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Subject – Bioinformatics

**Topic – Multiple Sequence
Alignment**

Practical No: 4

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

Code:

```
import java.io.*;
import java.util.*;
public class
Consensus
{
    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
    e()); else if(cons[j].length()==3)
        System.out.print(cons[j].replace("-
    ","")); else
        System.out.print(cons[j]);
    }
    }
    }

```

Output:

```
C:\Windows\system32\cmd.exe
Enter the no of Sequences
5
Enter sequences
ACTG
TCGA
TATG
TGCA
TA
count=1
count=3
count=2
count=1
count=1
Max=3
index=1
count=2
count=1
count=1
count=1
count=1
Max=2
index=0
count=3
count=1
count=2
count=1
count=1
Max=3
index=0
count=2
count=3
count=1
count=2
count=1
Max=3
index=1
Consensus=
t c t a
C:\Users\admin\Desktop>Pause
Press any key to continue . . .
```