

**Paper: BI-524 Computational Methods for Sequence Analysis**

- CO1** Students will be made aware about the analysis of various types of biological data  
**A1** List different types and levels of biological data generated through experimental procedures  
**T1** Align the given protein sequences using Smith Watermann and Needle Wunsch Algorithms

	Roll No	Assignment 1	Test 1	Total marks of attempted questions	Total Marks	Percentage	Score (3,2,1)	Target >= 60% (Y/N)
<b>Marks</b>			10	20	30	30		
	25151		9	17	26	30	86.66666667	3 Y
	25152		9	19	28	30	93.33333333	3 Y
	25153		7	10	17	30	56.66666667	2 N
	25154		7	15	22	30	73.33333333	3 Y
	<b>Average</b>						<b>2.75</b>	

%age	score
>=60	3
50-59.9	2
40-49.0	1

- CO2** Students will be familiar with various software and databases used in analysis of data  
**AC1** Browse Different webservers for Multiple Sequence Alignment and write their features and the underlying algorithms  
**A1** Retrieve protein Sequences from a given family from Swissprot and align them using Clustal Omega and TCOFEE and compare the results.

	Roll No	Activity 1	Assignment1	Total marks of attempted questions	Total Marks	Percentage	Score (3,2,1)	Target
<b>Marks</b>			10	10	20	20		
	25151		9	9	18	20	90	3 Y
	25152		8	9	17	20	85	3 Y
	25153		8	8	16	20	80	3 Y
	25154		8	9	17	20	85	3 Y
	<b>Average</b>						<b>3</b>	

- CO3** Learners will be able to predict the structure of proteins  
**T1** Differentiate between Prokaryotic and Eukaryotic Gene Structure  
**A1** Write detailed flowchart of PHD secondary structure prediction algorithm

	Roll No	Test1	Assignment1	Total marks of attempted questions	Total Marks	Percentage	Score (3,2,1)	Target
<b>Marks</b>			10	10	20	20		
	25151		9	9	18	20	90	3 Y
	25152		9	8	17	20	85	3 N
	25153		6	5	11	20	55	2 N
	25154		8	8	16	20	80	3 Y