Telephone No: 2419208/2419315/2419219/2419361
Fax: 0821-2419363/2419301

e-mail : registrar@uni-mysore.ac.in
www.uni-mysore.ac.in

UNIVERSITY OF MYSORE

Established: 1916

Vishwavidyanilaya Karyasoudha
Crawford Hall, Mysore-570 005

No.AC.2(S)/151/2021-22

Dated: 18.08.2021

NOTIFICATION

Sub: Minor changes in the Syllabus of PG Diploma of Genetics and Genomics from the academic year 2021-22.

Ref: 1.Decision of Board of Studies in Genetics and Genomics (PG) meeting held on 26.11.2020.
2. Decision of the Faculty of Science & Technology Meeting held on 08.02.2021.
3. Decision of the Academic Council meeting held on 07.04.2021.

*****

The Board of Studies in Genetics and Genomics (PG) which met on 26.11.2020 has approved Minor changes are made in PG Diploma program from the academic year 2021-22.

The Faculty of Science and Technology and Academic Council meeting held on 08.02.2021 and 07.04.2021 respectively have approved the above said proposal and the same is hereby notified.

The detailed Syllabus of Genetics and Genomics (PG) course is annexed. The contents may be downloaded **from the University Website i.e., www.uni-mysore.ac.in**.

DRAFT APPROVED BY THE REGISTRAR

18/8

DEPUTY REGISTRAR (ACADEMIC)

Deputy Registrar (Academic)
University of Mysore
Mysore-570 005

To:

1. The Registrar (Evaluation), University of Mysore, Mysore.
2. The Dean, Faculty of Science & Technology, DoS in Psychology, MGM.
3. The Chairperson, DoS Genetics and Genomics (PG), Manasagangotri, Mysore.
4. The Deputy/Assistant Registrar/Superintendent, AB and EB, UOM, Mysore.
5. The P.A. to the Vice-Chancellor/Registrar/Registrar (Evaluation), UOM, Mysore.
6. Office file.

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

2020-21

PREAMBLE:

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. Decoding the human genome in the context of the molecular mechanisms of disease, disease staging, disease progression, and patient outcome has been fundamental to research and practice in genomic medicine. This evolving field has seen significant strides in recent years.

Programme Outcome:

On successful completion of this programme each student will be able to

- Genomic innovation for diagnosis, prognosis, treatment, and drug administration
- Understand and to apply basic, clinical and translational research in the innovation
- Know technological progress from sequencing to the storage, analysis, and reporting of big data
- Achieve skill to handle and explore various NGS platforms to help in advancing the quality of health care

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	Paper Code
1.1	**Human Genetics and Diseases**	3	1	0	**4**	50301
1.2	**Human Genomics**	3	1	0	**4**	50302
1.3	**Molecular Genomics**	3	1	0	**4**	50303
1.4	**Precision Genomic Medicine**	3	1	0	**4**	50304
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	Paper code
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**	

I Semester
24 credits

Paper 1.1: Human Genetics and Diseases 48 Hrs

Course Outcomes:

At the end of the course, the students will be able to

- Perform pedigree analysis to know the inheritance pattern
- Analyze the chromosomal aberrations through karyotyping
- Identify different human genetic disorders and inheritance which will help in diagnosis and therapeutics

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

Course Outcomes:

At the end of the course, the students will be able to understand

- The organization of human genome, structural genomics and functional genomics
- The gene expression and gene regulation mechanisms
- The electronic resources of human gene variations like HapMap, 1000 genome database, and db SNP
- The intricate relationship of microbial and human genome.

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

Course Outcomes:

At the end of the course, the students will be able to

- Perform the WGS and Exome sequencing techniques
- Analyze the Cancer gene panels, Nutrigenomic panels
- Perform Transcriptome and proteome analysis
- Analysis of Metabolomics / pathway and its construction
- Understand the Role of mutations in Translational Regulatory regions
- Understand cancer genomics

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

Course Outcomes:

At the end of the course, the students will be able to

- Perform Individualized analysis based on each person's genome will lead to a very powerful form of preventive medicine.
- Understand The SNPs effect on the protein structure, protein- protein interactions using various software tools and databases.
- Perform the pipeline of structure-based drug designing & docking.
- Knowledge of the ethical issues related to human exome sequencing.
- Understand that Precision medicine is gradually shifting from the reactive testing of single genes toward the proactive testing of multiple genes to improve treatment outcomes, reduce adverse events, and decrease the burden of unnecessary costs for healthcare systems

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, DGIdb, 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 Challe nges in the Genomic Era.

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

At the end of the course, the students will be able to

- Prepare human chromosome karyotype
- Perform all the recombinant DNA techniques
- Learn human genome variations
- Perform the Integrating expression data with variant annotations, enrichment analysis.

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. Competent cell preparation
6. Performing transformation using cloned DNA.
7. Isolation of recombinant DNA
8. Performing restriction digestion, and electrophoresis.
9. Browsing of various Nucleotide and Protein Databases.
   NCBI, EBI, UNIPROT, PDB.
10. Genomic databases: ENSEMBLE, NCBI Genome, Human Genome Databases, Introduction to Genome Browsers.
11. Sequence alignment: pair wise alignment, local and global.
12. Multiple sequence alignment, Clustal-omega.
13. Introduction to motifs, domains, PROSITE, PRODOM, CATH, PRINTS.
14. 3D structure visualization, Rasmol, DS/BIOVIA Discovery Studio Visualizer.
15. Homology modeling of protein 3D structure, Swiss model, SPDBV.
16. Ligand designing, Using Ligand designing softwares, ISIS Draw, Biovia Draw.
17. Docking using Argos-Lab or any other docking tools.

Paper 1.6
Practical -2: Personalized genomic Medicine 4x2x16=128 Hrs

At the end of the course, the students will be able to

- Process the Genomic and exomic NGS data
- Perform all the alignment and pathway and network establishment
- Genome-wide Hot-spot detection
- Protein Interaction Network Programs

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

Course Outcomes:

At the end of the course, the students will be able to

- Adopt to the clinical practices of Clinical laboratories have adopted next generation sequencing (NGS) as a gold standard.
- Through interactive sessions a student will be well versed with the diagnosis of hereditary disorders because of NGS analytic accuracy, high throughput, and potential for cost-effectiveness.
- Counseling skills and Discussion of utility of NGS in clinical diagnostics and personalized medicine

Paper 2.2: Seminar presentation 2x2x16=64 Hrs

Course Outcomes:

At the end of the course, the students

- Will do literature survey and R& D with the papers published in the discipline of personalized Genomic Medicine.
- Will present a review seminar based on papers surveyed.
- This activity will give a skill to the student to conceptualize research projects and solution.

1) Published paper in the personalized Genomic Medicine presentation

2) Major Project presentation

Paper 2.3: Project/Dissertation 12x2x16= 384 Hrs

Course Outcomes:

At the end of the course, the students will be able to

- Do research on a specific disease.
- Identify the genetic variations and changes at molecular level responsible for disease expression.
- Further analyses on effect of genetic variations at protein structure and function level followed by pathway mapping
- Finally consolidates all the findings as a project report.

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 Onozygotic 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 **Paper 1.2 – Human Genomics** **Paper 1.3 – Molecular Genomics** **Paper 1.4 – Precision Genomics Medicine**	C1	4-6 weeks	**15 Multiple Choice Questions**	15	15
			Take home assignment Hard copy submission	05	05
	C2	7-11 weeks	**Open book test**	20	20
	C3	12-16 weeks	**15 Short questions**	15	15
			Take home assignment Online submission	05	05
	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 **Paper 1.6 Personalized Genomic Medicine** **Practical- II**	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
	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
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 evalaute 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*

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) Genotpyic 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.