



UNIVERSITY OF MYSORE

Syllabus for

“Post-graduate Diploma Program in Personalized Genomic Medicine”
For Skill Development (DBT Sponsored Scheme)

FCBCS-CAGP SYSTEM

Department of Studies in Genetics and Genomics
University of Mysore
Manasagangotri, Mysuru – 570 006

2019-20

PREAMBLE:

The Information and potential use of genomic discoveries are no longer issues left for scientists and medical professionals to handle, but have become ones for the public at large. Rarely a day passes without genomics related story reported in the media. The proposed diploma program is designed to provide advanced knowledge dissemination in the field of genome sciences, applications and laboratory skills needed for molecular diagnostics and precision medicine procedures conducted in a clinical or research environment. The program is intended for those individuals who wish to enhance their laboratory expertise and knowledge in molecular-based methods.

Precision medicine has the potential to fundamentally change how health care is practiced, but requires a trained health care workforce that understands the complexities of this field. One important component of precision medicine is the use of an individual's genomic information to offer targeted treatment, tailored to the individual. Our course aims to provide participants with advanced knowledge of genomics, an overview of the clinical applications of genomic medicine, the skills to evaluate the clinical validity and utility of new tests, and an appreciation of the associated ethical and social issues inherent in this field.

The course is geared towards individuals with a background in the biological sciences and a basic understanding of genetics. It is designed to be succinct and clinically focused, offering both conceptual and practical information about real-world applications of genomics. The syllabus offers a basic knowledge on genomics relevant to the individual patient as well as to patient populations. Further, the lessons also focus on applications of genomics and present the material as case studies, highlighting the strengths, limitations, and issues that arise in the use of each test.

Next-generation sequencing (NGS) has the potential to make genome sequencing an integral aspect of personalized medicine in the near future. The sensitivity and specificity of genetically characterizing mutations in patients has profound implications for treatment choices and predicting potential responses. NGS is arguably one of the most significant technological advances in biological sciences of the last 30 years; we therefore should provide scientific workforce capable of exploiting various NGS platforms to help in advancing the quality of health care.

1. Title of proposed course: **Post-graduate Diploma Program in Personalized Genomic Medicine (PGDPGM)**
2. **DBT, New Delhi has agreed to fund this courses for three years and University has agreed to continue this course after DBT funding**
3. Duration of the Course: **12 months (1 Year/2 semesters)**
4. Objectives of the course:
 - a. **To impart extensive theoretical and practical knowledge required for genomic personalized precision medicine**
 - b. **To create and train scientific workforce to meet the growing pace of Next-generation sequencing (NGS) in clinical genomics**
 - c. **To train and conduct research on valid clinical subjects**
5. Number of seats per year: **12**
6. Mode of selection of students: **Written entrance test**
7. Eligibility for admission
 - **Post-Graduate in Medical Science (MD/MD-Ayurveda/MDS)**
 - **Post-Graduate in Basic Sciences in Biotechnology/Genetics/ Applied Genetics/Genomics/Molecular Biology/Biochemistry/ Zoology/Life Sciences or in equivalent areas**
 - **Post-Graduate in Engineering Sciences (e.g. M.Tech in Biotechnology)**
 - **Post-Graduate in Pharmaceutical Sciences (MPS)**

8. Proposed fee structure: **Rs.50,000 for the course**
9. Recognition of program: **PG Diploma in Personalized Genomic Medicine from University**

**CREDIT MATRIX FOR
Post-graduate Diploma Program in Personalized Genomic Medicine
(PGDPGM) 2019-20**

Semester I					
Paper code	Title of the Course	L	T	P	Credit
1.1	Human Genetics and Diseases	3	1	0	4
1.2	Human Genomics	3	1	0	4
1.3	Molecular Genomics	3	1	0	4
1.4	Precision Genomic Medicine	3	1	0	4
1.5	Genetics and Genomics - Practical - I	0	0	4	4
1.6	Personalized genomic medicine- Practical - II	0	0	4	4
	Total Credits				24
Semester II					
Paper code	Title of the Course	L	T	P	Credit
2.1	Interactive Session	0	2	0	2
2.2	Seminar presentation	0	2	0	2
2.3	Project/Dissertation	0	2	10	12
	Total				16
	Grand Total Credits				40

Detailed syllabus

Paper 1.1: Human Genetics and Diseases

48 Hrs

Unit I

16Hrs

Human Genetics: Introduction to human genetics, human chromosomes, karyotyping, chromosome structure and function, Pedigree analysis, Patterns of Inheritance, Mendelian inheritance, Sex linked Inheritance, Linkage and Interaction of genes, Types of human genetic Diseases.

Unit II

16 Hrs

Genetic basis of Diseases and disorders: a) Monogenic diseases, b) Inborn errors of metabolism, c) Neurogenetic disorders, d) Genetic disorders of Haemopoetic systems, e) Genetic disorders of eye, f) Muscle genetic disorders, g) Genetic disorders in skeleton and skin, h)) Congenital heart diseases,i) Learning disorders, j) Genetics of Infertility, k) Cognitive disorders, l) Complex syndromes, m) Mitochondrial syndromes.

UNIT III

16 Hrs

Diagnosis, Counseling, Therapy and Ethics: a) Prenatal diagnosis: Noninvasive methods and Invasive methods, b)Technology in reproductive assistance, c) Genetic counseling in Mendelian and multifactorial syndromes, d) Gene therapy - Viral and Non-viral methods, Stem cell therapy, RNAi in treatment, miRNAs in cancer: tumor suppressors and oncogenes, e) Ethics -Legal, social and ethical considerations. Protection against Discrimination based on Genetic Information: The Genetic Information and Nondiscrimination Act (GINA).

Paper 1.2: Human Genomics

48Hrs

Unit I

16 Hrs

i) Human genome: Genome organization, gene organization, gene expression and regulation- at chromatin level, transcription and translational levels, epigenetics and epigenomics.

ii) Genome projects: The Human genome project, HapMap Project, The 1000 genome project, and The ENCODE Project.

iii) Epidemiology: Diseases in Populations, population specific diseases and protection, Minor allele frequency, genome architecture between populations, adaptive evolution of human genome.

Unit II

16 Hrs

i) Genomic variations: Single Base Variations (Synonymous, Nonsynonymous, Stop gain, read through, splice site, promoter and TFBs mutations/polymorphisms), Multi Base Variations (Insertions, Deletions, Frame shift), Copy Number Variations (Duplications, Deletions), Structural Variations (Translocations, Inversions).

ii) Human genome mapping methods: Genetic mapping: Linkage analysis (RFLP/MS/SNP), Gene identification using positional and functional cloning approach, Physical mapping: Fluorescence in situ hybridization, comparative genome hybridization, High resolution mapping - STS/EST/MS/SNP/sequencing, Genome-wide association studies: SNP Genotyping- Massarray-Snapshot technique, Axiom genotyping, Sequenom MassARRAY iPLEX Platform.

Unit III

16 Hrs

i) Structural genomics: (a) Assembly of a contiguous DNA sequence, whole –genome shotgun sequencing. (b) Understanding a genome sequence: locating the genes in a genome sequence, determining the functions of individual genes.

ii) Functional genomics: Study of transcriptome (By RNAseq, and Microarray analysis) and Proteome (Interacting proteins by phage display and Yeast two hybrid system, In vitro translation).

iii) Human-Microbial Genomics: Introduction to Metagenomics, Comparative Microbial Genomics: From Sequence to Significance, Infectious Diseases, Emerging Infectious Diseases, Microbial gut flora, Gut-Brain axis, Molecular Phylogenetic Techniques.

Paper 1.3: Molecular Genomics

48 Hrs

Unit I

16 Hrs

i) Genome Structure and Sequence: Whole Genome Sequencing (WGS) (Illumina, Ion, PacBio, MinION), Whole Exome Sequencing (WES) (Agilent capture kits, Illumina-Truseq, Nextera), Targeted Sequencing, Disease specific panels (Cardiac, Brain, Lung diseases), Cancer panels (all onco panels), and Nutri-genomics panel to identify mutations.

ii) Transcriptome: Real-Time RT-PCR, Microarray, and RNAseq of Disease Cells Vs Normal Cells and Tumor cells Vs Normal Cells.

iii) Proteome: Protein characterization by Mass spectrometry – fundamentals, mass spectrometry ionization techniques, mass analyzers – MALDI-TOF, MS-MS, LC-MS-MS; In-gel digestion, peptide mass fragmentation. Mass-spectrometry data: basics, spectra; Sequence data: databases, tools and resources; Mass-spectrometry search engines, Mass spectra analysis – identification, molecular weight, determination of peptide sequence, determination of post-translational modifications, Human Protein Atlas, Human Proteome Map, Protein Networks: String and GeneMANIA Proteome: Co-expression, Co-localization, Physical Interactions, Genetic Interactions, Pathways and Shared Protein Domains of proteins.

Unit II

16 Hrs

i) Biological pathways: Ingenuity Pathway Analysis, Elsevier Pathway Studio, Biocyc, KEGG, WikiPathways, Pathway Commons, and networks based pathway builder.

ii) Regulatory regions: Identifying transcription factors for a coding gene using Transcription Factor Databases like PAZAR and others. Identifying enhancers in the human genome and annotating them to identify mutations in genome. Identifying promoters and transcription factor binding sites for genes.

iii) Role of mutations in Translational Regulatory regions: 5'-cap, secondary structures, multiple uAUGs (up-stream AUGs), IRESs (internal ribosome entry sites), positioning of AUG sequence in Kozak's context, polyadenylation signals and motifs, such as IREs (iron-responsive elements), and Ribosome Binding Sites using MIRVAS and other tools.

Unit III

16 Hrs

i) Cancer Genome: Identifying driver and passenger gene mutations using CRAVAT and other tools, Identifying translocations (balanced and unbalanced) and inversions, Identifying enhancer elements near translocations and inversions.

ii) miRNA genome: Identifying gene targets for miRNAs (miRdb and others), identifying regulatory miRNA's for coding genes, identifying miRNA-mRNA binding sites, Understanding the role of 3'UTR mutations and miRNA gene mutations in altered miRNA-mRNA pairing using BiBiServ-RNA Hybrid.

Paper 1.4: Precision Genomic Medicine

48 Hrs

Unit I

16 Hrs

i) Using WGS/WES: NGS Raw data FASTA Sequence alignment, Genome assemblies of NCBI and UCSC, Variants calling, .VCF files, .VCF annotations, Pipelines for disease specific and traits specific mutation identification, mutation annotation (wANNOVAR, SG-ADVISER and others), gene enrichment analysis, disease gene and candidate gene identification strategies, gene-protein and protein-protein network construction, gene-based drug selection (PharmGKB, DrugBank, DGldb, Druggable Human Proteome), Building pathways using genes bearing mutations, strategies for identifying both known and novel genes for diseases, strategies for identifying both known and novel mutations/polymorphisms in genes, disease risk and protection assessment.

ii) Nutrigenomics: Identifying good and poor metabolizers, Interpretation, Statistics and Data Quality Assurance in Genome Analysis

Unit II

16 Hrs

i) Genotype based: drug toxicity estimation, drug response efficacy, and drug dosing recommendations. Personalized Genomic Medicine map creation, clinical development of drugs and biologics, drug repositioning, personalized report preparation, strategies

for deciding treatment options, counseling patient and family members, ethics and conversing with clinicians and healthcare personnel.

ii) Microarray Transcriptome: Clinical & molecular diagnostics using microarray, microarray based gene expression in cancer cells for personalized treatment, identifying molecular targets for cancer, tumor profiling for targeting cancer treatment and the use of blood-based gene expression profiles in cancer prognosis.

Unit III

16 Hrs

i) Next Generation Sequencing: Handling Big Data, The use of next-generation sequencing for solving diagnostic dilemmas, Methods used in patient populations to uncover associations between genome variation and common diseases, Predictive tests for common, complex diseases.

ii) Drug Development: Pharmacogenomic testing for drug selection, dosing and predicting adverse effects of commonly prescribed drugs, drug-drug interactions. In silico protein modelling, drug target prediction, 3D drug molecule structure and drug-protein docking

iii) Minding The Business of Genomics: The Commercialization of Genetic Testing, Obstacles in Establishing Genetic Testing as Consumer Product, Connecting Consumer Needs with Genetic Testing through Marketing, Challenges to Marketing Genetic Testing, Stimulating Market Growth for Genetic Testing, Integrating Genetic Testing with Clinical Practice. Opportunities and Challenges in the Genomic Era.

Paper 1.5: Practical -1 Genetics and Genomics - 4x2x16=128 Hrs

1. Visit to Institution of Excellence, Vijnana Bhavan, University of Mysore for whole Genome/Exome Sequencing demonstration using NGS.
2. Leukocyte culture and Karyotyping
3. Isolation of DNA from Human Blood by phenol-chloroform extraction method and/ or spin column based.
4. Primer design and DNA amplification by PCR method.
5. Cloning by TA method (Ligation)
6. Competent cell preparation
7. Performing transformation using cloned DNA.

8. Isolation of recombinant DNA
9. Performing restriction digestion, and electrophoresis.
10. Isolation of mRNA from blood sample.
11. cDNA conversion and quantification of expression with real-time PCR of any gene of interest.
12. CNV duplication mapping and Deletion Mapping techniques
13. Whole genome expression analysis using microarray.
14. Integrating expression data with variant annotations, enrichment analysis.
15. Identifying eQTLs to understand the regulatory protein relationships.
16. Whole genome expression analysis using RNASeq.
17. Visit to genetics and genomics Diagnostics Company.

Paper 1.6 Practical -2: Personalized genomic Medicine

4x2x16=128 Hrs

1. Processing .fastq/.bam/.vcf files in several genome aligning programs to perform genome alignment using NGS PROGRAMS: StrandNGS, SVS Golden Helix, Genome Browser, CLC Genomics Workbench, and NCBI Workbench.
2. Performing genome alignment, Whole genome/exome sequence analysis, variant annotations of SNP, InDels and CNVs (VeP, wANNOVAR, SG-ADVISER, IVA etc.), pathway and network establishment.
3. Whole genome/exome sequence analysis.
4. Variant annotations of SNP, InDels and CNVs using Variant Analysis Programs: customized pipelines, Ingenuity Variant Analysis, wANNOVAR, Ensembl-VeP (Variant effector Predictor), and regulomeDB.
5. Gene sequencing with sanger method, gene panel sequencing with NGS.
6. Whole Genome Scans using Microarray based Genome-Wide SNP 6.0 chip.
7. SNP Data Analysis using Golden Helix program and Affymetrix Genotyping Console and CNV Association Software, Genome-wide Association study, CNV studies and CNV annotation.
8. Integrating NGS and expression data in Ingenuity Pathways Analysis and Ingenuity Variant Analysis to identify upstream and downstream targets.
9. Whole Genome sequence analysis to identify structural variations (Gene, Mutations, and Polymorphisms) and their enrichment analysis.
10. Genome-wide Hot-spot detection using HD-CNV and Circos plot generation.
11. Expression and Enrichment analysis: GenespringGX, Affymetrix Transcriptome Analysis Console, WebGestalt, EnrichR, Gorrila, and DAVID.
12. Protein Interaction Network Programs: Cytoscape-GeneMANIA, Ingenuity Pathway Analysis (IPA), Pathway Studio, KEGG and Wikipathways, and Pathway Commons.

Semester II

16 Credits

Paper 2.1: Interactive Session

2x2x16=64 Hrs

Counseling skills and Discussion of utility of NGS in clinical diagnostics and personalized medicine

Paper 2.2: Seminar presentation

2x2x16=64 Hrs

- 1) Published paper in the personalized Genomic Medicine presentation
- 2) Major Project presentation

Paper 2.3: Project/Dissertation

12x2x16= 384 Hrs

Case Studies - Addressing a scientific issue using experimental tools and submission of the report.

Reference:

1. Maxam, A. M., and W. Gilbert. "A New Method for Sequencing DNA." *Proceedings of the National Academy of Sciences of the United States of America* 74, no. 2 (1977): 560–4.
2. Sanger, F., S. Nicklen, et al. "DNA Sequencing with Chain-Terminating Inhibitors." *Proceedings of the National Academy of Sciences of the United States of America* 74, no. 12 (1977): 5463–7.
3. Li, R., A. Montpetit, et al. "Somatic Point Mutations Occurring Early in Development: A Monozygotic Twin Study." *Journal of Medical Genetics* 51, no. 1 (2014): 28–34.
4. Quail, M. A., M. Smith, et al. "A Tale of Three Next Generation Sequencing Platforms: Comparison of Ion Torrent, Pacific Biosciences and Illumina MiSeq sequencers." *BMC Genomics* 13 (2012): 341.
5. Vance, C., A. Al-Chalabi, et al. "Familial Amyotrophic Lateral Sclerosis with Frontotemporal Dementia is Linked to a Locus on Chromosome 9p13.2–21.3." *Brain* 129, no. 4 (2006): 868–76.
6. DeJesus-Hernandez, M., I. R. Mackenzie, et al. "Expanded GGGGCC Hexanucleotide Repeat in Non-Coding Region of C9ORF72 Causes Chromosome 9p-Linked Frontotemporal Dementia and Amyotrophic Lateral Sclerosis." *Neuron* 72, no. 2 (2011): 245–56.
7. Blauw, H. M., C. P. Barnes, et al. "SMN1 Gene Duplications are Associated with Sporadic ALS." *Neurology* 78, no. 11 (2012): 776–80.
8. Nishiguchi, K. M., R. G. Tearle, et al. "Whole Genome Sequencing in Patients with Retinitis Pigmentosa Reveals Pathogenic DNA Structural Changes and NEK2 as a New Disease Gene." *Proceedings of the National Academy of Sciences of the United States of America* 110, no. 40 (2013): 16139–44.

9. Zhang, J., P. Meltzer, et al. "Application of Chromosome Microdissection Probes for Elucidation of BCR-ABL Fusion and Variant Philadelphia Chromosome Translocations in Chronic Myelogenous Leukemia." *Blood* 81, no. 12 (1993): 3365–71.
10. Shah, N. P., J. M. Nicoll, et al. "Multiple BCR-ABL Kinase Domain Mutations Confer Polyclonal Resistance to the Tyrosine Kinase Inhibitor Imatinib (STI571) in Chronic Phase and Blast Crisis Chronic Myeloid Leukemia." *Cancer Cell* 2, no. 2 (2002): 117–25.
11. Kotowski, I. K., A. Pertsemlidis, et al. "A Spectrum of PCSK9 Alleles Contributes to Plasma Levels of Low-Density Lipoprotein Cholesterol." *American Journal of Human Genetics* 78, no. 3 (2006): 410–22.
12. Stein, E. A., S. Mellis, et al. "Effect of a Monoclonal Antibody to PCSK9 on LDL Cholesterol." *New England Journal of Medicine* 366, no. 12 (2012): 1108–18.
13. O'Huallachain, M., K. J. Karczewski, et al. "Extensive Genetic Variation in Somatic Human Tissues." *Proceedings of the National Academy of Sciences of the United States of America* 109, no. 44 (2012): 18018–23.
14. Ng, B. G., K. J. Buckingham, et al. "Mosaicism of the UDP-Galactose Transporter SLC35A2 Causes a Congenital Disorder of Glycosylation." *American Journal of Human Genetics* 92, no. 4 (2013): 632–6.
15. Do, C. B., J. Y. Tung, et al. "Web-Based Genome-Wide Association Study Identifies Two Novel Loci and A Substantial Genetic Component for Parkinson's Disease." *PLoS Genetics* 7 no. 6 (2011): e1002141.
16. Kwak, D., A. Kam, et al. "Open-Phylo: A Customizable Crowd-Computing Platform for Multi Sequence Alignment." *Genome Biology* 14, no. 10 (2013): R116.
17. Chen, Z., J. L. Wang, et al. "Using next-Generation Sequencing as a Genetic Diagnostic Tool in Rare Autosomal Recessive Neurologic Mendelian Disorders." *Neurobiology of Aging* 34, no. 10 (2013): 2442.e11–7.
18. Bainbridge, M. N., W. Wiszniewski, et al. "Whole-Genome Sequencing for Optimized Patient Management." *Science Translational Medicine* 3, no. 87 (2011): 87re3.

Course Format

1. This is a Professional diploma course with 40 credits spanning 12 months including examination.
2. The program consists of lecture-based sessions, hands-on laboratory sessions and research dissertation. Classroom lectures and laboratory sessions are offered based on realistic scenarios. For the diploma, students must complete all credit hours (40) with a 5.5 grade point average.
3. Course is aimed at generating genome analysis specialists in the field of clinical genetic diagnosis.
4. This diploma course will be equivalent to M.Phil degree.

**Operational Guidelines for Flexible Choice Based Credit System (FCBCS)–
Continuous Assessment Grading Pattern (CAGP) for PGDPGM**

Semester I

1. Following are the guidelines set for individual components for theory papers 1.1 to 1.4 and 1.5 to 1.6.

Paper Code and Title	Component	Evaluation Period	Mode of Assessment	Weight- age (%)	Marks
Paper 1.1 – Human Genetics and Diseases	C1	4-6 weeks	15 Multiple Choice Questions	15	15
			Take home assignment Hard copy submission	05	05
Paper 1.2 – Human Genomics	C2	7-11 weeks	Open book test	20	20
			15 Short questions	15	15
Paper 1.3 – Molecular Genomics	C3	12-16 weeks	Take home assignment Online submission	05	05
			MCQs (8) Short notes (3) Long descriptive questions (2)	40	40
Paper 1.4 – Precision Genomics Medicine	C4	17-19 weeks	MCQs (8) Short notes (3) Long descriptive questions (2)	40	40
	Make up in C4	19-20 weeks	Same as C4	40	40

2. Following are the guidelines set for individual components for practical papers

Paper Code and Title	Component	Evaluation Period	Mode of Assessment	Weight-age (%)	Marks
Paper 1.5 – Genetics and Genomics - Practical- I	C1	4-6 weeks	Viva	05	05
			Individual Practical Performance Evaluation (05), Practical Experiment Results Presentation (05) and Practical Records Evaluation (05)	15	15
	C2	7-11 weeks	Viva	05	05
			Individual Practical Performance Evaluation (05)and Practical Experiment Results Presentation (05) Practical Records Evaluation (05)	15	15
Paper 1.6 Personalized Genomic Medicine Practical- II	C3	12-16 weeks	Viva	05	05
			Individual Practical Performance Evaluation (05), Practical Experiment Results Presentation (05) and Practical Records Evaluation (05)	15	15
	C4	17-19 weeks	Viva	05	05
			One major one minor experiment and spotting	35	35

Semester II

Following are the guidelines set for individual components for Tutorial papers and Major Project

Paper Code and Title	Component	Evaluation Period	Mode of Assessment	Weight-age (%)	Marks
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Paper 2.1 – Interactive session Paper 2.2 - Seminar presentation	C1	4-6 weeks	10 minute seminar on the topic of students choice using board	20	20
	C2	7-11 weeks	Group Discussion on the topic of students/ faculty choice	20	20
	C3	12-16 weeks	20 Multiple Choice/ Descriptive Questions/ assignments	20	20
	C4	17-19 weeks	15 minute seminar on the topic of students/ faculty choice using PPT	40	40
Paper 2.3 - Project/ Dissertation	C1	4-6 weeks	10 minute project presentation on background, significance & Objectives	20	20
	C2	7-11 weeks	10 minute project presentation on progress of project	20	20
	C3	12-16 weeks	10 minute project presentation on Progress of project	20	20
	C4	17-19 weeks	15 minute project presentation, Project report submission (All faculty will evaluate project)	40	40

Guidelines for Examination

Guidelines for Multiple Choice Questions (MCQs) test for C-1

- 1). Number of MCQs in a paper shall be 15 for C1.
- 2). No question in the MCQ format shall have “none of the above” as option.
- 3). MCQs for C-1 will be limited to a specific day and time.

Guidelines for Problem solving questions for C-1 to C-3

- 1). Problem solving questions will be given as part of the take home assignment or in class open book test for theory papers lecture hour or in tutorials for respective papers.
- 2). Same problem solving questions can be given to all students or separate questions from respective papers.
- 3). Problem solving questions can be either “take home” or “class-based” for respective papers.
- 4). Problem solving questions will be written.
- 5). Problem solving questions is applicable only theory papers.
- 6). Problem solving questions for C-1 to C-4 will be limited to a specific day of the test or week during which the student works on the take home assignment.

Guidelines for Assignments for C-1 and C-3

- 1). Assignments will be written.
- 2). Assignments are applicable for only theory papers.
- 3). Submission of written assignments is either hard or soft copy based.

4). Assignments for C-1 and C-3 shall be given to the student for one week and the student has to submit the assignment on the stipulated date.

Guidelines for Seminar presentation for C-1 to C-3

- 1). Seminars should be based on respective papers or on research papers of similar syllabus topics.
- 2). Seminars assignments can be group-based or individually delivered.
- 3). Seminars for C-1 to C-3 shall be continuous having single or multiple evaluations and need not be limited to a specific day or time.

Guidelines for Open book test for C-2

- 1). Open book test can be conducted on any day during specified lecture or tutorial hours.
- 2). Open book test is applicable for both theory and practical papers.

Guidelines for Descriptive test for C-3

- 1). A descriptive test will include three questions.
- 2). Descriptive test will be a single entity.
- 3). Descriptive test for C-2 shall have a single evaluation and will be limited to a specific day and time.

Guidelines for evaluation of Practical papers

For each of the C1, C2 and C3 components:

- 1). 5% out of the 20% is awarded for quality of execution of experiments. During each practical class, faculty will evaluate the results obtained by the student. A score will be awarded to the student on a scale of 1 to 10. At the end of the duration of the evaluation period for each component, the score obtained by each student will be totaled and scaled to 5%. (This is for both 1.5 and 1.6 practicals).
- 2). 5% out of 20% is awarded for Practical Experiment Results Presentation. At the end of the duration of the evaluation period for each component, the score obtained by each student will be totaled and scaled to 5%
- 3). Another 10% out of 20% is awarded for the quality writing in the Practical Record Book. In this case also, each experiment documented by the student in the book will be given a score on a scale of 1-10 or 1-5. At the end of the duration of the evaluation period for each component, the score obtained by each student will be totaled and scaled to 10%.
- 4). The final 5% of the grade will be awarded to the student on the basis of his or her performance in the VIVA conducted on the designated day for the particular component. Each student will be given a score on a scale of 1-5.

Guidelines for C4 examination

Scheme of Theory examinations for M.Sc. Genetics

Time: 2 Hours

Max. Marks: 40

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|---|--------|
| I) Multiple Choice 8 Questions covering all the units | 1x8=8 |
| II) Write Short notes on any THREE of the following | 4x3=12 |

Six questions covering all the Units with internal choice

III) Write descriptive answers on any TWO of the following 2x10=20

Three questions covering all the Units

Guidelines for C4 examination

Scheme of Practical examinations for M.Sc. Genetics

Time: 4 Hours

Max. Marks: 40

I) Major experiment	20
II) Minor experiment/ report evaluation	09
III) Identify/Comment on A to C Spotting	2x3=06
IV) Viva	05

General Guidelines

- 1). C-1 to C-3 assessments can be a combination of minimum of any two entities involving assignments, Problem solving questions, Group discussion, Seminar presentation, MCQs, and Descriptive test.
- 2). C-1 to C-3 assessment format should be given by respective faculty one week before the assessment begins.
- 3). C-4 shall be a descriptive theory and practical exams, project report or seminar presentation and the format should be given by respective faculty one month before the assessment begins.
- 4). C-1 to C-3 assessments shall be for a total of 20% of total marks for respective papers.
- 5). C-4 assessment shall be for 40% for respective papers. It is a summative assessment. **The answer keys for the theory questions set by the concern faculty should be provided to the chairman prior to the evaluation by the concerned faculty to avoid ambiguity in grading. The Central valuation will be done in the Department immediately after all the theory examinations. The staff secretary/ course coordinator will compile the marks in the ledger book of the department. The extract of this will be sent to the University to declare the result and print the marks cards.**

Problem solving questions are those that are required to measure the student's ability to solve theoretical or numerical problems, interpret graphical or tabular data.

Assignments can be either written, or demonstration based for both theory and practical papers on a specific topic.

MCQs are Multiple Choice Questions that has four options but without the "none of the above".

Descriptive test are questions having lengthy answers, conducted on a continuous having single or multiple evaluations.

In case unavoidable circumstances prevent the conduction of tests, exams etc. on the above given dates, the same will be conducted on a newly scheduled appropriate date.

Plan and strategy for placement of students graduating with post - graduate diploma in personalized genomic medicine

A). The following 5 companies have expressed interest through the Letter of Intent to receive the trained students for internship and potential employment. These companies have extended their co-operation and copy of their letters are enclosed.

- a) Interpretomics
- b) Genotypic Technology Pvt. Ltd.
- c) Eurofins Clinical Genetics India Pvt. Ltd
- d) PathCare Labs, Hyderabad
- e) Strand Life Sciences, Bengaluru

B). The Centre for Proficiency Development and Placement Services (CPDPS) of the University of Mysore will assist in placement of the diploma students.

C). The CPDPS will direct the trained batch of students for internship and potential employment in these companies.
