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**
8. Report its location.
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 for 2 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**
9. Report it. Goto Step 14.
10. **ElseIf** the least mismatch hit is non-unique
11. Reported it as non-unique. Goto Step 14.
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**