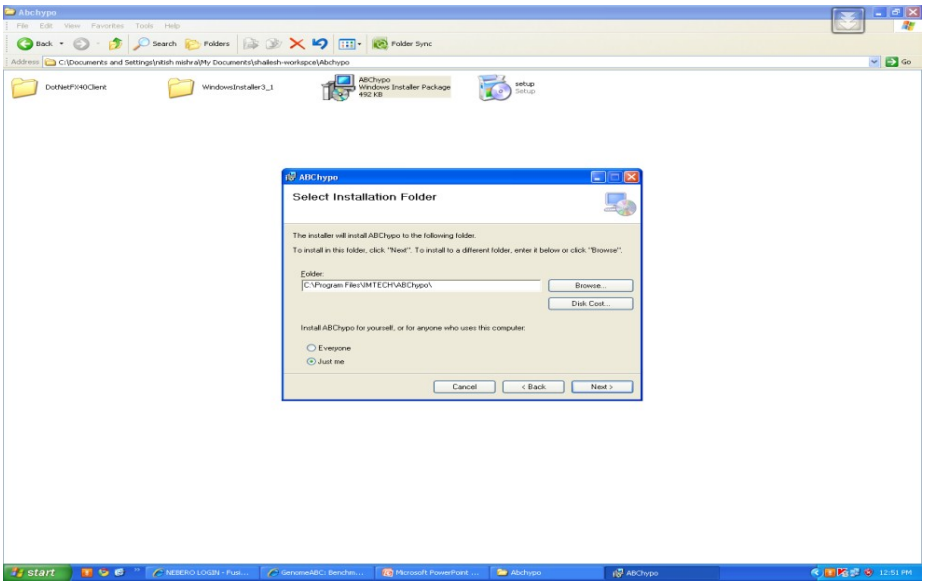
Step 2

Click the ABChypo software to install.



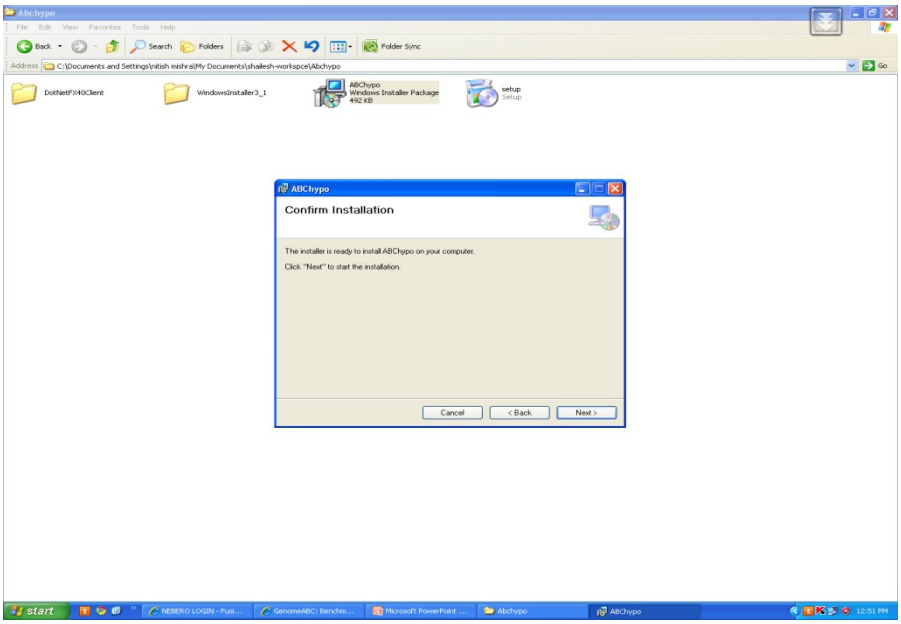
Step 3

Provide the location to download the software.

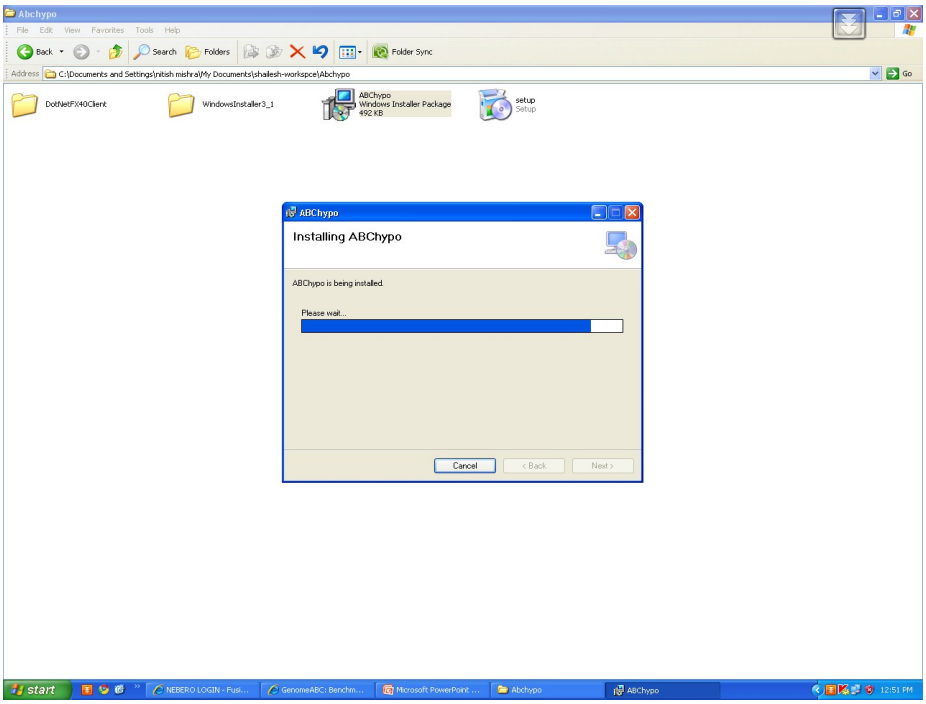


Step 4

Conform to install.

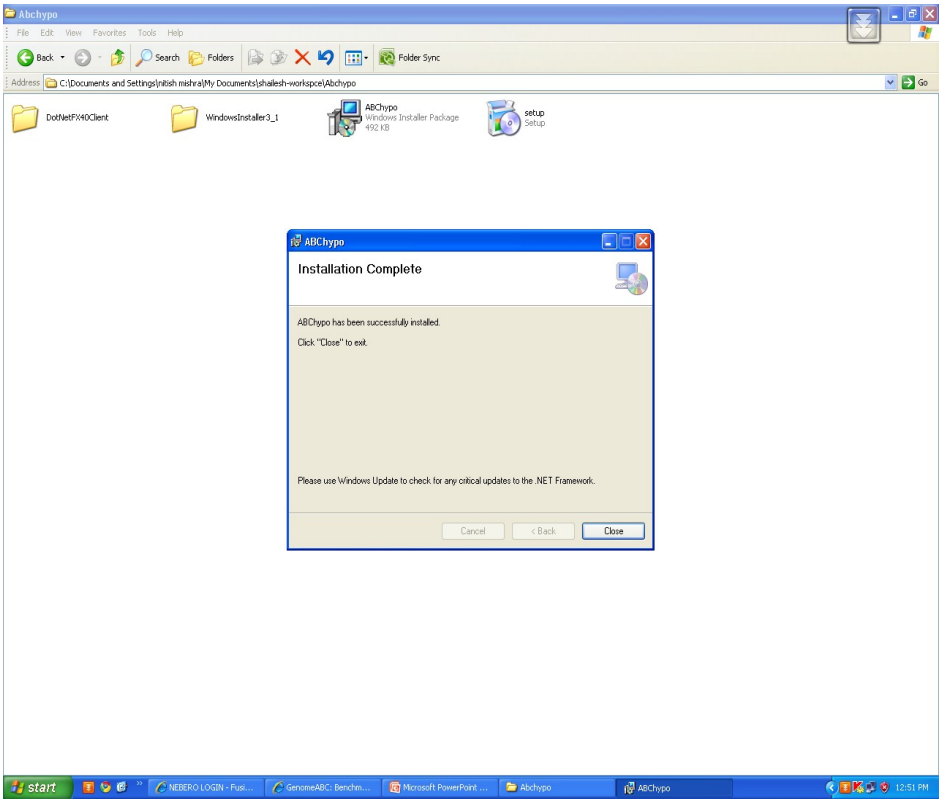


Step 5



Step 6

Click close to complete the installation.



About ABChypo

This software can be used for generation of hypothetical/artificial genome and simulated short reads of hypothetical genome. This data (hypothetical genome and simulated short reads) is important for benchmarking of genome assembler. This software will generate, Illumina type

single end or paired end reads. Error free reads are generated by this software, will be the same type as produced by Illumina's Solexa technology. This software requires some parameters which are necessary for the generation of Solexa type reads. Sequencing strategy adopted in this software is same as Solexa technology. The reads generated will be error free, as the reads are generated by the fragmentation of genome and doesn't have vector contamination. 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 random genome.

1. Size of genome: - Genome size should be given in form of nucleotides.

Example: - If you wish to create a genome of 6Mb then you have to give the value 6000000 in the box provided.

2. Composition (%):- This is the content of all nucleotides i.e. percentage composition of A, T, G and C. Total of all four values should be 100 i.e. 100%.
Example:-If you want to create a genome with a (75 %), G (5%), T (5%) and C (15%) then you should provide the values 75, 5, 5 and 15 in the corresponding boxes.

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.