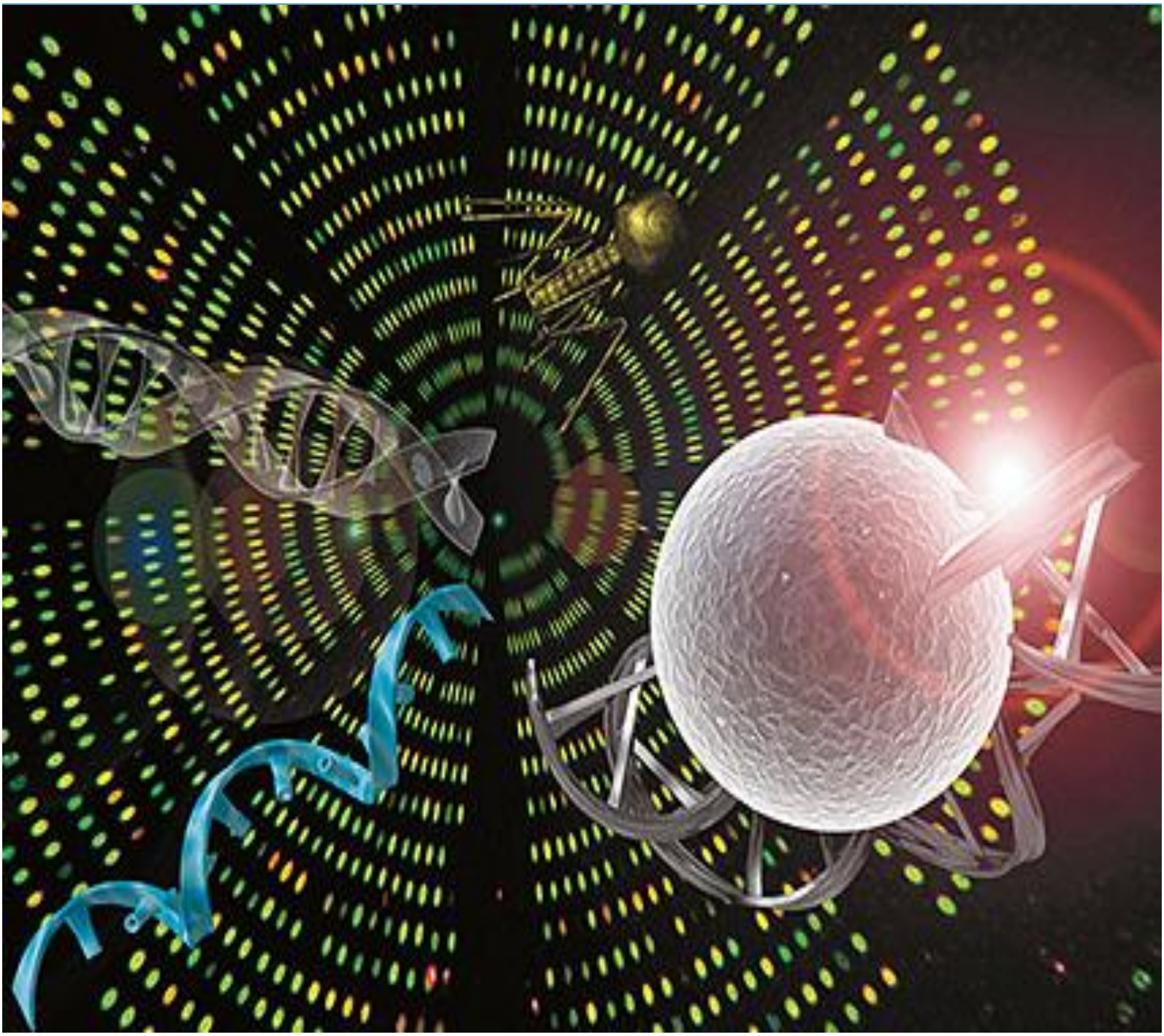

BVDU-RGITBT-ADB (Advanced Diploma in Bioinformatics, Post Graduate Diploma) Syllabus

2019

Bharati Vidyapeeth
(Deemed to be University)
Pune, India.
Founder Chancellor : Dr. Patangrao Kadam
★ Accredited with 'A+' Grade (2017) by NAAC ★
★ Category-I University Status by UGC ★
★ NIRF Ranking - 66 ★
"Social Transformation Through Dynamic Education"

Estd. 1964 Celebrating 50 and Beyond BHARATI VIDYAPEETH

Prof. Dr. Shivajirao Kadam M.Sc., Ph.D.
Chancellor

Prof. Dr. M. M. Salunkhe M.Sc., Ph.D., F.R.S.C.
Vice Chancellor

Dr. Vishwajeet Kadam B.Tech., M.B.A., Ph.D.
Pro Vice Chancellor

G. Jayakumar M.Com., Dip.Pub.Admn.
Registrar

NOTIFICATION NO. 988

It is hereby notified for the information of all concerned that the University authorities have approved the revised course structure, syllabus and rules of examinations of M.Sc. Bioinformatics and Advanced Diploma in Bioinformatics under the Faculty of Interdisciplinary Studies to be implemented from the academic year 2019-20.

A copy of the revised course structure, syllabus and rules of examinations of M.Sc. Bioinformatics and Advanced Diploma in Bioinformatics is enclosed.

All the concerned are requested to make a note of this.

Registrar

Ref. No. BVDU/2019-20/ 162
Date : June 8, 2019

To,

1. The Dean, Faculty of Interdisciplinary Studies, College of Engineering, Pune 411043.
2. The Principal, Rajiv Gandhi Institute of IT & BT, Pune 411043.
3. The Controller of Examinations, BVDU.
4. The IT Cell for uploading in the website.

Notification2019-20

BHARATI VIDYAPEETH DEEMED TO BE UNIVERSITY
PUNE

REVISED SYLLABUS FOR

Advanced Diploma in Bioinformatics
(Post Graduate Diploma)

UNDER

FACULTY OF INTERDISCIPLINARY STUDIES

SYLLABUS OF SEM I – SEM II

UNDER

CREDIT SYSTEM

To be effective from Academic Year

2019-20

Bharati Vidyapeeth Deemed To Be University is a multidisciplinary, multicampus university having 32 Institutions imparting quality education in various disciplines. All programmes of the University are approved by UGC and respective statutory councils. BVDU has been re accredited for the third time with 'A+' grade by NAAC in 2017. UGC has accorded 12B Status [UGC ACT1956] to the university. Ministry of Human Resource and Development, Government of India has awarded "A" category to the University in 2012 based on parameters including innovative programs, research and infrastructure facilities. The University is a member of Association of Indian Universities [AIU] which has ranked BVDU among top 10 universities of India for International students' enrollment. BVDU is also a member of International Association of Universities.

Rajiv Gandhi Institute of IT and Biotechnology is a constituent unit of BVDU established in 2003. The Institute is approved by UGC to conduct graduate and post graduate courses in Biotechnology. The Institute has excellent infrastructure, state-of-the-art laboratories and competent faculty facilitating appropriate learning environment. The Institute offers one undergraduate and four postgraduate programmes in Biotechnology.

INTRODUCTION

The Advanced Diploma in Bioinformatics (ADB) is a full time post graduate diploma offered by **Bharati Vidyapeeth (Deemed to be University (BVDU))** in its constituent unit, Rajiv Gandhi Institute of IT and Biotechnology (RGITBT). The course was initiated in the year 2010 and was designed to facilitate empowerment of students to face cutting edge technological applications in bioinformatics sector. 21st century biology has been transformed into integrative biology due to paradigm shift from reductionist to holistic approach. The data explosion is one of the obvious causes of the transformation to holistic or systems biology mode. In order to have deeper insights in to biological systems, integration of the data from genome to phenome levels to generate dynamic models has surfaced as key area of bioinformatics. On its implementation for 10 years, the curriculum is being revised two times to embrace newer emerging disciplines and value added courses. The revised **ADB** is a full time **60 credits** Program to be implemented in Rajiv Gandhi Institute of IT and Biotechnology from the academic year 2019-20. The feedback of students, alumni, faculty, employers and parents has a substantial contribution in designing of this curriculum.

OBJECTIVES

1. To impart deep knowledge of the discipline
2. Develop skills in relevant areas to enhance employment opportunities
3. Introduce emerging areas of NGS, Drug designing and data mining
4. Build interdisciplinary approach
5. Foster global competence among students
6. Inculcate social and moral values and sense of scientific responsibilities in students

ELIGIBILITY FOR ADMISSION TO THE COURSE

Candidates satisfying following criteria are eligible to apply for ADB Course

1. A student who has obtained Bachelor’s degree with minimum **45%** in (i) B.Sc. (Biotechnology / Microbiology / Biochemistry / Zoology / Botany / Chemistry /Agriculture/ Mathematics /Statistics / Computer Science). (ii)B. Pharm (iii).

MBBS (iv) BDS (v) BAMS (vi) BHMS (vii) B.E. in Computer Science or Information technology or Biomedical Engineering will be considered eligible for admission to M.Sc. Bioinformatics course or **40%** aggregate marks for **SC / ST** category respectively at graduate level university examination.

2. Subject to above conditions, the admission will be based on first come first serve basis.

DURATION OF THE COURSE

The course will be executed in two semesters. The medium of instruction and examination will be only English.

RULES FOR THE COURSE

1. The entire course is of 60 credits.
2. One credit for theory course is equivalent to 15 lectures/tutorials; while one credit for practical course is equivalent to 25 – 30 hrs. of lab /field work or demonstration.
3. The curriculum comprises of core, advanced and value added courses. The Core and Advanced Courses are compulsory where as Value Added are elective.
4. The Core Courses are aimed at providing fundamental knowledge of the discipline. The advanced courses are designed to develop manpower for bioinformatics industries as per current need. The Value Added Courses are intended to inculcate the thrust of new domains of bioinformatics within students.
5. The teaching schedule for the 3 credits and 2 credits theory courses will be 3 and 2 lectures per week respectively. All courses will have one tutorial fortnightly.
6. The respective elective course will be implemented only if more than 10 students enroll for that course.
7. All core courses will be evaluated by University Examination. The elective courses will be evaluated by University Examination and Continuous Assessment.
8. Two extra credits will be awarded to students if there is any significant outcome of their dissertation study. The research outcome in terms of publication in indexed national/International journal; filing of patent; or commercialization of technology will be considered for the award of credits.

RULES FOR EXAMINATION

A: Nature of Examination:

1. Each course will have 40% marks for internal assessment and 60% marks for semester-end examination.
2. The assessment for 1, 2 and 3 Credits courses will be as given in following table:

Table 1: Evaluation pattern for one to three Credit Courses

Course Credits	Marks for UE (60% Weightage)	Marks for IE (40% weightage)	Total Marks for evaluation
1	**15**	**10**	**25**
2	**30**	**20**	**50**
3	**45**	**30**	**75**
4	**60**	**40**	**100**

3. The duration of **60 Marks UE theory paper will be 3.00 Hrs; for 30 Marks 1.30 Hrs.** respectively.
4. The Internal Assessments (IA) will be conducted by the Institute and an end-of-the term University Examination (UE) conducted by the university. The UE will be based on the entire syllabus.
5. The performances at UE and IA will be combined to obtain the Grade Point Average (GPA) for the course.

STANDARD OF PASSING

A: Grading System: A **10-point absolute grading system** will be adapted for grading in each head of passing. The system will have seven grade points, the highest being 10. The grading system shall be as shown in Table-2 below. The performance indicators O, A+, A, B+, B, C, and D shall respectively mean Outstanding, Excellent, Very Good, Good, Average, Satisfactory, and Poor.

Table-2: The grading system under CBCS

Range of Marks (out of 100)	Grade Point	Grade
80 ≥*Marks* ≤ 100	10	O
70 ≥ *Marks* ≤ 80	9	A+
60 ≥*Marks* ≤ 70	8	A
55 ≥*Marks* ≤ 60	7	B+
50 ≥*Marks* ≤ 55	6	B
40 ≥*Marks* ≤ 50	5	C
***Marks* <40**	0	D

1. The grade point average (GPA) for a course shall be calculated by first finding the total marks **out of 100 for the course**. **The corresponding GP (as per the table-2) shall be the GPA for the course**.
2. Two kinds of performance indicators, namely, the Semester Grade Point Average (SGPA) and the Cumulative Grade Point Average (CGPA) shall be computed at the end of each term. The SGPA measures the cumulative performance of a learner in all the courses in a particular semester, while the CGPA measures the cumulative performance in all courses up to and including the current semester. The CGPA of a student when he/she completes the program is his/her final result.
3. The SGPA is calculated by the formula , $SGPA = \frac{\sum Ck \times GPAk}{\sum Ck}$ where *Ck* is the Credit-value assigned to a course and *GPAk* is the GPA obtained by the student in the course. In the above, the sum is taken over all the courses that the student has undertaken for the study during the semester, including those in which he/she might have failed or those for which he/she remained absent. **The SGPA shall be calculated up to two decimal place accuracy.**
4. The CGPA is calculated by the formula , $CGPA = \frac{\sum Ck \times GPAk}{\sum Ck}$ where *Ck* is the Credit-value assigned to a course and *GPAk* is the GPA obtained by the student in the course. In the above, the sum is taken over all the courses that the student has undertaken for the study from the time of his/her enrolment and also the

during the semester for which CGPA is calculated, including those in which he/she might have failed or those for which he/she remained absent. **The CGPA shall be calculated up to two decimal place accuracy.**

5. The CGPA, calculated after the minimum credits specified for the program are 'earned', will be the final result grace marks of 1, 2 or 3 may be awarded to a candidate at UE as per the university rules.

B: Standards of Passing and ATKT rules:

1. For all Core Courses, both UE and IA

Constitute separate heads-of-passing (HoP). In order to pass in such courses and to 'earn' the assigned credits

(a) the learner must obtain a minimum grade point of 5.0 (40% marks) at UE and also a minimum grade point of 5.0 (40% marks) at IA;

OR

(b) If he/she fails in IA, then also the learner passes in the course, **provided that a minimum of 25% is obtained in IA and GPA for the course is at least 6.0 (50%marks) in aggregate**. The GPA for a course will be calculated only if the learner passes in that course.

2. A student who fails at UE in a course has to reappear only at UE as a backlog candidate and clear the HoP. Similarly, a student who fails in a course at IA has to reappear only at IA as a backlog candidate and clear the HoP. **A student who passes in aggregate in a course need not reappear even if he failed at IA if he/she obtains 25% at IA.**

3. The students of Semester I and II & III will be admitted to next Semester even if he/she gets backlog in any of the course. They can reappear in the next semester examination as a backlog candidate.

C: AWARD OF HONOURS:

1. A student who has completed the minimum credits specified for the program shall be declared to have passed in the program. The final result will be in terms

of letter grade and CGPA only and is based on the CGPA of all courses studied and passed. The criteria for the award of honors are given in Table 3.

Table 3: Criteria for the award of honors at the end of the program

Range of CGPA	**Final Grade**	**Performance Descriptor**	**Equivalent Range of Marks (%)**
9.50 ≥ *CGPA*≤ 10.00	O	Outstanding	80 ≥ *Marks* ≤ 100
9.00 ≥*CGPA*≤ 9.49	A+	Excellent	70 ≥ *Marks* ≤ 80
8.00 ≥*CGPA*≤ 8.99	A	Very Good	60 ≥*Marks* ≤ 70
7.00 ≥*CGPA*≤ 7.99	B+	Good	55 ≥ *Marks* ≤ 60
6.00 ≥*CGPA*≤ 6.99	B	Average	50 ≥ *Marks* ≤ 55
5.00 ≥*CGPA*≤ 5.99	C	Satisfactory	40 ≥ *Marks* ≤ 50
CGPA Below 5.00	F	Fail	Marks below 40

THE FORMAT OF THE TRANSCRIPTS

The transcripts may be acquired by the students indicating his/her performance in every semester examination. The transcript shall show the performance indicators given in the following table, in addition to any other information.

Course Number	Course Description	Number of Credits	University Examination		IA/CA		Grade Point Average (GPA)	Result
			Grade	Grade Point	Grade	Grade Point		

Total Cumulative Credits Completed	SGPA	CGPA	Equivalent Marks (%)	**Note: GPA is calculated by adding the UE marks out of 60 and IA marks out of 40. The total marks out of 100 are converted to Grade Point, which will be GPA**

PATTERN FOR ASSESSMENT

A: Pattern of Evaluation for Internal Assessment of Theory Courses:

The weightage for Internal Assessment is 40%. Students for IA of every theory course will be assessed for total of 40 marks for 3 credit course and for 20 marks for 2 credit course which will be cumulative marks obtained in two separate assessments specified below.

1. Two internal written examinations of 20 marks each for 3 credit course and 10 marks each for 2 credit course. A total of the two tests will be considered.
2. An optional assignment/ oral/ open book examination may be undertaken if desired.

B. Pattern of Evaluation for Internal Assessment of Practical Courses:

The Internal Assessment for every practical course will be of 20 Marks for 2 credits and 40 marks for 4 credits practical courses. The students for IA will be assessed on the basis of;

1. Performance for every practical: 10 Marks/20 Marks for 2/4 Credits practical courses respectively. (Marks to be distributed depending on total number of practical)
2. Assignment/ Oral examination/Tour Report: 10/20 Marks for 2/4 Credits courses

C: Pattern of question paper at University Examination

University Examination for 3 credit and 2 credit theory course will be of 60 marks and 30 marks respectively. **For 3 credit course**, the question paper will comprise of 6 questions, 3 questions each in section I and section II. Each question will be of 10 marks. All questions will be compulsory. The pattern of question paper will be as given on next page.

PATTERN OF QUESTION PAPER FOR 3 CREDIT COURSE OF UNIVERSITY THEORY EXAMINATION OF ADB 2019 Credit System Based Course (TOTAL MARKS: 60, TME: 2.00 HRS.)

Instructions to Paper Setter:

1. Question paper of each course will comprise of total 6 questions,
2. Section I will have 3 questions and Section II 3 questions.
3. All questions will be compulsory. Each question will carry an internal option of one extra sub-question.
4. Q. no 1 will be objective, comprising of 7 questions of 2 mark each. They will be based on entire portion of Section I. Students will have to attempt any 5 out of these.
5. Q no 4 will be objective, comprising of 7 questions of 2 mark each. They will be based on entire portion of Section II. Students will have to attempt any 5 out of these.
6. Questions 2 & 3 of **Section I** and 5 & 6 of **Section II** will be descriptive and contain 3 sub-questions of 5 marks each out of which students will attempt any two.
7. Q 2 and 3 will be based solely on Unit I and II whereas Q 5 and 6 will be based on Unit III and IV of the syllabus respectively.
8. Students will attempt answers to Section I and Section II in separate answer books

SECTION I

Q.1 Attempt **Any FIVE** of the following:(Define, Explain why, Fill in the blanks, Give examples, Answer in brief) (10)

a
b
c
d
e
f
g

Q.2 Attempt **Any Two** of the following: (Answer the following, Differentiate Between, Give neat labeled diagram of) (10)

a
b
c

Q.3 Write short notes on **Any Two** of the following (10)

a
b
c

SECTION II

Q.4 Attempt **Any five** of the following: :(Define, explain why, Fill in the blanks, Give examples, Answer in brief) (10)

a
b
c
d
e
f
g

Q.5 Attempt **Any Two** of the following: (Answer the following, Differentiate Between, Give neat labeled diagram of) (10)

a
b
c

Q.6 Write short notes on **Any Two** of the following (10)

a
b
c

QUESTION PAPER PATTERN FOR 2 CREDITS THEORY COURSE AT UNIVERSITY EXAMINATION

For 2 credit course, the question paper will comprise of 4 questions, 2 questions each in section I and section II. Q1 of section I and Q3 of section II will be of 7 marks each while Q2 and Q4 will be of 8 marks each .All questions will be compulsory. The pattern of question paper will be as given on next page.

Pattern of question paper for 2 credit course of university theory examination of ADB 2019 Credit System Based Course (Total Marks: 30, Tme:1.50 Hrs.)

Instructions to Paper Setter:

1. Question paper of each course will comprise of total 4 questions,
2. Section I will have 2questions and Section II 2 questions.
3. All questions will be compulsory. Each question will carry an internal option of one extra sub-question.
4. Questions 1 of section I and 3 of section II will be objective, and contain 7 questions of 1 mark each out of which students will attempt any 5. They will be based on entire portion of Section I and section II respectively.
5. Questions 2 of **Section I** and 4 of **Section II** will be descriptive and contain 3 sub-questions of 5 marks each out of which students will attempt any two.
6. Q 2 and 4 will be based solely on Unit I and II of the syllabus respectively.
7. Students will attempt answers to Section I and Section II in separate answer books

SECTION I

Q.1 Attempt **Any Five** of the following: :(Define, Explain why, Fill in the blanks, Give examples, Answer in brief) (05)

a
b
c
d
e
f

g

Q.2 Attempt **Any Two** of the following: (Answer the following, Differentiate Between, Give neat labeled diagram of, Write short notes on) (10)

a
b
c

SECTION II

Q.3 Attempt **Any Five** of the following: :(Define, Explain why, Fill in the blanks, Give examples, Answer in brief) (05)

a
b
c
d
e
f
g
h

Q.4 Attempt **Any Two** of the following: (Answer the following, Differentiate Between, Give neat labeled diagram of, Write short notes on) (10)

a
b
c

D: PATTERN FOR QUESTION PAPER OF UNIVERSITY PRACTICAL EXAMINATION OF ADB 2019 Credit System Based Course

(Total Marks: 30/60 for 2/4 credit courses, Time: 3 .00/6.00 Hrs.)

Q. 1	Major Practical	(10/20)
Q. 2	Spotting/Minor Experiment	(10/20)
Q. 3	Viva	(05/10)
Q. 4	Journal	(05/10)

Course structure of Advanced Diploma in Bioinformatics Under Credit System Based Course 2019-20

SEMESTER I

Course No. & Description	Title	Credits	IA	Univ. Exam	Total Credits
ADB 101 Basic Course-Theory	Cell Biology **(C)**	**2**	20	30	**28**
ADB 102 Basic Course –Theory	Biochemistry**(C)**	**2**	20	30	
ADB 103 Basic Course –Theory	Biomathematics**(C)**	**2**	20	30	
ADB 104 Basic Course –Theory	Biostatistics**(C)**	**2**	20	30	
ADB 105 Basic Course –Theory	C Programming and Data structure**(C)**	**3**	40	60	
ADB 106 Basic Course – Theory	Biological Informatics**(C)**	**2**	20	30	
ADB 107 Basic Course – Theory	DBMS & MongoDB **(C)**	**3**	40	60	
ADB 108 Core Course - Theory	Python	**2**	20	30	
ADB 109 Basic Course –Practical	Cell Biology and Biochemistry Lab **(C)**	**2**	20	30	
ADB 110 Basic Course –Practical	C Programming and Data Structure Lab **(C)**	**2**	20	30	
ADB 111 Basic Course –Practical	Biological Informatics Lab **(C)**	**2**	20	30	
ADB 112 Basic Course –Practical	DBMS & MongoDB lab**(C)**	**2**	20	30	
ADB 113 Core Course - Practical	Python Lab	**2**	20	30	

SEMESTER II

Course No. & Description	Title	Credits	IA	Univ. Exam	Total Credits
ADB 201 Core Course –Theory	Statistical Analysis System (SAS) **(C)**	**2**	20	30	**32**
ADB 202 Core Course –Theory	R and Data Analytics **(C)**	**3**	40	60	
ADB 203 Core Course –Theory	JAVA and BioJAVA Programming **(C)**	**3**	40	60	
ADB 204 Core Course –Theory	Science of Omics **(C)**	**3**	40	60	
ADB 205 Core Course - Theory	Proteomics **(C)**	**2**	20	30	
ADB 206 Advance Course -Theory	Advanced Bioinformatics	**2**	20	30	
ADB 207 Advance Course -Theory	Data Mining through Machine Learning	**2**	20	30	
ADB 208 Advance Course-Theory	Molecular Modeling & Drug Designing	**3**	40	60	
ADB 209 Core Course - Practical	SAS and Data Analytics lab **(C)**	**2**	20	30	
ADB 210 Core Course - Practical	JAVA and BioJAVA Programming lab **(C)**	**2**	20	30	
ADB 211 Core Course - Practical	Omics Analysis Lab **(C)**	**2**	20	30	
ADB 212 Advance Course - Practical	Advanced Bioinformatics Lab	**2**	20	30	
ADB 213 Advance Course- Practical	Data Mining through Machine Learning Lab	**2**	20	30	
ADB 214 Advance Course- Practical	Molecular Modeling & Drug Designing Lab	**2**	20	30	

Total Credits Offered: 28 C, Sem I+ 32 C, Sem II = 60

SEMESTER I

ADB 101: Cell Biology (C) **Total**

Basic Course – Theory; 2 Credits **30L**

UNIT I

1. **Cell as a basic unit of life.** Basic structure, organization and composition of prokaryotic and eukaryotic cell. Plasma membrane structure and functions, Membrane models. Components of blood & their functions (Plasma, RBC, WBC, Platelets). **4**
2. **Cytoskeleton:** Organization and functions cytoskeleton, Actin filaments, actin binding proteins, Intermediate filaments, Microtubules **3**
3. **Cell Junctions:** Gap junctions, Tight junctions, Cell adhesion-integrins, selectins, cadherins. desmosomes and hemidesmosomes, plasmodesmata **2**
4. **Membrane Transport:** Transport across membrane- passive diffusion, osmosis, active transport, Ion Channels, Na+ and K+ pump, Ca2+ ATPase pump, co-transport, symport, antiport, endocytosis and exocytosis. **6**

UNIT II

6. **Cell Cycle:** Molecular events of cell division and cell cycle, regulation of cell cycle events- Cyclins, Cyclin dependent kinases, inhibitors. **5**
7. **Cell Signaling**: General principles of cell signaling, signaling via G-protein coupled receptors, kinase receptors, role of secondary messengers. **6**
8. Ageing and apoptosis, abnormal development and teratogenesis in animals **4**

References:

1. Alberts, B., Bray, D., Lewis, J., Raf, M., Roberts, K., Watson, J.D. (1994). Molecular Biology of the Cell
2. Cooper, G.M. (1997).The Cell: A molecular approach, ASM Press, USA.
3. Darnell, J., Lodish, H., Baltimore, D. (1990). Molecular Cell Biology. Scientific American Books Inc. NY.
4. Hallwell, B., Gutteridge, J.M.C. (2002). Free Radicals Biology and Medicine. Oxford Press.UK.
5. Karp, G. (1996). Cell and Molecular Biology concepts and experiments, John Wiley and Sons Inc. NY.

ADB 102: Biochemistry (C) **Total**

Basic Course – Theory; 2 Credits **30L**

UNIT I

1.	**Introduction to Biomolecules: Carboydrates, Lipids and Proteins – their biological roles and functions**	**1**
2.	**Carbohydrates:** Classification-on basis of carbon no & functional grs.; Structure with molecular formulae; Stereochemistry (structural and conformational isomers); isomers with one and more chiral centres, properties of stereoisomers; cyclization of sugars; conformations of cyclic forms (chair & boat forms).	**3**
3.	**Important monosaccharides:** 6 C sugars- glucose, fructose, mannose, galactose, 5 C sugars- ribose, deoxyribose, important modified monosaccharides (2-keto-3-deoxy-D-*manno*-octulosonic acid (KDO), 2-keto-3-deoxy-D-*glycero*-D-*galacto*-nonulosonic acid (KDN), sialic acids, aminosugars, sugar acids (their biological role/ occurrence)	**1**
4.	**Linkages in Sugars:** Structure and functions of important di-saccharides (sucrose, lactose, maltose, cellobiose) and poly-saccharides (homo and heteropolymers, storage and structural polymers – starch, glycogen, cellulose, chitin, peptidoglycan)	**1**
5.	**Physico-chemical properties of carbohydrates:**Reducing-non-reducing properties; Exploitation for detection and separation –Benedict's test; Introduction to conjugate sugars (Glycoproteins and glycolipids and their importance)	**2**
6.	**Significance of carbohydrates in microbial, plant and animal system:** ABO blood groups, heparin, lectins, carbohydrate vaccines	**2**
7.	**Lipids:** Occurrence/sources: plant derived oils, ghee	**1**
8.	**Structure :**Structure of fatty acids, triglycerides; Classification viz., simple and compound, structural and storage with examples; unsaturated-saturated, Oils (refined/unrefined significance); fats, waxes, rancidity/spoilage of fats (microbial, oxidative)	**2**
9	**Functions:**Functions in a living system: significance of hydrophobicity and water immiscibility for compartmentalisation, in vitamins, cofactors, for signalling, pigments	**2**
10.	**Lipid conjugates:**Important conjugates and their functions: phospholipids, glycerophospholipids, sphingolipids; structure of membranes, micellar	**3**

structures, Cholesterol- Structure, function and significance

11. **Liposomes:**Liposomes in drug delivery, soaps, bio-surfactants **1**

Physico-chemical properties of carbohydrates and lipids: Compare and contrast of properties arising due to differences in C:O ratio

UNIT II

12. **Amino acids, peptides and proteins:** Occurrence/sources, Naturally occurring amino acids; structures; abbreviated names; stereoisomerism; amphoteric nature of amino acids, Classification of amino acids (on basis of functional groups, essential/non-essential); Chemical reactivity due to functional group (amide, acid, amine); peptides & proteins peptide bond, bond properties, N-Terminal, C-Terminal, Complex proteins– Proteoglycans, Lipoproteins, metalloproteins, phosphoproteins, chromoproteins and their significance **3**

13. **Protein structure:** Primary, secondary (α helix and β conformation), tertiary and quaternary structure. Forces stabilizing molecular structure (covalent bond, ionic bond, hydrogen bond, salt linkage, van der Waal's forces) a brief over view of Ramchandran plot, Structure-Function relationship in proteins with examples of Fibrous proteins, Collagen, Hemoglobin; importance of sequence of amino acids for structure and function of protein (eg. Sickle cell anaemia), **4**

14. **Introduction to enzymes as biocatalysts:** Enzyme-substrate interaction, Rates of enzyme reaction, Concept of Km, Vmax **4**

References:

1. Biochemistry, Berg, J.M., Tymoczko, J. L. and Stryer, L. W.H. Freeman and Co., New York, USA (2003).

2. Principles of Biochemistry by Lehninger, A., Nelson, D. L. and Cox, M.M. W.H. Freeman and Co., New York, USA (2008).
3. Biochemistry, Satyanarayan, U. Books and Allied (P) Ltd., Kolkata, India (2008).

ADB 103: Mathematics (C)

Basic Course – Theory; 2 Credits

Total 30L

UNIT I

1.	Calculus: Limits, Continuity, Differentiation (1D & Partial), Definite Integrals.	**8**
2.	Numerical Techniques: Vector algebra, Matrices, Finding Eigen values & Eigen vectors	**3**
3	2Dimensional & 3Dimensional Geometry: Cartesians and Polar Coordinates, Locus, Equation of a straight line, Pair of straight lines, Circle, Ellipse, Parabola, Hyperbola. 3D Coordinate System, Spherical and Cylindrical Coordinates.	**4**

UNIT II

4.	Ordinary & Partial Differential Equation: 1'st Order & 2'nd Order Ordinary Differential Equations. Nature of Partial Differential Equations, Method of Separation of Variables, Methods for Solving Equations, Solving ODE & PDE.	**5**
5.	Integral transform: Fourier Series, Fourier Transform, Laplace Transform	**7**
6.	Applications To Mathematical Biology: Enzyme kinetics, Immunology, Population genetics, Tumor modeling, Applications of ordinary & partial differential equations to Biology.	**3**

References:

1. Introduction to mathematical methods in bioinformatics by Isaev, Alexander Berlin Springer, 2004.
2. Mathematics in chemistry by K. V. Raman & Pal, Sourav, New Delhi, Vikas publishing house Pvt. ltd., 2005
3. Calculations in molecular biology and biotechnology: a guide to mathematics in the laboratory by Stephenson, F.H. Amsertdam, Academic Press, 2003.
4. Mathematics and computer science in medical imaging by Viergever, Max A.& Todd-Pokropek, Andrew.,1988.
5. Mathematical Methods for Physicists by G. Arfken, Academic Press, New York,1970.
6. Mathematical Biology, by J. D. Murray Springer Verlag, 1989.
7. Mathematical Models in Molecular and Cellular Biology by Segal, L., ed. 1980. Cambridge: Cambridge University Press.
8. Numerical Methods by Balaguruswamy, TMH.

ADB 104: Biostatistics (C) **Total**

Basic Course – Theory; 2 Credits **30L**

UNIT I

1. Probabilities, Random Variables, Multiple Random Variables, Distributions, Random Sampling, Maximum Likelihood Estimators, Bayes Estimators, Mean Squared Error. Hypothesis Testing., t-tests, Likelihood Ratio Tests , Interval Estimation **7**

2. Analysis of Variance ,One-Way Analysis of Variance , Two-Way Analysis of Variance , Regression Models, Simple Linear Regression, Logistic Regression **8**

UNIT II

3. Bayesian Method with Examples, basics of Markov chains, Dynamic Programming and Hidden Markov Model, Metropolis–Hastings Algorithm and Gibbs Sampling. **7**
Gene Expression and Microarray Analysis ,Unsupervised Learning , Supervised Learning Sequence Alignment, Pair-Wise Sequence Analysis, Multiple Sequence Alignment , Sequence Pattern Discovery

4. Some Common Tools and Techniques : (Brief introduction and case studies only) **8**
Classification and clustering (Use WEKA)
Artificial Neural Networks.
Fuzzy Sets and Fuzzy Logic
Genetic Algorithms

Note: Practice on XLminer analysis tool-pack or R (no hand computations). Theory to focus on basic concepts, applications and interpretations/inferencing with secondary data, no mathematical derivations

References:

1. Basics of Bioinformatics, Rui Jiang Xuegong Zhang Michael Q. Zhang Editors
2. “Basic Statistics for Bioinformatics,”(free open-source package called R. /XL Miner for solving problems / No hand computation, Use of XL-miner in practicals - 10 excercises, focus should be on estimating and interpreting outputs)

3. Probability statistics, and reliability for engineers by Boca Raton, Ayyub B. M. & McCuen, R H, CRC Press, 1997.

4. Statistics: concepts and applications by Frank, Harry & Althoen, S. C., Cambridge University Press, 1995.

5. Statistical methods in bioinformatics: an introduction by Ewens, W. J. & Grant, G. R., New York. Springer, 2001.

ADB 105: C Programming and Data Structure (C) **Total**

Basic Course – Theory; 3 Credits **45L**

UNIT I

1. Introduction and First Program **3**
  - Why Programming
  - Types of Programming
  - Introduction to C
  - C programming features
  - Benefits of C
  - Some Facts about C
  - Understanding First C Program

2. Variables and Data Types **3**
  - Identifiers
  - Keywords
  - Data Types
  - Variables
  - Constants

3. Console IO Operations **2**
  - printf function
  - scanf function
  - Unformatted Functions

4. Operators and Expressions **2**
  - Expressions
  - Types of Operators
  - Type Casting

5. Control Flow Statements **2**
  - Decision Making in C
  - If Statement
  - Switch Statement
  - Unconditional Branching
  - While Loop
  - Do…While Loop
  - For Loop
  - Break and continue statements

UNIT II

6. Working with Functions **5**
  - What is a Function

- Benefits of a Function
- Function Terminology
- Array of Structures
- How does Function Works
- Scope and Lifetime of Variables in function
- Storage Classes of Variables
- Call by value and call by reference
- Recursion

7. Working with Arrays and Strings **5**

- Understanding Arrays
- Arrays Declaration and Initialization
- Sample Programs
- Multidimensional Arrays.
- Arrays and Functions
- String operation

UNIT III

8. Pointers **4**

- Understanding Pointers
- Declaring and Initializing Pointers
- Function and Pointer Parameters
- Pointer Arithmetic
- Pointer and Arrays
- Two Dimensional Arrays and Pointers
- void Pointer
- Dynamic allocation of memory
- Difference between malloc and calloc

9. Structure and Unions **4**

- Overview of Structures
- Defining and Using a Structure
- Structures within a Structure
- typedef keyword
- Passing Structures to Functions
- Structure and Pointers
- Unions

10. File Handling **4**

- What is a Stream
- Opening and Closing of Files
- Writing and Reading in Text Format
- Writing and Reading in Binary Format

Unit IV

11. Introduction to Data Structures **2**
Data Structures- Data structure, Abstract Data Types (ADT), Concept of linear and Non-linear, static and dynamic data structures, and relationship among data, data structure

10. Linked Lists **3**
Concept, Comparison of sequential and linked organizations, Primitive operations, Realization of Linked Lists, Linked list operations, Head pointer and header node, Types of linked list- Linear and circular linked lists, Doubly Linked List and operations, Circular Linked List, Singly circular linked list, Doubly circular linked list.

11. Stacks **2**
Stacks- concept, Primitive operations, stack operations, Applications of Stack- Expression, Evaluation and Conversion, Need for prefix and postfix expressions, Postfix expression evaluation, Recursion- concept, Backtracking algorithmic strategy, use of stack in backtracking.

12. Queues **2**
Concept, Realization of Queues Using Arrays , Circular Queue, Advantages of using circular queues, operations on queue

13. Sorting and Searching **2**
Searching- Search Techniques, Sequential search, Binary search.
Sorting methods- Bubble sort, Insertion sort, Selection sort, Quick sort, Heap sort, Shell sort, Comparison of All Sorting Methods.

References:

1. C& Data structures - P. Padmanabham, B.S. Publications.
2. The C Programming Language, B.W. Kernighan, Dennis M.Ritchie, PHI/Pearson Education.
3. C Programming with problem solving, J.A. Jones & K. Harrow, Dreamtech Press.
4. Programming in C - Stephen G. Kochan, III Edition, Pearson Eductaion.
5. Data Structures and Program Design in C, R.Kruse, C.L. Tondo, BP Leung, Shashi M, Second Edition, Pearson Education.
6. Computer science, A structured programming approach using C, B.A. Forouzan and R.F. Gilberg, Third edition, Thomson.
7. DataStructures Using C - A.S.Tanenbaum, Y. Langsam, and M.J. Augenstein, PHI/Pearson education.
8. Let us C – Yashwant Kanetkar

ADB 106: Biological Informatics (C) **Total**
Basic Course – Theory; 2 Credits **30L**

UNIT I

1. Introduction to Bioinformatics **5**

- Nature of biological data types
- Overview of available Bioinformatics resources on the web
- Primary Resource Institutes: NCBI, EMBL & DDBJ
- Hierarchy of Biological databases: Primary, Secondary & Derived

2. Biological Databases & Tools **10**

- Database search engines: Entrez, SRS
- Nucleic acid databases: GenBank, ENA, Gententry
- Protein sequence databases: NCBI Protein, EMBL Protein, PIR-PSD , SwissProt/ UniProtKB/ TrEMBL, Expasy
- Structural Databases: PDB, SCOP, CATH, NDB, CCSD, CSD
- Molecular visualization tools: RasMol, Cn3D, SPDBV, Chime, Mol4D, etc
- Databases and search methods for chemical compounds: PubChem Compound, PubChem Substance, ChEBI, ChEMBL, PDBeChem, RESID, EuroCarbDB
- Sequence Submission Tools: Sequin, BankIt, ENA, IMGT/HLA, DGVa, SPIN, Metagenomics

UNIT II

3. Overview/concepts in Sequence Analysis **7**

- Local & Global alignment, DotPlot, Gap Penalties
- Dynamic Programming, Heuristic Methods
- Pairwise Sequence Alignment algorithms: Needleman & Wunsch, Smith & Waterman
- Scoring matrices for Nucleic acids and proteins: PAM/MDM, BLOSUM, CSW

4. Database Similarity Searches **8**

- BLAST & FASTA

Other Tools: LALIGN, Dotlet

- Multiple Sequence Alignment: ClustalW, ClustalX, PRAS
  Other Tools: DbClustal, Kalign, MAFFT, MUSCLE, MView, T-Coffee
- Motifs, Pattern & Profiles
- Derived Databases: PROSITE, BLOCK, ProDom, Pfam, PRINTS, SBASE

References:

1. Introduction to Bioinformatics by Attwood, T.K. & Parry-Smith, D.J., Delhi, Pearson Education (Singapore) Pte.Ltd., 2001.
2. Bioinformatics: Sequence and Genome Analysis by Mount, David, New York, Cold Spring Harbor Laboratory Press, 2004.
3. Current Protocols in Bioinformatics by Baxevanis, A.D., Davison, D.B., Page, R. D. M. & Petsko, G.A., New York, John Wiley & Sons Inc., 2004.
4. Claverie, J.M. and Notredame C. 2003 Bioinformatics for Dummies. Wiley Editor.
5. Letovsky, S.I. 1999 Bioinformatics. Kluwer Academic Publishers.
6. Baldi, P. and Brunak, S. 1998 Bioinformatics. The MIT Press.
7. Setubal, J. and Meidanis, J. 1996 Introduction to Computational Molecular Biology. PWS Publishing Co., Boston.
8. Lesk, A.M. 2002 Introduction to Bioinformatics. Oxford University Press.
9. Rastogi, S.C., Mendiratta, N. and Rastogi, P. 2004 Bioinformatics: Concepts, Skills & Applications. CBS Publishers & Distributors, New Delhi.
10. Vyas, S.P. and Kohli, D.V., Methods in Biotechnology and Bioengineering.
11. Genetic Library Construction and Screening: Advanced Techniques and Applications: Lab Manual
12. Mont, D.W., Bioinformatics: Sequence and Genome Analysis.
13. Pierre Baldi and Soren Brunak, Bioinformatics: The Machine Learning Approach.

ADB 107: DBMS & MongoDB (C) **Total**

Basic Course – Theory; 3 Credits **45L**

UNIT I

1. DBMS **10**

- Database designing, data capturing
- Data Abstraction
- Data Models
- Instances & Schemes
- E-R Model - Entity and entity sets
- Relations and relationship sets
- E-R diagrams

Reducing E-R Diagrams to tables

UNIT II

2. Basic concepts in Indexing and hashing **15**

- Types of Indexing
- Data warehousing
- Data mining
- Oracle Architecture
- Basic concepts in Oracle:
  - Table space
  - Data files
  - Blocks
  - Extents
  - Segments
  - Oracle Background Processes
  - Control files
  - Oracle Memory Management
  - Rollback
  - Redo logs etc.
- Oracle Report generation, Grants, Roles, Privileges
- Introduction to SQL

UNIT III

3. MongoDB **10**

- Introduction of mongoDB
- Uses and Advantages

- RDBMS/SQL vs. MongoDB
- Structure of MongoDB
- Database, Collection – operation
- Data type

UNIT IV

4.
- CRVD commands **10**
- Limit Records, Sorting Record
- Indexing, Aggregation
- Covered queries
- ObjectID
- Regular Expression

References:

1. Database System Concepts by Hanery Korth and Abraham Silberschatz, McGraw Hill publication.
2. An Introduction to Database Systems by C.J. Date, Addison-Wesley.
3. Database systems by Nilkamal Surve, Tech Max publications.
4. Data Mining: Concepts and Techniques by Jiawei Han and Micheline Kamber, Morgan Kaufmann Publishers.
5. Oracle PL/SQL Programming by Steven Feuerstein, Bill Pribyl, O-Reilly Media.
6. The Relational Database Dictionary by C.J. Date, O'Reilly Media
7. Fundamentals of Database Systems by Elmasri and Navathe, Pearson Education.
8. Database Design and Relational Theory by C.J. Date, O'Reilly Media.
9. Oracle Database 11g A Beginners Guide by Ian Abramson, Michael Abbey, Michael J. Corey and Michelle Malcher, McGraw Hill publication.
10. Developing Bioinformatics Computer Skills by Gibas, & Jambeck, O-Reilly.
11. Linux : The Complete Reference 6th Edition by Richard Petersen, Tata McGraw-Hill Education (2007)

ADB 108: Python **Core Course – Theory; 2 Credits**	**Total** **30L**

UNIT I

1.	**Introduction and Overview of Python**	4

- Installation and understanding Python Environment
- Introduction to Python variables
- basic Operators, keywords, python blocks

2.	**Data types and Program Flow Structures**	**6**

- Numeric data types: int, float, complex, string data type and string operations,
- Control Structure: if, else and elif , nested control structures
- Python Loop : for loops in python using ranges, string, list and dictionaries, while loops in python, Controlling loop using pass, continue, break and else

3.	**String , Lists, Tuples & Dictionaries**	**5**

- String: String operators, String manipulation using in built methods
- Lists: list operations, slicing, list methods, - list comprehension.
- Tuples: definition, assignment, tuple operations.
- Dictionaries: definition, operations and methods

UNIT II

4.	**Functions , Modules & Packages**	**4**

- Function: Definition, Function calling, lambda function
- Modules: Introduction to inbuilt Modules, User defined Modules
- Package: Understanding in built package, building own package,

importing package

5. File Handling & Exceptional Handling **6**

- File Handling: Opening a file, Read and Write operations, File and Directory related methods
- Exceptional Handling: try-except-else, Assert, try-finally, Raise, Exception Names & descriptions, User defined exceptions.

6. Python Database Interaction **5**

- Python Database interaction, Insertion and retrieval information in database.
- Reading and storing information on database.

References:

1. Python: The Complete Reference Paperback – 20 Mar 2018, Martin C. Brown
2. Python Programming: A modular approach by Pearson Paperback – 26 Sep 2017, **by** Taneja Sheetal , Kumar Naveen
3. Python Machine Learning By Example Paperback – Import, 31 May 2017
4. by Yuxi (Hayden) Liu
5. Artificial Intelligence with Python Paperback – Import, 27 Jan 2017, **by** Prateek Joshi
6. Python Deep Learning Paperback – Import, 28 Apr 2017, **by** Valentino Zocca , Gianmario Spacagna , Daniel Slater, Peter Roelants

ADB 109:Cell Biology and Biochemistry Lab (C) (2 Credits, 1 P, 4.00 Hr., Basic Course Practical)

Total 20 P

Cell Biology Lab

1.	Chloroplast isolation from spinach leaves	**1**
2.	Staining of prokaryotic cell organelles**:** Staining of capsule, spore, cell wall and metachromatic granule	**2**
3.	Study of mitosis with onion root tip chromosomes	**2**
4.	Observation of permanent slides of meiosis	**1**
5.	Isolation of nuclei from rat liver	**2**
6.	To determine Erythrocyte (*RBC*) count of a blood sample	**1**
7.	To determine Leucocytes (*WBC*) count of a blood sample	**1**
8.	Temporary mounting of mitochondria by Janus green B	**1**

Biochemistry Lab

9.	Preparation of buffers-acetate buffer & Preparation of biochemical reagents (Benedict’s reagent)	**2**
10.	Isolation of biomolecules a. Isolation of starch from corn (separation on the basis of density) b. Isolation of protein from a suitable source c. Extraction of triglycerides from oilseeds (separation on the basis of differential solubility)	**2**
11.	Quantitative estimation of Glucose by DNSA method	**1**
12.	Quantitative estimation of Protein by Biuret method and absorption at 280 nm	**2**
13.	Acid value or saponification value. Determination with reference to fatty acids.	**2**

References:

1. An Introduction to Practical Biochemistry, Plummer, D.T., Tata-McGraw-Hill Publishing Co., New Delhi (2005).
2. Principles and Techniques of Biochemistry and Molecular Biology, Wilson, K. and Walker, J., Cambridge University Press, New York (2005).

3. Laboratory Manual in Biochemistry, Jayraman J., New Age International (P) Ltd., New Delhi (2007).
4. Alberts B. and Jhonson A. 4th edition (2002) Molecular Biology of the cell, Garland science.
5. Berg J., Tymcoczko J, and Styrer L, 5th edition (2002) Biochemistry, W. H. Freeman and company, New York.
6. Cooper G.M., Hausman R. E. The cell: A molecular approach. 5th edition. ASM Press and Cinauer Associates Inc. 2009
7. Practical Microbiology: Principles and Techniques, (2005), 1st Edn., Kale, V and Bhusari, K. Himalaya Publishing House, New Delhi.

ADB 110: C Programming and Data Structure Lab (C) Total
(2 Credits, 1 P, 4.00 Hr., Basic Course Practical) 15 P

1. **Laboratory assignments based on the following topics in 'C' programming: 5**
   - Data types, operators and expressions, Hierarchy of operators,
   - control statements including decision (if, if-else), loops (while, do-while, for), branching statements(switch, break, continue),
   - Functions,
   - Arrays (1D, 2D- all matrix operations including inverse of a matrix),
   - Strings,
   - File handling etc.

10

2. **Writing C programs for Bioinformatics applications:**
   - Extract a protein or nucleic acid sequence from any of the databank files (GenBank entry, Swiss-Prot, EMBL entry etc.)
   - Interconverting the sequence from one databank format to the other eg. GenBank format to FASTA format, FASTA to PIR format etc.
   - Determining the base composition in a nucleic acid sequence and amino acid composition in a protein sequence.
   - Generating the complimentary sequence of a DNA sequence o Pattern search algorithms o Search for a specific oligonucleotide pattern (eg. GAACATCC) in a given DNA sequence.
   - Find the position where a specific sequence say "GGTCCCGAC" will hybridize a given DNA sequence.
   - Find the restriction enzyme cleavage sites eg. where PVUZ, ECORI etc. will cut the DNA.
   - Locate palindromic sequence stretches in a DNA sequence. Count the number of Open Reading frames (ORF's) in a DNA sequence.
   - Calculate the codon usage in a nucleic acid sequence.
   - Translate a DNA sequence into protein sequence in the forward and reverse frames.
   - Implementation of the Needleman-Wunsch algorithm for pair wise

alignment and testing alignment score with randomized pairs of sequences also.

- Numerical Techniques (4 assignments)
- Basic Formalism, Methods for Solving Equations, Finding Eigen values & Eigenvectors (5 assignments)

References:

1. Let Us C by Yashavant Kanetkar, BPB Publications.
2. The C programming language by Kerighan and Richie, PHI Publication.
3. Programming in ANSI C by Balaguruswamy, Tata McGraw-Hill Education.
4. Sams Teach Yourself C in 21 Days Peter Aitken and Bradley L. Jones, Macmillan Computer publishing.

ADB 111: Biological Informatics lab (C)
(2 Credits, 1 P, 4.00 Hr., Basic Course Practical)

		Total **15 P**
1.	Exploring the integrated database system at NCBI server and querying the PUBMED and GenBank databases using the ENTREZ search engine.	**1**
2.	Exploring the integrated database system at EBI server and searching the EMBL Nucleotide database using the SRS search engine.	**1**
3.	Exploring & querying SWISSPROT & UniProtKB.	**1**
4.	Exploring and querying the PIR database.	**1**
5.	Exploring tools on ExPASY.	**1**
6.	Exploring utilities in EMBOSS packages.	**1**
7.	Explore Pair-wise global alignments.	**1**
8.	Explore Pair-wise local alignments.	**1**
9.	Database (homology) searches using different versions of BLAST and FASTA interpretation of the results to derive the biologically significant relationships of the query sequences (proteins/DNA) with the database sequences. Exploring other databases: LALIGN, Dotlet	**2**
10.	Multiple sequence alignments: CLUSTALW, Clustal Omega, DbClustal, Kalign, MAFFT, MUSCLE, MView, T-Coffee.	**2**
11.	Exploring Alignment Analysis tools: AMAS, CINEMA, MaxAlign, PhyloGibbs, SVA, PVS.	**1**
12.	Exploring and using the derived databases: PROSITE, PRINTS, BLOCKS, Pfam and Prodom for pattern searching, domain searches etc.	**1**
13.	Studying the format & content of structural databases & visualization of structure using Rasmol, Cn3D and other utilities.	**1**

References:

1. Bioinformatics: A Practical Guide to the analysis of Genes and Proteins (3^{rd} Ed.) by Baxevanis, A.D. & Ouellettee, B., F. F., New York, John Wiley & Sons, Inc. Publications, 2004.
2. Practical Bioinformatics, Michael Agostino, 1stEdition,

ISBN:9780815344568 , September 26, 2012

3. Bioinformatics: A Practical Approach, Shui Qing Ye, CRC Press, 20-Aug-2007
4. Bioinformatics: Methods Express, Paul Dear (Editor) , Publication Date: September 18, 2007 | ISBN-10: 190484216X | ISBN-13: 978-1904842163 | Edition: 1st Edition
5. Current Protocols in Bioinformatics by Baxevanis, A.D., Davison, D.B., Page, R. D. M. & Petsko, G.A., New York, John Wiley & Sons Inc., 2004.
6. Bioinformatics: Sequence, Structure and Databanks: A Practical Approach [Paperback]

ADB 112: DBMS & MongoDB lab (C) **Total**

(2 Credits, 1 P, 4.00 Hr., Basic Course Practical) **20 P**

1. **Part I: ORACLE** **2**

   Assignment based on “Data Definition Language”.
   - A set of SQL commands used to create table, modify table structure, drop table, rename table.
2. Assignment based on “Data Manipulation Language” **2**
   - A set of SQL commands used to change the data within the database.
   - Insertion of records in the tables, updating of all or specific set of records in tables.
   - Viewing the attributes of table’s column.
3. Assignment based on “Data Query Language” **2**
   - Different forms of Select statement
   - Arithmetic and logical operators.
   - Range searching and pattern matching.
4. Assignment based on defining Constraints. **2**
   - Types: I/O constraints like Primary Key, Foreign key, Null and Unique
   - Constraints. Business constraints like check constraints.
5. Assignment based on using joins. **2**
   - Joining multiple tables, joining a table to it.
6. - Granting rights on user objects such as Tables, Views, and Sequences. **2**
   - Revoking rights on user objects such as Tables, Views, and Sequences.
   - XAMPP for MySQL
   -
7. **Part II: MongoDB based practical** **8**

References:

1. Database System Concepts by Hanery Korth and Abraham Silberschatz, McGraw Hill publication.
2. An Introduction to Database Systems by C.J. Date, Addison-Wesley.

3. Database systems by Nilkamal Surve, Tech Max publications.
4. Data Mining: Concepts and Techniques by Jiawei Han and Micheline Kamber, Morgan Kaufmann publishers.
5. Oracle PL/SQL Programming by Steven Feuerstein, Bill Pribyl, O-Reilly Media.
6. The Relational Database Dictionary by C.J. Date, O'Reilly Media
7. Fundamentals of Database Systems by Elmasri and Navathe, Pearson Education.
8. Oracle Database 11g A Beginners Guide by Ian Abramson, Michael Abbey, Michael J. Corey and Michelle Malcher, McGraw Hill publication.

ADB 113: Python lab — Total
(2 Credits, 1 P, 4.00 Hr., Core Course Practical) — 20 labs

1. Basic Python Programming **10**

- Python Basic
- Python Basic (Part -II)
- Python Data Types - String
- Python Data Types - List
- Python Data Types - Dictionary
- Python Data Types - Tuple
- Python Data Types - Sets
- Python Array
- Python Conditional statements and loops
- Python functions

2. Python Data Structures and Algorithms **3**

- Data Structure
- Search and Sorting
- Recursion

3. **7**

- Python Date Time
- Python Class
- Python Math
- Python File Input Output
- Python Regular Expression

References:

1. https://www.w3resource.com/python-exercises/
2. Python: The Complete Reference Paperback – 20 Mar 2018, Martin C. Brown
3. Python Programming: A modular approach by Pearson Paperback – 26 Sep 2017, **by** Taneja Sheetal , Kumar Naveen
4. Python Machine Learning By Example Paperback – Import, 31 May 2017
5. by Yuxi (Hayden) Liu
6. Artificial Intelligence with Python Paperback – Import, 27 Jan 2017, **by** Prateek Joshi
7. Python Deep Learning Paperback – Import, 28 Apr 2017, **by** Valentino Zocca , Gianmario Spacagna , Daniel Slater, Peter Roelants

SEMESTER II

ADB 201: Statistical Analysis System (SAS) (C) **Total**

Core Course – Theory; 2 Credits **30L**

UNIT I

1. **Introduction to SAS** **1**
   - An overview of SAS foundation
   - Introduction to SAS programs submitting a SAS program
   - Working with SAS program syntax
2. **Accessing Data** **1**
   - Examining SAS data sets
   - Accessing SAS libraries- Proc contents
3. **Reading and Creating SAS Data sets** **2**
   - Introduction to SAS Data sets
   - Reading from existing SAS Data Sets
   - Reading Spreadsheet and Database Data
   - Reading Raw Data Files
     - Reading standard delimited data
     - Reading nonstandard delimited data
     - Handling missing data
     - Reading raw data files with formatted input
     - Controlling when a record loads
4. **Formatting Data Values** **1**
   - Using SAS formats
   - Creating user-defined formats
5. **Manipulating Data** **2**
   - using SAS functions
   - conditional processing
6. **CoADBning SAS Data Sets** **2**
   - Concatening
   - Merging - one-one, one-many, merging with non-matches
7. **Processing Data in groups** **1**

8. Processing Data Iteratively 2

- DO loop processing
- conditional DO loop processing
- SAS array processing
- using SAS arrays

9. Restuction / Rotating SAS Data Set 1

10. Creating Summary Reports 2

- Proc Print
- Proc Freq
- Proc Report
- Proc Tabulate
- Report Enhancement

UNIT II

11. SAS Macros Language 1

- Purpose of Macro Facility
- Program Flow

12. Macro Variables introduction to macro variables 2

- Automatic macro variables
- Macro variable references
- User-defined macro variables
- Delimiting macro variable references

13. Macro Definitions defining and calling a macro 2

- Macro parameters
- DATA Step and SQL Interfaces creating macro variables in the DATA step

14. DATA Step and SQL Interfaces creating macro variables in the 2

DATA step

- Indirect references to macro variables
- Creating macro variables in SQL

15.	**Macro Programs conditional processing**	**2**

- Parameter validation
- Iterative processing
- Global and local symbol tables

16.	**SAS SQL – Language**	**1**

- Introduction to SAS- SQL
- Basic Queries
- Overview of the SQL procedure
- Specifying columns
- Specifying rows

17.	**Types of Joins**	**1**
18.	**Introduction to Subqueries**	**2**
19.	**Set Operators**	**2**

References:

1. Berger, J. O. (1985), Statistical Decision Theory and Bayesian Analysis, 2nd Edition, New York: Springer-Verlag.
2. Cameron, A. C. and Trivedi, P. K. (1998), Regression Analysis of Count Data, Cambridge: Cambridge University Press.
3. Gallant, A. R. (1987), Nonlinear Statistical Models, New York: John Wiley & Sons.
4. Gelman, A., Carlin, J. B., Stern, H. S., and Rubin, D. B. (2004) , Bayesian Data Analysis, 2nd Edition, London: Chapman & Hall.
5. Powers, D. A. and Xie, Y. (2000), Statistical Methods for Categorical Data Analysis, San Diego: Academic Press.
6. Schervish, M. J. (1995), Theory of Statistics, New York: Springer-Verlag.

ADB 202: R and Data Analytics (C) **Total**

Core Course – Theory; 3 Credits **45 L**

UNIT I

1. An Introduction to R and Basic Programming **5**

- Overview
- Environment set up (Note: Only for Lab Demonstration)
- Data Types
- Variables
- Operator
- Decision making

2. R Core Programming **5**

- Loops
- Functions
- Strings
- Vector
- List
- Matrix

UNIT II

3. R Core Programming **5**

- Arrays
- Factors
- Data Frames
- Packages
- Data Shaping
- Library

4. R Charts and Graphs **5**

- R-Pie Chart
- R – Bar Chart

- R- Box Plots
- R - Histogram
- R- Line Graph
- R- Scatter Plots

UNIT III

5. R Data Interfaces 1 **5**
- R-CSV
- R-Excel
- R-Binary files
- R-XML files

6. R Data Interfaces 1 **5**
- R-JSON files
- R-Web Data
- R-Database
- R- NoSQL

UNIT IV

7. Analytics with R Statistics **6**
- Mean, Median, Mode
- Normal Distribution
- Multiple regression
- Supervised Model
- Unsupervised Model

8. Algorithm **9**
- Logistic regression
- Linear Regression
- Decision tree
- Random Forest
- SVM model

References:

1. Data Analysis with R: A comprehensive guide to manipulating, analyzing, and visualizing data in R, Tony Fischetti, 2nd Edition Paperback – Import, 28 Mar 2018
2. Python Machine Learning, Uxi (Hayden) Liu By Example Paperback,– Import, 31 May 2017
3. Data Analytics for Beginners: Basic Guide to Master Data Analytics Paperback – November 3, 2016, by Paul Kinley
4. Data Analytics Made Accessible: 2019 edition Kindle Edition by Anil Maheshwari
5. Learn R in a Day, 2013, Kindle Edition, by Steven Murray
6. Beginning R: The Statistical Programming Language, 2013 by Mark Gardener, Paperback
7. Statistical Programming in R, 5 June 2017 by K.G. Srinivasa and G.M. Siddesh Paperback

ADB 203: JAVA and BioJAVA Programming (C) **Total**

Core Course – Theory; 3 Credits **45L**

UNIT I

1. An Introduction to Java **2**

A Short History of Java

- Features or buzzwords of Java
- Comparison of Java and C++
- Java Environment
- Simple java program
- Java Tools – jdb, javap, javadoc
- Java IDE – Eclipse/NetBeans (Note: Only for Lab Demonstration)

2. An Overview of Java **4**

- Types of Comments
- Data Types
- Final Variable
- Declaring 1D, 2D array
- Accepting input using Command line argument
- Accepting input from console (Using Buffered Reader class)

3. Objects and Classes **6**

- Defining Your Own Classes
- Access Specifiers (public, protected, private, default)
- Array of Objects
- Constructor, Overloading Constructors and use of ‘this’ Keyword
- Static block, static Fields and methods
- Predefined class – Object class methods (equals(), toString(), hashcode(),getClass())
- Creating, Accessing and using Packages
- Creating jar file and manifest file

- Wrapper Classes
- Garbage Collection (finalize() Method)

UNIT II

4. Inheritance and Interface **7**

- Inheritance Basics (extends Keyword) and Types of Inheritance
- Superclass, Subclass and use of Super Keyword
- Method Overriding and runtime polymorphism
- Use of final keyword related to method and class
- Use of abstract class and abstract methods
- Defining and Implementing Interfaces
- Runtime polymorphism using interface
- Object Cloning

5. Exception Handling **4**

Dealing Errors

- Exception class, Checked and Unchecked exception
- Catching exception and exception handling
- Creating user defined exception
- Assertions

UNIT III

6. Strings, Streams and Files **5**

- String class and StringBuffer Class
- Formatting string data using format() method
- Using the File class
- Stream classes
- Byte Stream classes
- Character Stream Classes
- Creation of files
- Reading/Writing characters and bytes

- Handling primitive data types
- Random Access files

7. Collection **6**

Introduction to the Collection framework

- List – ArrayList, LinkedList and Vector,Stack,Queue
- Set - HashSet, TreeSet, and LinkedHashSet
- Map – HashMap, LinkedHashMap, Hashtable and TreeMap
- Interfaces such as Comparator, Iterator, ListIterator, Enumeration

UNIT IV

8. Database Programming **6**

- The design of jdbc, jdbc configuration
- Types of drivers
- Create and Execute sql statements, query execution
- The Result Set Object

9. Multithreading **3**

- What are threads?
- Life cycle of thread
- Running and starting thread using Thread class
- Thread priorities
- Running multiple threads
- The Runnable interface
- Synchronization and interthread communication

10. Networking **2**

Networking basics – Protocol, Addressing, DNS, URL, Socket, Port

- The java.net package – InetAddress, URL, URLConnection class
- SocketServer and Socket class
- Creating a Socket to a remote host on a port (creating TCP client and server)

- Simple Socket Program Example

References:

1. Introduction to Bioinformatics by Attwood, T.K. & Parry-Smith, D.J., Delhi, Complete reference Java by Herbert Schildt(5th edition)
2. Java 2 programming black books, Steven Horlzner
3. Programming with Java , A primer ,Forth edition , By E. Balagurusamy
4. Core Java Volume-I-Fundamentals, Eighth Edition, Cay S. Horstmann, Gary Cornell,
   Prentice Hall, Sun Microsystems Press
5. Core Java Volume-II-Advanced Features, Eighth Edition, Cay S. Horstmann, Gary
6. Cornell, Prentice Hall, Sun Microsystems Press

ADB 204: Science of Omics (C) **Total**

Core Course – Theory; 3 Credits **45L**

UNIT I

1. **Introduction to Genomics:** **5**

- Genome sequencing:
  - Strategies & Approaches
  - Conventional DNA sequencing methodologies
  - NGS(Next generation sequencing)
    - ✓ Introduction, Next-generation sequencing methods,
    - ✓ NGS File formats (Recognizing different file formats related to genome sequencing data),
    - ✓ NGS data quality check & cleaning,
  - Third generation sequencing

2. Genome Assemblies: **6**

  - Reference assembly, Assembly statistics & visualization,
  - De-novo assemblies & assemblers for genome makeup(MIRA, RAYMETA etc)
- Basic Aspects of Genome Annotation
- Genome mapping techniques: Genetic Mapping and Physical mapping
- Structural Genomics and Functional Genomics

UNIT II

3. **Genomics and Comparative genomics Databases:** **6**

- Genome Databases: Genome Sequence DataBase (GSDB), Genome Database (GDB), 1000 Genomes Project , AceDB, FlyBase, UCSC Genome Browser, Wormbase, MaizeGDB, MGI
- Comparative Genomics Databases: COG, VirGen, CORG, HOBACGEN, Homophila, XREFdb, Gramene
- Genetic Disorders Databases: OMIM, OMIA, Genetic Association

Database, Genetic Disorder Guide, IGDD, DisGenet, Genetic Disorder UK

4. Genomics and Comparative genomics Tools: 6

- Genome Alignments tools:BLAST2, MUMmer, PipMaker, VISTA
- Comparison of Gene Order :GeneOrder, Gene Synteny
- Prediction of genes: ORFs, Prediction of Signal sequences (Promoters, Primers, splice sites, UTRs etc.), Operons
- Primer Designing Tools: Primer, Primer3, NetPrimer, Primerfinder
- DNA/RNA Sequence Analysis: CENSOR, Gene Finder, GENEID, GenHunt, GENIE, GRAIL, ORD ID, ORF Finder, ORFGene, Pol3Scan, tRNAscan
- Translation Tools: Translation Tool, The Protein Machine, 6 Frame Translation Tool, Reverse Translation Tools
- Restriction Analysis Tools: WEB Cutter, ENZFINDER, TACG

UNIT III

5. Transcriptomics: 6

- Biology of Transcription
- Search for transcription factor binding sites
- RNA Sequencing & Techniques of RNA analysis RNA-Seq, Microarrays, Regulatory RNAs: small or large, Computational prediction of miRNA target genes, RNA Darkmatter
- Generating Transcriptome expression Data

6. Metagenomics: 6

- Introduction & Study of metagenomics
- Metagenomics Samples
- Qualitative and quantitative analysis of metagenome: DGGE, T-RFLP, RT-PCR, NGS
- Sequence to identification of biodiversity
- Metagenomics Algorithms (metagenomics data analysis): RAST, IMG/M,

MEGAN

UNIT IV

7. Metabolomics: 5

- Fundamental concept,
- Tools of metabolomics- Capillary electrophoresis, Gas chromatography, Electrochemical detectors
- Case studies.

8. Lipidomics: 2

Basic concepts and tools Case studies

9. Degradomics: 3

- Techniques and concepts
- Approaches to identify the protease and protease-substrate repertoires, or
- 'degradomes', on an organism-wide scale
- Uncover new roles for proteases in vivo.
- Identification of new pharmaceutical targets to treat disease (Emerging degradomic)

References:

1. She Has Her Mother's Laugh: The Powers, Perversions, and Potential of Heredity Hardcover – May 29, 2018, Dutton; 1st Edition by Carl Zimmer
2. The Gene: An Intimate History Paperback – May 2, 2017, **by** Siddhartha Mukherjee
3. Introduction to genomics by Arthur M. Lesk, 2007, Published by OUP Oxford
4. Bioinformatics and Functional Genomics, Textbook by Jonathan Pevsner, 2003, Wiley publication
5. Metabolomics- Methods and Protocols by Wolfram Weckwerth, Humana Press.
6. Lipidomics- Technologies and Applications by Kim Ekroos, Wiley-VCH.
7. Web/Journal Resources.
8. Transcriptomics: Expression Pattern Analysis, Virendra Gomase, Somnath Tagore; VDM Publishing, 2009 – Science

ADB 205: Proteomics (C) **Total**

Core Course – Theory; 2 Credits **30L**

UNIT I

1. Overview of Proteomics: **7**

- Introduction and scope of proteomics
- Protein separation techniques:
    - ion-exchange
    - size-exclusion and
    - affinity chromatography techniques
    - Polyacrylamide gel electrophoresis
    - Two dimensional PAGE for proteome analysis; Image analysis of 2D gels

2. **1**

- Determination of Amino acid composition
    - Hydrolysis
    - Separation
    - Quantitative analysis

3. **1**

- Protein sequencing Methods
    - Sanger’s method
    - Edman’s method

4. **3**

- Protein structure determination methods:
    - X ray crystallography,
    - Mass spectrometry
    - NMR

5. **Proteomics tools:** **3**

- Protein Databases
- Structural databases: PDB, MMDB, SCOP, CATH.
- 3D structure visualization tools: Rasmol, Pymol, SPDBV, Cn3D (already covered in ADB 106)
- Secondary structure prediction algorithms: Chou-Fasman, Jpred, Psipred, GOR methods; PHD

- 3D structure validation databases: PROSA, Ramchandran Plot, Procheck
- Proteomics tools on Expasy

UNIT II

6.
- Protein modifications: Post transcriptional and post translational **9**
- Applications of proteome analysis to drug; Protein-protein interaction (Two hybrid interaction screening)
- Protein engineering, Protein chips and functional proteomics
- Clinical and biomedical application of proteomics
- Proteome databases
- Proteomics industries

7. Protein-protein interaction Databases : 6
- BIND - Biomolecular Interaction Network Database,
- STRING
- DIP (Database of Interacting Proteins)
- PPI Server
- BIND - Biomolecular Interaction Network Database
- PIM -Hybrigenics
- PathCalling Yeast Interaction Database
- MINT - a Molecular Interactions Database
- GRID - The General Repository for Interaction Datasets
- InterPreTS - protein interaction prediction through tertiary structure

References:

1. Fundamentals of Data Mining in Genomics and Proteomics, By Werner Dubitzky, Martin Granzow, Daniel P. Berrar, 2007, Springer Science + Bussiness Media, LLC.

2. Protein Arrays, Biochips and Proteomics: The Next Phase of Genomic Discovery edited by Joanna S. Albala, Ian Humphery-Smith, ISBN-0-8247-4212-1, 2003,

Marcel Dekker.

3. Proteomics: Methods Express (Methods Express Series) Paperback – Import, 2007, by C. David O'Connor (Editor), B. David Hames (Editor)
4. Proteomics: A Comprehensive Study of Proteins Hardcover – Import, 30 Jun 2017 by Tanner Perry (Editor)
5. Principles of Proteomics, English, Paperback, Twyman, 2004
6. Introduction to Proteomics -Tools for the New Biology by Daniel C. Liebler, Humana Press
7. Mass Spectrometry for Biotechnology by Gary Siuzdak, Academic Press.
8. Proteomics for Biological Discovery by Timothy Veenstra and John Yates, Wiley.

ADB 206: Advanced Bioinformatics **Total**

Advance Course – Theory; 2 Credits **30L**

UNIT I

1.	**Linux:** Linux Essentials, Hands-on Exercises Querying Biological Databases with SQL	**3**
2.	Statistics and graphing software: GraphPad Prism Creating Phylogenetic Trees with MEGA	**3**
3.	**NGS:** ➢ QC'ing Reads ➢ Mapping Next Generation Sequence Reads ➢ Analysis of ChIP-seq data in Galaxy ➢ Analysis of RNA-seq data in Galaxy ➢ Analysis of differential gene expression ➢ Finding and annotating indels in Human genome ➢ Bedtool: Toolset for genome arithmetic	**4**
5.	**Structural Variant Analysis** ➢ Variant detection: VarScan and SVDetect ➢ Variant annotation: TASSEL, GATK	**5**

UNIT II

6.	**Advanced Genomics** Visualizing Genomes: Browsers Introduction to ENSEMBL Integrative Genomics Viewer (IGV) Juggling Genome Coordinates Gene list enrichment analysis Visualizing Genomes: Circos Plots	**5**
7.	**Introduction to Microarray** DNA and Protein Array Microarray data Analysis pipeline Microarray Techniques Data analysis with R/Bioconductor Clustering and Displaying Microarray Data Expression Atlas Cool BaRC Web Tools	**6**
8.	Sequence analysis using DotPlot GeneGo: Bioinformatics Technology for Systems Biology Visualizing Networks: Cytoscape	**4**

References:

1. Next-Generation DNA Sequencing Informatics,Stuart M. Brown, New York University School of Medicine *2013 ISBN 978-1-936113-87-3*
2. Chip Technology, Volume 77,Jörg D. Hoheisel, Alvis Brazma, illustratedPublisherSpringer, 2002, ISBN3540432159, 9783540432159
3. Microarray biochip technology, Mark Schena , illustratedPublisherEaton Pub., 2000, Original fromthe University of California, ISBN1881299376, 9781881299370
4. Discovering Statistics Using R, Andy Field, Jeremy Miles, Zoë Field, SAGE, 2012, ISBN1446258467, 9781446258460
5. The R Book, Michael J. Crawley, John Wiley & Sons, 2012ISBN1118448944, 9781118448946
6. A Guide to MATLAB: For Beginners And Experienced Users, Brian R. Hunt, Ronald L. Lipsman, Jonathan M. Rosenberg, Edition2, illustratedPublisherCambridge University Press, 2006, ISBN1139452533, 9781139452533
7. MATLAB Guide, Desmond J. Higham, Nicholas J. Higham, Edition2, illustratedPublisherSIAM, 2005ISBN0898715784, 9780898715781
8. MATLAB Primer, , Kermit Sigmon, Timothy A. Davis, Edition7, CRC Press, 2004ISBN1420034952, 9781420034950
9. Foundations of Comparative Genomics, Arcady R. Mushegian, Academic Press, 2010ISBN0080546099, 9780080546094
10. Essentials of Genomic and Personalized Medicine, Geoffrey S. Ginsburg, Huntington F Willard, Academic Press, 2009ISBN0080958117, 9780080958118

ADB 207: Data Mining through Machine Learning **Total**

Advance Course – Theory; 2 Credits **30L**

UNIT I

1. Introduction to Machine Learning (ML) **2**

- .Introduction to Artificial Intelligence & Machine Learning,
- Elements of ML,
- Life Cycle of ML,
- Applications of Machine Learning.

2. Introduction to Data Mining **3**

- Data Science and Visualization
- Important Python Libraries
- pandas
- numpy
- scikit-learn
- matplotlib
- seaborn.

3. Biological Data and its Application in Machine Learning **1**

4. Genetic Algorithm **1**

- What is genetic algorithm?
- Types of genetic algorithm
- Introduction to feature selection

5.
- Introduction to Linear Regression **3**
- loss functions
- over fitting
- gradient descent

6. Classification Algorithm **6**

- Logistic Regression,
- Support Vector Machine

- Naïve Bayes Classifier.

UNIT II

7.	Introduction & Types of Unsupervised Learning	**1**
8.	Neural Computation - Introduction to Neural computation - Neural network model	**2**
9.	Evolutionary computation - Introduction to evolutionary Processes - Genetic Operators - Evolutionary Optimization Algorithms	**4**
10.	Fuzzy Computation - Introduction - Fuzzy sets & systems - Ant colony Optimization (ACO)	**3**
11.	Introduction to Human Language Technology & Machine Learning - Stochastic Grammar & linguistics,Language models - Statistical language Model, - Markov model - Hidden Markov Model	**2**
12.	Optimization Techniques - Conjugate Gradient, - Newton Raphson, - Steepest descent, - Simulated annealing	**2**

References:

1. Data Mining: Concepts and Techniques by Han and Kamber, Morgan Kaufmann.
2. Machine Learning by Tom Mitchell, McGraw Hill.
3. Data Mining: Practical Machine Learning Tools and Techniques by Witten and Frank, Elsevier.
4. Biological Sequence Analysis: probabilistic models of proteins and nucleic acids by Durbin, R., Eddy, S., Krogh, A. & Mitchison, G.Cambridge Univ. Press, 1998.
5. Optimization Theory and Application by Rao, S.S., 1984.
6. Discrete optimization by Parker, R. G. & Rardin, R. L., 1988.
7. Stochastic simulation by Repley, Brian D, Wiley series, 1987.
8. Methods of microarray data analysis III by Johnson, K.F. & Lin, S.M. Boston. Kluwer academic publishers, 2003.
9. Exploration and analysis of DNA microarray and protein array data by Amaratunga, D. & Cabrera, J.New Jersey. John Wiley & Sons Inc., 90 BVDU-RGITBT-M.Sc. BIOINFORMATICS- SEM III 2004.
10. Ant colony optimization by Dorigo, Marco & Stutzle, Thomas New Delhi, Prentice-Hall of India Pvt Ltd, 2004.
11. Data mining: introductory and advanced topics by Dunham, M.H.:New Delhi, Pearson Education, 2003.
12. An introduction to bioinformatics algorithms by Jones, Neil.C. & Pevzner, Pavel A. New Delhi, Anne Books, 2005.
13. Fuzzy sets and fuzzy logic: theory and applications by Klir, G.J. & Yuan Bo, New Delhi. Printice Hall of India, 2002. 81-203-1136-1.
14. Fuzzy and neuro-fuzzy systems in medicine by Teodorrescu, HoriaNicolai, Kandel, Abraham. & Jain, Lakhmi, C New York, CRS Press

ADB 208:Molecular Modeling& Drug Designing **Total**

Advance Course –Theory;3 Credits **45L**

UNIT I

1.	Homology Modeling, fold recognition, and ab-initio structure prediction methods - protocols/algorithms.	**3**
2.	General features- bond stretching, angle bending, improper torsions, cross terms, non-bonded interactions, point charges, calculation of atomic charges, polarization, Van Der Waals interactions, hydrogen bond interactions, Water models.	**3**
3.	Types of force field - all atoms force field, united atom force field, etc.	**2**
4.	Molecular Energy minimization methods:steepest descent, conjugate gradient– derivatives, First order steepest decent and conjugate gradients.	**3**

UNIT II

5.	Second order derivatives Newton-Raphson, Minima, maxima saddle points and convergence criteria.-non derivatives minimization methods, the simplex.	**3**
6.	Molecular Dynamics Simulation:Newtonian dynamics, Periodic boundary conditions and minimum image convention, Potential truncation, Neighbor list, Force calculations.	**3**
7.	Classical Monte Carlo: Random numbers, Evaluating integrals using random numbers, Importance sampling, Metropolis algorithm.	**3**
8.	Analysis of simulated trajectories: Radial distribution functions, Self diffusion coefficient.	**3**

UNIT III

9.	**Drug discovery and QSAR** ➢ Drug discovery process, role of Bioinformatics in drug design.	**11**

- Target identification and validation, lead optimization and validation.
- Structure-based drug design and ligand based drug design.
- Concept of *de novo* design for lead identification.
- Structure Activity Relationship:QSARs and QSPRs, QSAR Methodology, Training data, test data and external validation data, applicability domain in QSAR
- 3D QSAR techniques: CoMFA and CoMSIA.

UNIT I V

10. Pharmacophore and molecular docking 11

- Pharmacophore features, Pharmacophore model, Receptor-based and ligand-based pharmacophore modeling.
- Virtual screening based on pharmacophore model.
- Receptor site, molecular docking study, flexible docking, rigid docking, molecular interactions.
- Scoring functions, correlation between ligand-based and receptor-based studies.

References:

1. Molecular Modeling Principles and Applications (2nd Ed.) by Andrew R. Leach, 2001, Prentice Hall, USA.
2. Principles of Protein Structure by G. E. Schulz, 2009, Springer
3. Textbook of Structural Biology by Anders Liljas, Lars Liljas, Jure Piskur and GÃranLindblom, World Scientific Publishic Co. Pvt. Ltd.
4. Structural Bioinformatics, Edited by Jenny Gu, Philip E. Bourne, Wiely Blackwell
5. Computational Structural Biology: Methods and Applications by orstenSchwede, TorstenSchwede, Manuel C. Peitsch, 2008, World Scientific Publishing Company.
6. Molecular Modeling Of Nucleic Acids, Leontis N.B. and SantaLucia J. Jr. (eds), 1998, American Chemical Society.
7. Molecular Modeling of Proteins by Andreas Kukol, 2008, Humana Press.
8. Molecular Modeling and Simulation: An Interdisciplinary Guide by Schlick T., 2012, Springer.
9. Biological Modeling and Simulation: A Survey of Practical Models, Algorithms, and Numerical Methods (Computational Molecular Biology)by Russell Schwartz, The MIT Press, Cambridge, Massachusetts, London, England

ADB 209: SAS and Data Analytics lab (C) **Total**

(2 Credits, 1 P, 4.00 Hr., Core Course Practical) **20P**

1. SAS based practical **10**

2. Data Analysis lab **10**

- Install R from CRAN and setup R studio
- Write a Program to print list of Student, Marks and Percentage considering
    - Different data types variables in R using logical, numeric
    - integer, complex, character and raw
    - Valid/invalid variables declaration
    - Variable assignment
    - Getting variables in environment
    - Class of variables
    - Deleting variables
    - Vectors declaration
    - Different operators demonstration using Arithmetic Operators, Relational Operators, Logical Operators, Assignment Operators, Miscellaneous Operators
    - if-else demonstration for negative, positive and zero number test
    - Switch case for different operations
- Write program to classify odd and even number to demonstrate For, While and Repeat loops with break and next keywords
- Create a function to calculate Area and circumference of circle/rectangle
    - calling a function with/without arguments
    - calling by argument position and names
- Write R program to demonstrate string functions in R , String manipulations in R
    - Vector declaration
    - Accessing vector elements

  - Vector manipulations
- Create a list and modify
  - Name elements
  - Access elements
  - Manipulate the list
  - Merging list
  - convert list to vector
- Create a numeric matrix
  - Access elements
  - Matrix computation
  - Demonstration
- Create array name columns, rows, matrix, Access array elements matrix computations
- Create a categorical vector and convert it to
  - Factor
  - Factor validations
  - Generating levels
  - Order change
- Create a data frame
  - Get structure and summary
  - Extract data from DF
  - Expand the data frame add column and rows
  - Check packages
  - Install packages
  - Load package
  - Join cols/rows in DF
  - Merge DF
  - Melting and casting
- Read/write files and access from
  - CSV files
  - Binary file
  - Xls file

- Read access and manipulate JSON data
    - Download and load data from website
    - Connect to mysql/oracle DB and access data from table
    - Working with MongoDB/Redis
- Create data records and create
    - Plot Pie chart for Profit sharing among individuals. Percentage plotting , pie chart
    - Plot a bar graph for monthly revenue. Group bar graph/stacked chart
    - Plot a boxplot for match data mpg vs cylinder
    - Create a vector and plot a histogram , Ranged histogram
    - Create a vector and plot line, point both graph
    - Plot scatterplot for mtcars$wt and mtcars$mpg
- Create data from Hospital, Patient, and disease use case
    - Calculate mean, median, mode of a distribution for data
    - Demonstration of dnorm, pnorm, qnorm and rnorm
    - Demonstration of multiple regression with mtcar dataset
- Get records and perform below
    - Use case of admission into university
    - Use case for weight calculation
    - Use case for Titanic survival prediction
    - Use case for Car acceptability
    - Use case for Heart disease recognition with caret package

References:

1. Data Analysis with R: A comprehensive guide to manipulating, analyzing, and visualizing data in R, Tony Fischetti, 2nd Edition Paperback – Import, 28 Mar 2018
2. Python Machine Learning, Uxi (Hayden) Liu By Example Paperback,– Import, 31 May 2017
3. Data Analytics for Beginners: Basic Guide to Master Data

Analytics Paperback – November 3, 2016, by Paul Kinley

4. Data Analytics Made Accessible: 2019 edition Kindle Edition by Anil Maheshwari
5. Learn R in a Day, 2013, Kindle Edition, by Steven Murray
6. Beginning R: The Statistical Programming Language, 2013 by Mark Gardener, Paperback
7. Statistical Programming in R, 5 June 2017 by K.G. Srinivasa and G.M. Siddesh Paperback

ADB 210: JAVA and BioJAVA programming Lab (C) **Total**

Core Course – Theory; 2 Credits **20 P**

1.	➢ Class and Method Implementation by – ○ Method overloading ○ Constructor Overloading ○ Static members and methods	**2**
2.	➢ Implementation of Multiple Inheritance using Interface.	**1**
3.	➢ Implementation of Inheritance by ○ Method overriding ○ super constructor and super keyword ○ abstract class	**2**
4.	➢ Implementation of Package	**1**
5.	➢ Program to read basic data types from keyboard using Scanner/BufferedReader and check the entered values' data type for its appropriateness.	**1**
6.	➢ Exception Handling for – ○ Divide by zero error ○ Null values	**2**
7.	➢ Program to read the data from user and save it to two different files, display the contents and exchange the contents of those two files using IO package.	**2**
8.	➢ Synchronization of threads. ➢ Develop an animation program using Multithreading viz. Bouncing Ball. ➢ Implementation of Client / Server mechanism using Socket classes. ➢ Design Database program for Employee details and implement INSERT, ➢ SELECT, DELETE, UPDATE queries. ➢ Design concurrent server that will handle multiple clients using ➢ Multithreading.	**9**

- Develop a simple client-server application using RMI.
- Programs using IO streams.
- Programs using files.

References:

1. Introduction to Bioinformatics by Attwood, T.K. & Parry-Smith, D.J., Delhi, Complete reference Java by Herbert Schildt(5th edition)
2. Java 2 programming black books, Steven Horlzner
3. Programming with Java , A primer ,Forth edition , By E. Balagurusamy
4. Core Java Volume-I-Fundamentals, Eighth Edition, Cay S. Horstmann, Gary Cornell,
   Prentice Hall, Sun Microsystems Press
5. Core Java Volume-II-Advanced Features, Eighth Edition, Cay S. Horstmann, Gary
6. Cornell, Prentice Hall, Sun Microsystems Press

ADB 211: Omics Analysis Lab (C) **Total**

Core Course – Theory; 2 Credits **20P**

1. Browsing & viewing genome data **1**

Ensembl@EBI

- MapViewer@NCBI

2. Explore comparative genomics resources and NCBI and EBI **1**

3. Viewing regions exhibiting Synteny **1**

- Genome assembly
- Genome Annotation:

Using integrated genome annotation servers such as the server

developed at IMTech, Chandigadh

(http://imtech.res.in/raghava/gp.html)

4. Gene Prediction and Gene Modeling **2**

- Prediction of genes and gene structures (gene modeling) using online (web) servers of different methods tailored for prokaryotic and eukaryotic organisms such as GLIMMER, GeneMark, Grail, GENSCAN etc. Interpretation of results and comparison with known gene models (where available). Evaluation of accuracy of the methods.
- Prediction of promoters using methods such as Neural Network Promoter Prediction (NNPP) at Berkeley Drosophila Genome Project server, Genome inspector for coADBned analysis of multiple signals in genomes etc. Using Promoter databases.
- Prediction of alternate splice sites using methods such as Splice Site Prediction by Neural Network (at Berkeley Drosophila Genome Project server), GenScan, NetGene2 GeneSplicer etc. Prediction of PCR primers using Primer 3, ePCR etc.

5.	Comparison of full / partial genomic sequences using following methods to identify conserved genes and map/compare the annotations of the two sequences ➢ BLAST2 ➢ MegaBLAST and Discontiguous MegaBLAST ➢ MUMmer ➢ PipMaker ➢ VISTA ➢ Artemis	**2**
6.	Compare gene order of given genomic sequences using the GeneOrder tool	**1**
7.	Explore and query the comparative genomics databases: COG, VirGen, CORG, HOBACGEN, Homophila, XREFdb, Gramene etc.	**1**
8.	Explore and query SNP and SNP-related databases	**1**
9.	RNA seq data Analysis	**1**
10.	Transcriptomics data analysis	**1**
11.	Metagenomics Data Analysis	**1**
12.	Explore and query the protein-protein interaction databases: DIP, PPI Server, BIND, PIM, PathCalling, MINT, GRID, InterPreTS	**2**
13.	Gene annotation of unknown sequence	**1**
14.	Functional Genomics Using primary databases (such as UniProt) and derived databases such as InterPro, PRINTS, BLOCKS, PRODOM, Pfam etc. along with advanced sequence analysis tools such as profiles searches, pattern searches for function annotation of genomic sequences. Validation and verification of results for known case studies ➢ Using sequence-based and structure-based Function Annotation Servers such as: ProKnow (http://www.doe-ADB.ucla.edu/Services/ProKnow/) ➢ Joined Assembly of Function Annotations (JAFA) at http://jafa.burnham.org/learnMore.html etc. which are integrated	**4**

services for function annotation

- ProFunc (http://www.ebi.ac.uk/thornton-srv/databases/ProFunc)

References:

1. Fundamentals of Data Mining in Genomics and Proteomics, By Werner Dubitzky, Martin Granzow, Daniel P. Berrar, 2007, Springer Science + Bussiness Media, LLC.
2. Protein Arrays, Biochips and Proteomics: The Next Phase of Genomic Discovery edited by Joanna S. Albala, Ian Humphery-Smith, ISBN-0-8247-4212-1, 2003, Marcel Dekker.
3. Proteomics: Methods Express (Methods Express Series) Paperback – Import, 2007, by C. David O'Connor (Editor), B. David Hames (Editor)
4. Principles of Proteomics, English, Paperback, Twyman, 2004.
5. Dale Jeremy, Schantz Malcolm Von. From genes to genomes: concepts and applications of DNA technology. Publisher: John Wiley & Sons Ltd., 2007. ISBN:9780470017340.

9. Brown, T.A., Genomes, 3rd edition Garland Science publishers, 2006. ISBN: 1859960294.
10. Primrose Sandy B., Twyman Richard. Principles of Gene Manipulation and Genomics. Publisher: Wiley-Blackwell. 7th edition 2006. ISBN: 1405135441.

ADB 212: Advanced Bioinformatics Lab **Total**

(2 Credits, 1 P, 4.00 Hr., Advance Course Practical) **20P**

1. **Linux:** Linux Essentials, Hands-on Exercises **2**

Querying Biological Databases with SQL

2. Statistics and graphing software: GraphPad Prism **2**

Creating Phylogenetic Trees with MEGA

3. **NGS:** **4**

- QC'ing Reads
- Mapping Next Generation Sequence Reads
- Analysis of ChIP-seq data in Galaxy
- Analysis of RNA-seq data in Galaxy
- Analysis of differential gene expression
- Finding and annotating indels in Human genome
- Bedtool: Toolset for genome arithmetic

5. **Structural Variant Analysis** **2**

- Variant detection: VarScan and SVDetect
- Variant annotation: TASSEL, GATK

6. **Advanced Genomics** **4**

Visualizing Genomes: Browsers

Introduction to ENSEMBL

Integrative Genomics Viewer (IGV)

Juggling Genome Coordinates

Gene list enrichment analysis

Visualizing Genomes: Circos Plots

7. **Introduction to Microarray** **4**

DNA and Protein Array

Microarray data Analysis pipeline

Microarray Techniques

Data analysis with R/Bioconductor

Clustering and Displaying Microarray Data

	Expression Atlas	
	Cool BaRC Web Tools	
8.	Sequence analysis using DotPlot	**2**
	GeneGo: Bioinformatics Technology for Systems Biology	
	Visualizing Networks: Cytoscape	

References:

1. Next-Generation DNA Sequencing Informatics,Stuart M. Brown, New York University School of Medicine *2013 ISBN 978-1-936113-87-3*
2. Chip Technology, Volume 77,Jörg D. Hoheisel, Alvis Brazma, illustratedPublisherSpringer, 2002, ISBN3540432159, 9783540432159
3. Microarray biochip technology, Mark Schena , illustratedPublisherEaton Pub., 2000, Original fromthe University of California, ISBN1881299376, 9781881299370
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ADB 213: Data Mining through Machine Learning Lab

Total

20P

(2 Credits, 1 P, 4.00 Hr., Advance Course Practical)

Implementation of following Algorithms using Python Programming

20

1. Logistic Regression,
2. Support Vector Machine,
3. Naïve Bayes Classifier. :
4. K- Nearest Neighbors,
5. Random Forest Classifier.
6. K-means Clustering
7. Association Rule Mining
8. Ant colony optimization
9. Simulated annealing algorithm for energy minimization
10. Estimator of transition probabilities for markov models based¬ on various sample sizes

References:

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2. Machine Learning by Tom Mitchell, McGraw Hill.
3. Data Mining: Practical Machine Learning Tools and Techniques by Witten and Frank, Elsevier.
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5. Optimization Theory and Application by Rao, S.S., 1984.
6. Discrete optimization by Parker, R. G. & Rardin, R. L., 1988.
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ADB 214: Molecular Modeling & Drug Designing Lab — Total

(2 Credits, 1 P, 4.00 Hr., Advance Course Practical) — 20P

Molecular Modeling:

- Homology Modeling **10**
- Conformational Analysis
- Molecular dynamics simulations
- Molecular Dynamics analysis

Drug Design:

- Development of 2D QSAR models. **10**
- Development of 3D QSAR models.
- Pharmacophore model.
- Molecular docking study.
  - Rigid Docking
  - Flexible Docking
  - Self Docking
- Virtual Screening.

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2. Principles of Protein Structure by G. E. Schulz, 2009, Springer
3. Textbook of Structural Biology by Anders Liljas, Lars Liljas, Jure Piskur and GÃran Lindblom, World Scientific Publishic Co. Pvt. Ltd.
4. Structural Bioinformatics, Edited by Jenny Gu, Philip E. Bourne, Wiely Blackwell

5. Computational Structural Biology: Methods and Applications by orsten Schwede, Torsten Schwede, Manuel C. Peitsch, 2008, World Scientific Publishing Company.
6. Molecular Modeling Of Nucleic Acids, Leontis N.B. and SantaLucia J. Jr. (eds), 1998, American Chemical Society.
7. Molecular Modeling of Proteins by Andreas Kukol, 2008, Humana Press.
8. Molecular Modeling and Simulation: An Interdisciplinary Guide by Schlick T., 2012, Springer.
9. Biological Modeling and Simulation: A Survey of Practical Models, Algorithms, and Numerical Methods (Computational Molecular Biology) by Russell Schwartz, The MIT Press, Cambridge, Massachusetts, London, England.