### a)

1. Prepare the converted *Reference Indexes for both plus and minus strands.*
2. For each input read do
3. Prepare the plus and minus conversions of the read
4. Count the number of hits using 4 possible ways to map the converted reads on the *Converted Genome*
5. Using List Filtering, we filter the lists whose number of hits > cutoff
6. For each hit in the unfiltered lists, compute the number of mismatches ignoring the BS-treatment mismatches.
7. If the least mismatch hit is unique then
9. Else
10. Report it as non-unique.
11. EndIf
12. EndFor

### b)

1. Prepare 4 *Reference Indexes* for the two fully-converted color genomes and the two non-CpG converted color genomes.
2. For every read do
3. Count the number of hits using 4 possible ways to map the read and its reverse on the fully-converted color genomes
4. Apply List Filtering on the counts obtained from Step 3.
5. Apply Mismatch Stage Filtering to the unfiltered list from Step 4.
6. Apply Conversion of Bisulfite Color reads to Base reads to the hits from Step 5.
7. Determine the Color Mismatch Counts for the hits on the ordered hits from Step 6.
8. If the least mismatch hit is unique then
10. ElseIf the least mismatch hit is non-unique
12. ElseIf no hits found on fully-converted color genomes then
13. Repeat Steps 3 to 14 with non-CpG-converted color genomes
14. EndIf
15. EndFor