A Programming Course in Bioinformatics for Computer and Information Science Students Appendix II: Student Evaluations of Course

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Table (A) Lecture topics are given (with same numbering as in text of article), along with name and affilation of lecturer. Student rated importance of topic, and quality of readings are given as percentages of 18 students who completed survey anonymously. (B) Assignments and Projects are listed along with student rated importance of assignment and difficulty.

A.	Topic of Lecture	Lecturer	Affiliation	Importance			Readings			
				Very	Okay	Not	Poor	Good	Exc.	Didn't Read
1.	Introduction	*Altman*	*Medical Informatics*	78	21	0	0	66	22	11
2.	Dynamic programming	*Altman*	*Medical Informatics*	88	11	0	0	78	21	0
3.	Exploring myoglobin	*Koza*	*Computer Science*	63	36	0	0	66	6	27
4.	Basic structural computations	*Altman*	*Medical Informatics*	68	31	0	NA	NA	NA	NA
5.	Protein folding problem	*Levitt*	*Structural Biology*	61	38	0	0	50	6	43
6.	Hemoglobin as mini-computer.	*Koza*	*Computer Science*	29	58	11	0	37	6	56
7.	Analysis of sequences	*Koza*	*Computer Science*	31	62	6	0	43	12	43
8.	Alternative sequence representations	*Klingler*	*Biochemistry*	31	68	0	0	50	6	43
9.	Simulating molecular dynamics	*Levitt*	*Structural Biology*	50	44	6	0	50	11	44
10.	Processing distance information	*Altman*	*Medical Informatics*	42	57	0	0	57	31	10
11.	Biology and genetic programming	*Koza*	*Computer Science*	42	47	0	0	57	31	10
12.	Hidden Markov models of sequences	*Haussler*	*Computer Science*	56	43	0	11	54	6	29
13.	Non-atomic protein features	*Altman*	*Medical Informatics*	37	62	0	0	38	16	44
14.	Molecular surfaces and volumes	*Gerstein*	*Structural Biology*	11	72	16	5	38	0	55
15.	Secondary structure prediction	*Koza*	*Computer Science*	21	78	0	0	66	0	33
16.	Computing and Genome Project	*Walker*	*Affymetrics, Inc.*	33	66	0	0	50	6	45
17.	Constructing evolutionary trees	*Cheeseman*	*NASA*	29	64	6	0	47	11	41
18.	Knowledge bases for metabolism	*Karp*	*SRI Int'l*	28	57	16	0	53	0	46
19.	Constraint satis-faction techniques	*Altman*	*Medical Informatics*	38	61	0	0	46	16	39

B.	Assignments/Projects	Importance			Difficulty		
		Very	OK	Not	Easy	OK	Hard
A1.	Information retrieval from the WWW	64	29	6	35	65	0
A2.	Exploring 3D structure graphically	52	48	0	17	76	6
A3.	Detailed 3D analysis of 4HHB and 2SOD	33	61	6	12	87	0
A4.	Dihedral angles, Ramachandran plots	41	52	6	0	100	0
A5.	Distances and contact maps	31	68	0	0	94	6
A6.	Hidden Markov Models	16	77	6	27	72	0
P1.	Dynamic Programming Alignment	82	17	0	0	88	11
P2.	RMS fitting of 3D structures	50	50	0	5	83	11
P3.	Threading to identify globins	27	72	0	5	100	0