**PRACTICAL 4**

**Aim:** Enter genome of five different organism and write a python/java program to find consensus sequence using Multiple Sequence Alignment (MSA) technique.

**Code:**

package prac.pkg4;

/\*\*

\*

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\*/

import java.io.\*;

import java.util.\*;

public class PRAC4 {

/\*\*

\* @param args the command line arguments

\*/

public static void main(String str[]) throws IOException {

int n, i,j,k,count;

String seq[],cons[];

ArrayList<Integer> a = new ArrayList<Integer>();

ArrayList s = new ArrayList();

BufferedReader br=new BufferedReader(new InputStreamReader(System.in));

System.out.println("Enter the no of Sequences");

n=Integer.parseInt(br.readLine());

seq=new String[n];

System.out.println("Enter sequences");

for(i=0;i<n;i++)

seq[i]=br.readLine();

cons=new String[seq[0].length()];

for(j=0;j<seq[0].length();j++)

cons[j]=" ";

for(j=0;j<seq[0].length();j++)

{

a.clear();

s.clear();

for(i=0;i<n;i++)

{

count=1;

for(k=i+1;k<n;k++)

{

if(seq[i].charAt(j)==seq[k].charAt(j))

count++;

}

System.out.println("count="+count);

a.add(count);

s.add(seq[i].charAt(j));

}

/\*\*Updated Snippet 1\*\*/

Set<String> set = new HashSet<>(s);

ArrayList setlist = new ArrayList(set);

Collections.sort(setlist);

if (setlist.contains('-') &&setlist.size()==2){

cons[j]+="-"+setlist.get(1);

}

else if (setlist.size()==1){

cons[j]+="-"+setlist.get(0);

}

else{

int m = Collections.max(a);

int index=a.indexOf(m);

System.out.println("Max="+m);

cons[j]+=s.get(index);

System.out.println("index="+index);

for(i=index+1;i<a.size();i++)

{

if(a.get(i)==m)

cons[j]+="/"+s.get(i);

}

}

}

System.out.println("Consensus=");

for(j=0;j<seq[0].length();j++){

/\*\*Updated Snippet 2\*\*/

if(cons[j].length()==2)

System.out.print(cons[j].toLowerCase());

else if(cons[j].length()==3)

System.out.print(cons[j].replace("-",""));

else

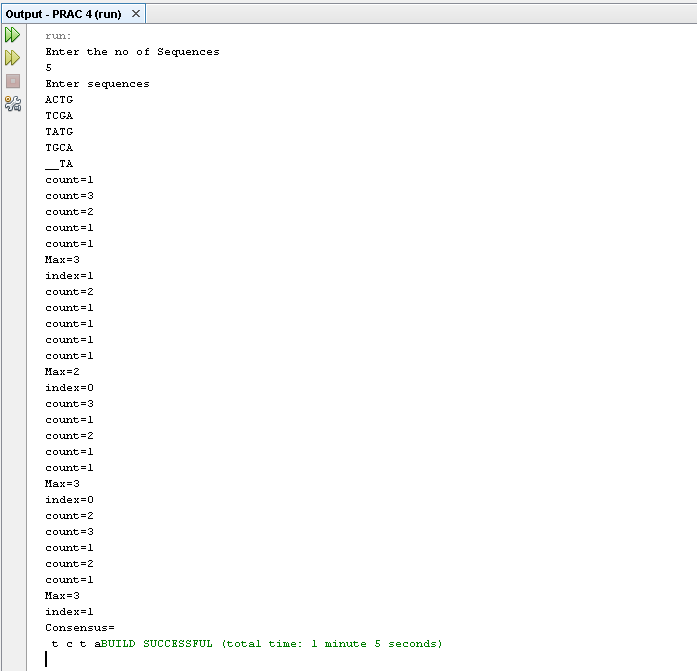
System.out.print(cons[j]);

}

}

}

**Output:**

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