Avinashilingam Institute for Home Science and Higher Education for Women

(Deemed to be University under Category 'A' by MHRD, Estd. u/s 3 of UGC Act 1956)
Re-accredited with 'A+' Grade by NAAC. Recognised by UGC Under Section 12B
Coimbatore - 641 043, Tamil Nadu, India

Master's Degree Examination – June 2021
IV Semester

Class : II M.Sc. **Time: 3 Hours**
Major : Bioinformatics **Max. Marks: 100**

17MBIC22 Systems Biology

PART A 10 x 1 = 10
Choose the Correct Answer

Course Outcomes:

1. Introduction to systems biology
2. Modeling Biochemical reactions
3. Modeling biochemical networks
4. Cellular simulation
5. Methods and software platform for systems biology

1. In SMBL which label is the support for creating and destroying entities during a simulation (CO5; K1)
   a. distrib b. multi c. req d. dyn

2. Select one suitable benefit of bottom- up approach (CO1; K4)
   a. risk identification b. employee buy in
   c. improving collaboration d. risk management

3. Match the following site, which is voluntarily avoided by effector molecule during allosteric regulation of an enzyme (CO2; K5)
   a. allosteric site b. active site c. regulatory site d. catalytic site

4. Choose the appropriate place, where Gillespie algorithm is useful for the simulating reaction (CO3; K3)
   a. within cells b. outside of cells
   c. within the organelles of cell d. none of these

5. Select any one of the peptide from the following which is encoded by GAL genes (CO3; K1)
   a. neuroendocrine peptide b. neurotropic peptide
   c. endocrine peptide d. brain peptide

6. Which one is not the supporting format of sharp module? (CO4; K5)
   a. JPEG b. PDF c. AVIF d. GIF

7. MAP kinase relays cellular proliferation, differentiation, development etc., pointout in what type of cells it takes place (CO3;K4)
   a. Mammalian cells b. Vertebrate c. Eukaryotic cells d. Prokaryotic cells

8. In SMBL i) label "arrays" – is the support for expressing arrays of components ii) label "groups"- denotes a means for grouping elements (CO5; K1)
   a. (i)- true and (ii)- false b. (i)- false and (ii)- true c. (i) & (ii) are false d. (i) & (ii) are true

9. Cell designer is a structure editor, estimate its proper application from the following (CO5;K2)
   a. gene regulatory b. biochemical network & gene regulatory
   c. biochemical pathway d. cell structure

10. Identify the gene which cannot able to code lac genes (CO3;K1)
    a. lacZ b. lacY c. lacI d. lacA

Part B 5 x 6 = 30

Answer ALL questions

Each answer should not exceed 400 words or two pages

11.a. Tabulate the difference between bottom- up approach and top- down approach. (CO1;K1)

(or)

11.b. Predict the importance of system analysis in biology. (CO1;K5)

12.a. Analyze the concept of protein- protein interaction with the application of bioinformatics tools. (CO2;K4)

(or)

12.b. Appraise the process of stochastic modelling. (CO2;K4)

13.a. Explain about reconstruction methods in metabolic networks. (CO3;K2)

(or)

13.b. What is GPCRs and collect the about in which pathway it is involved? (CO3;K6)

14.a. Illustrate the use of “The MONTE CARLO simulation”. (CO4;K4)

(or)

14.b. List the properties and functions of fuzzy sets. (CO4;K1)

15.a. List out the labels in SBML and report their application. (CO6;K6)

(or)

15.b. Explain Hierarchical and Qualitative models. (CO6;K2)

Part C 5 x 12 = 60

Answer ALL questions

Each answer should not exceed 800 words or four pages

16.a. Discuss the approaches and applications of measurement techniques. (CO1;K2)

(or)

16.b. Write a essay on biological networks and system structures identification methods. (CO1;K3)

17.a. Differentiate deterministic models from stochastic models. (CO2;K4)

(or)

17.b. Summarize different types of deterministic models. (CO2;K2)

18.a. Formulate the lac operon concept in detail with clear sketch. (CO3;K3)

(or)

18.b. Discuss about cell signaling with a help of examples and pathways. (CO3;K2)

19.a. Point out the properties and function of different module boundaries. (CO4;K4)

(or)

19.b. Define simulation and give a brief note on simulation analysis methods. (CO4;K1)

20.a. Justify DBRF-MEGN is an algorithm for deducing minimum equivalent gene networks from large scale gene expression. (CO5;K6)

(or)

20.b. Give an elaborate note on multi cellular organism simulation. (CO5;K4)

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