	VI	CHITRAGAD / VELGAD II (C.B.C.S.) (2013 COURSE): WINTER - 20 SUBJECT: GENOMICS & PROTEOMICS	015
Day Date	: T : 1	Time: 2:00 P.M.T 3-10-2015 Max Marks: 60	05.00
N.B:	1) 2) 3) 4)	Q. No.1 & Q.No.5 are COMPULSORY. Solve ANY TWO questions from remaining questions in each section. Both the sections should be written in the SEPERATE answer book. Figures to the RIGHT indicate full marks. Draw neet labeled diagram WHENEVER necessary.	om the
)	SECTION-I	
Q.1		Define: (ANY FIVE):	(10)
		 a) Single Molecule Sequencing b) Annotation c) ADMET d) Synteny e) COG f) HSS 	
Q.2	a) b) c)	Differentiate between: (ANY TWO) Illumina & Ion Torrent sequencing EST & STS DNA cloning & DNA fingerprinting	(10)
Q.3	a) b) c)	Answer the following: (ANY TWO) Explain ORF prediction algorithm. Briefly differentiate between structural genomics and functional genomics. Describe genome annotation concept.	(10)
Q.4	a) b) c)	Write short notes on: (ANY TWO) Pharmacogenetics VISTA Comparative Genomics	(10)
		SECTION-II	
Q.5		Explain Briefly: (ANY FIVE)a) Scope of Proteomicsd) GRIDb) 2D Gelse) Isoelectric Focusingc) Two Hybrid Methodf) Protein Interaction Networks	(10)
Q.6	a) b) c)	Answer the following: (ANY TWO) Define Proteomics. Explain its scope & applications. Write a note on size- exclusion chromatography. Explain Proteome analysis steps in detail.	(10)
Q.7		Explain in detail protein identification techniques.	(10)
		OR	
		Explain the concept of protein chips. How it is helpful in functional proteomics? Enlist proteomics industries working on same concept.	al
Q.8		Differentiate between any TWO of the following:	(10)
	a) b) c)	DIP and BIND PIM – Hybrigenics and MINT PPI Server and Interpre TS	
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VICHITRAGAD / VELGAD- II (2013 COURSE) (CBCS): WINTER - 2015 SUBJECT : PERL & BIOPERL PROGRAMMING

Day : Wednesday

Date : 14.10.2015

Time : 2.00 P. M. TO 5.00 P. M. . Max. Marks : 60

[10]

N.B.:

- 1) Q.No.1 and Q.No.5 are COMPULSORY. Attempt ANY TWO from the remaining questions from each section.
- 2) Answers to both the sections should be written in the SEPARATE answer books.
- 3) Figures to the right indicate **FULL** marks.

SECTION - I

Q.1 Answer the following:

- a) What are the basic differences between a compiled and interpreted languages? Which one is PERL? Why is this useful?
- b) BUG BUSTER; what's wrong with this program; if (\$val == 4) then {print \$val;} elseif (\$val >4) {print "more than 4 ";}
- c) What is the difference between = & == operators?
- d) What are the differences between print, printf & sprintf ? When would you use each one?
- e) What is a file handle? What are the STDIN, STDOUT & STDERR file handles used for?
- Q.2 Write a script that prompts you for two numbers. Test to make sure that neither [10] number is negative and the second number is not zero. If both numbers meet each of those requirements divide the first by the second and print the result.

OR

Write a note on scalar variable, lists. Explain different types of operators and datatypes.

- Q.3 a) Write a program that accepts input as multiple words on different lines and [05] combine those words into single string.
 - b) What do the following operators do?

* * ne || * =

Q.4 Write a subroutine that takes a test of numbers and squares them all, returning [10] the list of squares. If there are elements in the string that are not numbers, delete them from the final list.

P.T.O.

[05]

Q.5 Answer the following:

- a) What sorts of tasks in pattern matching useful for? Name them.
- **b)** What are Bioperl module?
- c) What are Packages?
- d) What does CGI stand for? What's it used for?
- e) BUG BUSTER; print 'Search for what?' ; chomp (\$ pat = < STDIN>) ; while (<>) { while (/ \$pat /) { \$ count ++ ; } }
- Q.6 What is object oriented programming? Explain methods, classes and objects [10] in PERL.

Q. 7	a)	Define the term pattern matching and regular expressions.	[05]
	b)	How to Print Complex Data Structures?	[05]

Q.8 What do AUTÓLOAD methods do?

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