THE TAMIL NADU Dr. M.G.R. MEDICAL UNIVERSITY, CHENNAI -600 032

REGULATIONS FOR THE POST GRADUATE DIPLOMA IN BIOINFORMATICS

1. SHORT TITLE AND COMMENCEMENT : These regulations shall be called **THE REGULATIONS FOR THE POST - GRADUATE DIPLOMA COURSE IN " BIOINFORMATICS".**

2. REGISTRATION: A candidate admitted into Post-Graduate Diploma Courses in any of the affiliated Institutions of the Tamil Nadu Dr. M.G.R. Medical University, Chennai shall register with the University by remitting the prescribed fees along with the application form for registration duly filled in and forwarded to the Controller of Examinations of t his University through the Head of the affiliated institution within the stipulated date. The candidate's name must be registered in the University within 3 months from the date of his/her admission.

3. ELIGIBILITY: Candidates for admission to the **One year Post-Graduate Diploma in Bioinformatics Course** shall be required to possess the Bachelor of Science in Life sciences from a recognised University acquired as a full-time student.

4. . AGE LIMIT:

No upper age limit for Admission

5. ELIGIBILITY CERTIFICATE:

Candidates who have passed any qualifying examination as stated in (1) other than the Tamil Nadu Dr. M.G.R. Medical University shall obtain an "Eligibility Certificate" from this University by remitting the prescribed fees along with the application form and required documents before seeking admission to any one of the affiliated institutions. The application form is available in the University website :web.tnmgrmu.ac.in.

6. DURATION OF THE COURSE : The period of certified study and training for the Post - Graduate Diploma course shall be **ONE YEAR**.

7. COMMENCEMENT OF THE COURSE:

The course shall commence from **1st September** of the academic year. Cut off date for Admission is **30th September every year**.

8. .MEDIUM OF INSTRUCTION:

English shall be the Medium of Instruction for all the Subjects of study and for examinations for the **POST-GRADUATE DIPLOMA COURSE IN "BIOINFORMATICS".**

9. CURRICULUM:

The Curriculum and the syllabus for the course shall be as prescribed in these regulations and are subject to modifications by the Standing Academic Board from time to time.

10. CUT-OFF DATE OF THE COURSE:

- **i) 30th September of the year concerned**
- ii) The candidates admitted upto **30th September** of the Academic Year shall be registered to take up the **1st year examination during October of the next year**.

11. COMMENCEMENT OF THE EXAMINATION:

15th October / 15 May

If the date of commencement of Examination falls on Saturdays, Sundays or declared Public Holidays, the examination shall begin on the next working day.

12. WORKING DAYS IN AN ACADEMIC YEAR. : The academic year shall consist of not less than **270 working days.**

13. ATTENDANCE REQUIREMENTS FOR ADMISSION TO EXAMINATIONS:

No candidate shall be permitted to appear for the Examination unless he/she put in 85% attendance during his/her period of study and training in the affiliated institution recognized by this University and produces the necessary certificate of study, attendance and progress from the Head of the Institution by maintaining log book.

14. MAINTAINENCE OF LOG BOOK:

1. Every Post-graduate Diploma candidate shall maintain a record of skills he has acquired during the one year training period certified by the various Heads of Departments he has undergone training.

The candidates should also be required to participate in the teaching and training programme of the institute.

In addition, the Head of the Department shall involve their post-graduate candidates in Seminars, Journal Clubs, Group discussions and conferences.

The Head of the Department shall scrutinize the Log Book once in every three months.

At the end of the course, the candidate should summaries the contents and get the Log Book certified by the Head of the Department.

The Log Book should be submitted at the time of practical examination for the scrutiny of the Board of Examiners.

15. MIGRATION/TRANSFER OF CANDIDATES:

1. A student studying in **POST-GRADUATE DIPLOMA COURSE IN "BIOINFORMATICS"** can be allowed to migrate/transfer to another institution of Allied Health Science under the same or another University.

2. Under extraordinary circumstances, the Vice Chancellor shall have the powers to place any migration/transfer he/she deems fit before the Governing Council and get its approval for grant of permission/ratification for Migration/Transfer to the candidates undergoing the course of study in affiliated institutions of this University.

16. RE-ADMISSION AFTER BREAK OF STUDY: The regulations for re-admission are as per the University Common Regulation for Re-admission after break of study for all courses**.**

17. VACATION:

There is no vacation

18. SCHEME OF EXAMINATION:

Paper	Title	Theory		I.A		Total		Practical	
		Max.	Min.	Max.	Min.	Max.	Min.	Max.	Min.
1	Molecular Biology	100	50	50	25	150	75		
2	Bioinformatics Databasis	100	50	50	25	150	75		
3	Genomics, Metagenomics & Sequence Analysis	100	50	50	25	150	75		
4	Proteomics, Structural Biology, Modeling and Drug Design	100	50	50	25	150	75		
5	Systems Biology, R and Data Analytics	100	50	50	25	150	75		
Practical - I	Basic Bioinformatics Laboratory							100	50
Practical - II	Molecular Modeling and Systems Biology Lab							100	50

PRACTICAL & VIVA

Practical		Viva Voce		Total	
Max.	Min.	Max.	Min.	Max.	Min.
100	50	50	25	150	75

DISTRIBUTION OF THE THEORY MARKS

Type of Questions	Distribution of Marks	Total Marks
Long Essays	2 x 20	40
Short Notes	10 x 6	60

Total 100 mark and Minimum pass mark 50

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SYLLABUS FOR POST GRADUATE DIPLOMA IN MEDICAL BIOINFORMATICS

ONE YEAR & NON – SEMESTER PATTERN

THEORY

MODULE – 1 - MOLECULAR BIOLOGY

MODULE – 2- BIOINFORMATICS DATABASES
MODULE – 3 – GENOMICS, METAGENOMICS & SEQUENCE ANALYSIS

MODULE – 4 – PROTEOMICS, STRUCTURAL BIOLOGY, MODELING AND DRUG DESIGN

MODULE – 5 – SYSTEMS BIOLOGY, R and Data Analytics

PRACTICALS & DISSERTATION

PRACTICAL – 1 Basic Bioinformatics Laboratory

PRACTICAL – 2 Molecular Modeling and Systems Biology Lab.

MODULE – 1 - MOLECULAR BIOLOGY

Unit I - Genome organization

Organization of bacterial genome; Structure of eukaryotic chromosomes; Role of nuclear matrix in chromosome organization and function; Matrix binding proteins; Heterochromatin and Euchromatin; DNA reassociation kinetics (Cot curve analysis); Repetitive and unique sequences; Satellite DNA; DNA melting and buoyant density

Unit II - DNA Structure; Replication; Repair & Recombination

Structure of DNA - A-,B-, Z- and triplex DNA; Measurement of properties-Spectrophotometric, CD, AFM and Electron microscope analysis of DNA structure; Replication initiation, elongation and termination in prokaryotes and eukaryotes; Enzymes and accessory proteins; Fidelity; Replication of single stranded circular DNA; Gene stability and DNA repair- enzymes; Photoreactivation; Nucleotide excision repair; Mismatch correction; SOS repair; Recombination: Homologous and non-homologous; Site specific recombination

Unit III - Prokaryotic & Eukaryotic Transcription

Prokaryotic Transcription; Transcription unit; Promoters- Constitutive and Inducible; Operators; Regulatory elements; Initiation; Attenuation; Termination-Rho-dependent and independent; Anti-termination; Transcriptional regulation-Positive and negative; Operon concept-lac, trp, ara, his, and gal operons; Transcriptional control in lambda phage; Transcript processing; Processing of tRNA and rRNA Eukaryotic transcription and regulation; RNA polymerase structure and assembly; RNA polymerase I, II, III; Eukaryotic promoters and enhancers; General Transcription factors; TATA binding proteins (TBP) and TBP associated factors (TAF);

Unit IV - Post Transcriptional Modifications

Processing of hnRNA, tRNA, rRNA; 5'-Cap formation; 3'-end processing and polyadenylation; Splicing; RNA editing; Nuclear export of mRNA; mRNA stability; Catalytic RNA. **Translation & Transport** - Translation machinery; Ribosomes; Composition and assembly; Universal genetic code; Degeneracy of codons; Termination codons; Isoaccepting tRNA; Wobble hypothesis; Mechanism of initiation, elongation and termination; Co- and post-translational modifications; Genetic code in mitochondria; Transport of proteins and molecular chaperones; Protein stability; Protein turnover and degradation.

Unit V - Mutations; Oncogenes and Tumor suppressor genes

Nonsense, missense and point mutations; Intragenic and Intergenic suppression; Frameshift mutations; Physical, chemical and biological mutagens; Transposition - Transposable genetic elements in prokaryotes and eukaryotes; Mechanisms of transposition; Role of transposons in mutation; Viral and cellular oncogenes; Tumor suppressor genes from humans; Structure, function and mechanism of action of pRB and p53 tumor suppressor proteins; Activation of oncogenes and dominant negative effect; Suppression of tumor suppressor genes; Oncogenes as transcriptional activators.

Text/References

1. Benjamin Lewin, Gene IX, 9th Edition, Jones and Barlett Publishers, 2007.
2. J.D. Watson, N.H. Hopkins, J.W Roberts, J. A. Seitz & A.M. Weiner; Molecular Biology of the Gene, 6th Edition,
Benjamin Cummings Publishing Company Inc, 2007.
3. Alberts et al; Molecular Biology of the Cell, 4th edition, Garland, 2002.

MODULE – 2- BIOINFORMATICS DATABASES

Unit 1 - Introduction to Bioinformatics data and databases

Types of Biological data:- Genomic DNA, Complementary DNA, Recombinant DNA, Expressed sequence tags, Sequence-Tagged Sites, Genomic survey sequences; Primary Databases:- GenBank, EMBL, DDBJ; Composite Databases:- NRDB, UniProt; Literature Databases:- Open access and open sources, PubMed, PLoS, Biomed Central, NAR databases; Bioinformatic Resources:- NCBI, EBI, ExPASy, RCSB.

Unit 2 - Genome Databases

Viral genome database:-ICTVdb; Bacterial Genomes database:-Genomes OnLine Database – GOLD, Microbial Genome Database-MBGD; Genome Browsers:- Ensembl, VEGA genome browser, NCBI-NCBI map viewer, KEGG, MIPS, UCSC Genome Browser; Archeal Genomics, Eukaryotic genomes with special reference to model organisms:-Yeast(SGD), Drosophila (FlyBase), C.elegans (WormBase), Rat, Mouse, Human (OMIM / OMIA)

Unit 3 Sequence Databases

Nucleotide sequence Databases:- GenBank, EMBL, DDBJ; Protein sequences Databases:- Swiss-Prot, TrEMBL, UniProt, UniProtKB, UniParc, UniRef, UniMES; Sequence motifsDatabases:- Prosite, ProDom, Pfam, InterPro, Gene Ontology; Sequence file formats:- GenBank, FASTA, PIR, ALN/ClustalW2.

Unit 4 Structure and derived databases

Primary structure databases:- PDB, NDB, MMDB; Secondary structure databases:-Structural Classification of Proteins –SCOP, Class Architecture Topology Homology –CATH, Families of Structurally Similar Proteins –FSSP, Catalytic Site Atlas –CSA; Molecular functions / Enzymatic catalysis databases:- KEGG ENZYME database; Protein-Protein interaction database:- STRING; Chemical Structure database:- Pubchem; Gene Epression database:- GEO, SAGE.

Unit 5 Bioinformatics Database search engines

Text-based search engines (Entrez, DBGET / LinkDB). Sequence similarity based search engines (BLAST and FASTA). Motif-based search engines (ScanProsite and eMOTIF). Structure similarity based search engines (Combinatorial Extension, VAST and DALI). Proteomics tools:- ExPASy server, EMBOSS.

Text Books:

2. Bioinformatics: Sequence and Genome Analysis by Mount D., Cold Spring Harbor Laboratory Press, New York. 2004

3. Bioinformatics- a Practical Guide to the Analysis of Genes and Proteins by Baxevanis, A.D. and Francis Ouellellette, B.F., Wiley India Pvt Ltd. 2009

4. Introduction to bioinformatics by Teresa K. Attwood, David J. Parry-Smith. Pearson Education. 1999

MODULE – 3 – GENOMICS, METAGENOMICS & SEQUENCE ANALYSIS

Unit 1 - Genomics and Metagenomics

Large scale genome sequencing strategies. Genome assembly and annotation. Genome databases of Plants, animals and pathogens. Metagenomics: Gene networks: basic concepts, computational model such as Lambda receptor and lac operon. Prediction of genes, promoters, splice sites, regulatory regions: basic principles, application of methods to prokaryotic and eukaryotic genomes and interpretation of results. Basic concepts on identification of disease genes, role of bioinformatics-OMIM database, reference genome sequence, integrated genomic maps, gene expression profiling; identification of SNPs, SNP database (DbSNP). Role of SNP in Pharmacogenomics, SNP arrays.

Unit 2 Epigenetics

DNA microarray: database and basic tools, Gene Expression Omnibus (GEO), ArrayExpress, SAGE databases DNA microarray: understanding of microarray data, normalizing microarray data, detecting differential gene expression, correlation of gene expression data to biological process and computational analysis tools (especially clustering approaches)

Unit 3 Comparative and Functional genomics

Basic concepts and applications, whole genome alignments: understanding the significance; Artemis, BLAST2, MegaBlast algorithms, PipMaker, AVID, Vista, MUMmer, applications of suffix tree in comparative genomics, synteny and gene order comparisons Comparative genomics databases: COG, VOG - Application of sequence based and structure-based approaches to assignment of gene functions – e.g. sequence comparison, structure analysis (especially active sites, binding sites) and comparison, pattern identification, etc. Use of various derived databases in function assignment, use of SNPs for identification of genetic traits. Gene/Protein function prediction using Machine learning tools viz. Neural network, SVM etc

Unit 4 – Sequence Analysis, Alignment

Basic concepts of sequence similarity, identity and homology, definitions of homologues, orthologues, paralogues and xenologues Scoring matrices: basic concept of a scoring matrix, Matrices for nucleic acid and proteins sequences, PAM and BLOSUM series, matrix derivation methods and principles. Repeats: Tandem and Interspersed repeat finding, Motifs, consensus, position weight matrices. Pairwise sequence alignment – Basic concepts of sequence alignment, gap penalties, Needleman and Wunsch, Smith and Waterman algorithms for pairwise alignments and application in Nucleic acid and protein sequences alignments. Multiple sequence alignments (MSA) – The need for MSA, basic concepts of various approaches for MSA (e.g. progressive, hierarchical etc.). Algorithm of CLUSTALW and PileUp and application, concept of dendrogram and its interpretation, Use of HMM-based Algorithm for MSA (e.g. SAM method)

Unit 5 – Comparative Genomics and Phylogenetics

Basic concepts, Applications of Comparative Genomics: Identifications of Protein coding genes, Regulatory Regions, virulence factors / pathogeneity islands; Reconstruction of metabolic pathways, Genome analysis tools : Artemis, MegaBLAST, Geneplot. Basic concept and definition of sequence patterns, motifs and profiles, various types of pattern representations viz. consensus, regular expression (Prosite-type) and sequence profiles; profile-based database searches using PSI-BLAST. Definition and description of phylogenetic trees and various types of trees, Phylogenetic analysis algorithms such as maximum Parsimony, UPGMA, Transformed Distance, Neighbor-Joining, Probabilistic models and associated algorithms such as Probabilistic models of evolution and maximum likelihood algorithm, maximum parsimony, Bootstrapping methods, use of tools such as Phylip, MEGA, Mr Bayes, ModelTest and ProtTest.

Text Books:

1. Discovering Genomics, Proteomics and Bioinformatics 2nd edition - by A. Malcolm Campbell and Laurie J. Heyer. by Cold Spring Harbor Laboratory Press 2006.

Reference books:

1. Principles of Genome Analysis and Genomics (3rd Ed.) by Primrose, S.B. and Twyman, R.M., Blackwell Publishing Company, Oxford, UK. 2003
2. Introduction to Proteomics – Tools for the new biology (1st Ed.) by Liebler, D.C., Humana Press Inc., New Jersey, USA. 2002
3. Bioinformatics and Functional Genomics by Pevsner, J., John Wiley and Sons, New Jersey, USA. 2003
4. Bioinformatics: Sequence and Genome Analysis by Mount, D., Cold Spring Harbor Laboratory Press, New York. 2004

MODULE – 4 – PROTEOMICS, STRUCTURAL BIOLOGY, MODELING AND DRUG DESIGN

UNIT 1 – Proteomics

Protein arrays: basic principles. Computational methods for identification of polypeptides from mass spectrometry. Protein arrays: bioinformatics-based tools for analysis of proteomics data (Tools available at ExPASy Proteomics server); databases (such as InterPro) and analysis tools. Protein-protein interactions: databases such as DIP, PPI server and tools for analysis of protein-protein interactions

UNIT 2 – Structural Biology

Macromolecules – DNA and RNA: types of base pairing – Watson-Crick and Hoogstein; types of double helices A, B, Z and their geometrical as well as structural features; structural and geometrical parameters of each form and their comparison; various types of interactions of DNA with proteins, small molecules. RNA secondary and tertiary structures, t-RNA tertiary structure. Proteins: Principles of protein structure; anatomy of proteins – Hierarchical organization of protein structure – Primary. Secondary, Super secondary, Tertiary and Quaternary structure; Ramachandran Map.

UNIT 3 - Structure Prediction Strategies and Protein 3D Structures

Secondary structure prediction: Algorithms viz. Chou Fasman, GOR methods; analysis of results and measuring the accuracy of predictions using Q3, Segment overlap, Mathew’s correlation coefficient Identification/assignment of secondary structural elements from the knowledge of 3-D structure of macromolecule using DSSP and STRIDE methods. Purpose of 3-D structure comparison and concepts; Algorithms such as FSSP, CE, VAST and DALI, Fold Classes. Databases of structure-based classification: CATH and SCOP. Structures of oligomeric proteins and study of interaction interfaces.

UNIT 4 – Drug Design

Drug discovery process. Target identification and validation, lead optimization and validation. Methods and Tools in Computer-aided molecular Design, Analog Based drug design:- Pharmacophores (3D database searching, conformation searches, deriving and using 3D Pharmacophore, constrained systematic search, Genetic Algorithm, clique detection techniques, maximum likelihood method) and QSAR. Structure based drug design:- Docking, De Novo Drug Design (Fragment Placements, Connection Methods, Sequential Grow), Virtual screening.

Unit 5 - Structure Activity Relationship

Introduction to QSAR, QSPR, Various Descriptors used in QSARs: Electronics; Topology; Quantum Chemical based Descriptors. Regression Analysis, The Significance and Validity of QSAR Regression Equations, Partial Least Squares (PLS) Analysis, Multi Linear Regression Analysis. Use of Genetic Algorithms, Neural Networks and Principle Components Analysis in the QSAR equations.

Text Books:

1. Computational Chemistry and Molecular Modeling-Principles and Applications by Ramachandran, Deepa and Namboori., 2008, Springer_Verlag.
2. Molecular Modeling Principles and Applications (2nd Ed.) by Andrew R. Leach., Prentice Hall, USA. 2001
3.

Reference:

1. Molecular Modelling for Beginners, (2nd Edition) by Alan Hinchliffe., John Wiley & Sons Ltd.2008
2. Molecular Modeling and Simulation – An Interdisciplinary Guide by Tamar Schlick., Springer-verlag 2000
3. Computational Medicinal Chemistry for Drug Discovery, edited by Patrick Bultinck., Marcel Dekker Inc. 2004

MODULE – 5 – SYSTEMS BIOLOGY, R and Data Analytics

Unit 1 - Introduction & Biological Networks – Systems Biology: Emergent property, Applications in health and diseases. Microarrays and its applications in systems biology. Self-organizing maps and Connectivity maps-definition and its uses. Biological Networks: Degree distribution, Clustering coefficient, Random networks, Scale-free networks, small-world effect. Virtual Erythrocytes, Global human metabolic model. Flux Balance Analysis (FBA): Translating biochemical networks into linear algebra

Unit 2 - Databases and softwares for Systems Biology – Introduction- databases: KEGG, EMP, MetaCyc. Expression databases and other databases related to systems biology. Cytoscape, visANT & CellDesigner.

Unit 3 - Overview of the R language – Defining the R project, Obtaining R, and Generating R codes, Scripts, Text editors for R, Graphical User Interfaces (GUIs) for R, Packages. R Objects and data structures – Variable classes, Vectors and matrices, Data frames and lists, Data sets included in R packages, Summarizing and exploring data, Reading data from external files, Storing data to external files, Creating and storing R workspaces.

Unit 4 - Manipulating objects in R – Mathematical operations (recycling rules, propagation of names, dimensional attributes, NA handling), Basic matrix computation (element-wise multiplication, matrix multiplication, outer product, transpose, eigenvalues, eigenvectors), Textual operations, Basic graphics (high-levelplotting, low-levelplotting, interacting with graphics). Hypothesis testing and data handling – Parametric and nonparametric tests, Chi-square test, t-tests, ANOVA, Correlation and regression, Principal component Analysis.

Unit 5 - Bioconductor – Introduction, Bioconductor packages, ExpressionSet Class, Data annotation, biomaRt, Applications of R in phylogenetics, microarray data analysis, next-generation sequencing (NGS) data (RNA-Seq) analysis and network analysis.

Text Books:

1. Introduction to Systems Biology: Design Principles of Biological Circuits by Uri Alon, Chapman & Hall/CRC, 2007.

2. Synthetic Biology: A Primer by P.S. Freemont & R.I. Kitney, Imperial College Press, 2012.

3. Robert Gentleman. Bioinformatics with R. Chapman & Hall/CRC, Boca Raton, FL, 2008. ISBN 1-420-06367-7.

4. Robert Gentleman. R Programming for Bioinformatics. Computer Science & Data Analysis. Chapman & Hall/CRC, Boca Raton, FL, 2008. ISBN 978-1-420-06367-7.

Reference Books:

3. Introduction to Systems Biology, S. Choi, Humana Press, 2007.

4. Linked – The New Science of Networks, Albert-László Barabási, Perseus Publishing, 2002.

5. Networks – an Introduction, Mark Newman, Oxford University Press, 2010.

Reference Books:

1. Florian Hahne, Wolfgang Huber, Robert Gentleman, Seth Falcon. Bioconductor case studies. Springer, 2008.

2. Paul D. Lewis, R for Medicine and Biology, Jones and Bartlett Series, 2010.

PRACTICAL – 1 Basic Bioinformatics Laboratory

1. Isolation & Purification of genomic DNA from bacteria

2. PCR for DNA amplification

3. Entrez and Literature Searches (PubMed, PubMed central, OMIM / OMIA)

4. SRS of Biological Databases (Nucleotide/ Genome Databases, Protein Sequence Database, Structure databases, Protein Pattern Databases)

5. File format conversion (FmtSeq, ReadSeq, Sequence manipulation Suite)

6. Sequence Analysis (DotPlot, Pairwise alignment, Multiple Sequence Alignment)

7. Softwares (Bio Edit, GeneDoc, ClustalW / X, MEGA, MEME

8. Visualization Tools (RasMol, Cn3D, PyMol)

9. Sequence Analysis Packages: EMBOSS, NCBI ToolKit

10. Pair wise alignment: Search tools against Databases: (BLAST, FASTA)

11. Multiple sequence alignment (Clustal, Dialign, Multalign)

12. Sequence patterns and profiles (generation of sequence profiles - PSI-BLAST

13. Derivation of and searching sequence patterns: (MEME/ MAST, PHI-BLAST, SCanProsite, PRATT)

14. Protein motif and domain analysis: (MEME/MAST, eMotif, InterproScan, ProSite, ProDom. Pfam

15. Phylogenetic analysis (MEGA, MESQUITE, PHYLIP)

PRACTICAL – 2 Molecular Modeling and Systems Biology Lab.

Molecular visualization Tools

1. Rasmol
2. SPDB viewer

Dimensional protein structure prediction using Homology Modeling techniques

1. Swiss model work space
2. Modeller9v7
3. Insight II

Protein structure Validation

1. Structure Analysis and Verification Server
2. Mol probity server

Energy Minimization techniques

1. First order derivation (Steepest Descent and Conjugate Gradient) methods.
2. Mutation Techniques.

Protein- Ligand Docking

1. Hex
2. Auto Dock

Systems Biology

1. Biological network modeling and visualization using Cytoscape.
2. Using Gepasi.
3. Construction and analysis of gene expression networks.
4. Using Cell Designer to visualize molecular interaction networks in a complex disease (Rhematoid Arthritis)

DISSERTATION

The exercise is designed to result in the satisfactory completion and defense of the diploma.

This process includes

1. a) the conceptualization of the independent research that will comprise the dissertation,

2. b) the preparation of and satisfactory defense of the dissertation proposal,
3. c) the collection, analysis, and interpretation of data,
4. d) presentation of findings in the dissertation format, and
5. e) oral defense of the dissertation.

Dissertation activity must be completed within prescribed time frame for the semester.