COURSES OF STUDY

POST GRADUATE DIPLOMA IN BIOINFORMATICS
(SESSION: 2018-2019)

DEPARTMENT OF BIOTECHNOLOGY & BIOINFORMATICS
SAMBALPUR UNIVERSITY, JYOTI VIHAR
BURLA- 768019, ODISHA

DEPARTMENT OF BIOTECHNOLOGY & BIOINFORMATICS
SAMBALPUR UNIVERSITY

OUTLINE OF COURSE STRUCTURE
POST GRADUATE DIPLOMA IN BIOINFORMATICS

SEMESTER-I

Course Code	Course Name	Credits Hours	Marks
DBI-101	Bioinformatics Resources	4 CH	100
DBI-102	Bioinformatics Programming (Python & R)	4 CH	100
DBI-103	DBMS and Data Warehouse	4 CH	100
DBI-104	Molecular Modeling & Simulation	4 CH	100
DBI-105	Practical (Bioinformatics Programming, DBMS & Data Warehouse)	2 CH	50
DBI-107	Practical (Bioinformatics Resources, Molecular Modeling & Simulation)	2 CH	50
Semester Total Credit		**20 CH**	**500**

SEMESTER-II

Course Code	Course Name	Credit Hours	Marks
DBI-201	Computational Biology	4 CH	100
DBI-202	Computational Genomics and Proteomics	4 CH	100
DBI-203 (Any one) (A to C)	**Elective Papers:**	4 CH	100
	(A) Computer Aided Drug Design		
	(B) Clinical Data Warehouse and Data Mining		
	(C) NGS and Microarray Data Analysis		
DBI-204	Practical (Computational Biology, Computational Genomics and proteomics)	2 CH	50
DBI-205	Practical (Based on Elective Paper, Linux operating system	2 CH	50
DBI-206	Review and Seminar	4 CH	100
Semester Total Credit		**20 CH**	**500**
Total Course Credit		**40 CH**	**1000**

FIRST SEMESTER

DBI-101 BIOINFORMATICS RESOURCES 4CH

Objective: To develop the ability to use the various resources of bioinformatics to retrieve, analyze and predict the sequence, structure and function of genes and proteins.

Learning outcome:

- The students will have a working knowledge of a variety of publicly available data and computational tools important in bioinformatics.
- Understand the underlying principles that are adequate for them to evaluate and use novel techniques as they arise in the future.

Course Description

Unit-I

Bioinformatics: Origin, Definition, Applications and research, scenario in India, Characteristics of bioinformatics databases, Categories of bioinformatics databases, Navigating databases, Information retrieval system, File formats: various file formats for biomolecular sequence (GenBank, FASTA, GCG, MSF).

Unit-II

Sequence databases: nucleic acid sequence databases: GenBank, EMBL, DDBJ; protein sequence databases: Uniprot, SWISS-PROT, TrEMBL, UniParc; repositories for high throughput genomic sequences: EST, STS GSS, etc.; genome databases at NCBI, EBI, TIGR, SANGER – viral genomes; archeal and bacterial genomes; eukaryotic genomes with special reference to model organisms (Yeast, Drosophila, Human, plants such as *Arabidopsis thaliana*, Rice, etc.)

Unit-III

Structure Database: PDB, NDB, PubChem, ChemBank, MMDB, CATH, SCOP, FSSP, DALI, protein-protein interaction database. **Other Database:** InterPro, Prosite, Pfam, ProDom, motif databases, drug databases, BRENDA, MEROPS, KEGG, CAzy, disease databases, PubMED

Unit-IV

Tools in bioinformatics: need for tools, knowledge discovery, industry trend, data mining tools, nucleotide sequence submission tools, protein submission tools, data analysis tools for nucleotide sequence and protein sequence. **Algorithms in bioinformatics**: classification of algorithms, implementing algorithms, biological algorithms, data analysis algorithms, prediction algorithms

Suggested readings:

1. Bioinformatics (Databases, Tools and Algorithms) by Orpita Bosu and Simminder Kaur Thukral, Oxford Univerrsity Press, 2007
2. Introduction to Bioinformatics, by Arthur M. Leask, Oxford University Press, 2002
3. Bioinformatics: Sequence and Genome Analysis, by David Mount, Cold Spring Harbor Labotratory, 2001
4. Fundamental Concepts of Bioinformatics, by Krane , Dan E and Michael L. Raymerr, Pearson Education, India, 2003
5. Bioinformatics: Concepts, Skills and Application by S. C. Rastogi, Namita Mendiratta and Parag Rastogi, CBS Publishers & Distributors, 2003
6. Bioinformatics: Principles and Application by Zhumur Ghosh and Bibekanand Mallick, Oxford Publication, India

DBI-102 BIOINFORMATICS PROGRAMMING (PYTHON & R) 4CH

Objective: To acquire programming techniques essential for analysis and processing of biological data from the best compatible programming languages (Phython and R).

Learning Outcome:

- Learning about different programming languages and their syntax.
- Logic development for coding the biological problems.
- Methods to retrieve data from resources programmatically and development of repositories for data storage.
- How to develop computational applications to analyze data and development of applications.

Course Description

Unit-I

Fundamentals in computing types: batch, real time, online, offline, types of modern computing, workstations, server, parallel processing computing, cluster computing, grid computing, cloud computing. **Introduction to operating system**: operating system concept, Dos and Window operating system and their utilities, Unix/Linux operating system, Installation and test on satisfactory operation of components, productive use of the unix environment, shell programming, unix utilities that are particularly useful in bioinformatics

Unit-II

Python Programming: Programming basics, Interpreter and Compiler, Variables, expressions, Operators, Statements; Conditional execution: Conditional and logical operators; Functions: In-built functions, User defined functions; Iteration: Iterative operators; Strings: String structure and functions; Files: Creation, Writing and updating files; Lists: Elements, Methods, Functions; Dictionaries: Structure and methods, Text parsing; Tuples: Methods and uses; Regular expressions: Matching and Extraction.

Unit-III

Applications of python and introduction to BioPython: installation of biopython package, working with sequence objects, sequence annotation objects, sequence input-output, multiple sequence alignment objects, BLAST and other sequence search tool, accessing NCBIs Entrez database, SWISSPROT and Expasy.

Unit-IV

R language: Installing R; R basics, Graphics; Simple plotting, Advanced plotting, Using color in plots, Using subscripts and superscripts in graph labels, Interactive graphics, Saving graphical output, loops. Working with data sets: Data structures, Moving to and from files, Statistical distributions.

Suggested Reading:

1. Bioinformatics with Python Cookbook by Tiago Antao, O Relly Publication.
2. Bioinformatics with R Cookbook by Paurush Praveen Sinha, Packt Publishing
3. Beginning Python, James Payne, Wiley Publishing, Inc.
4. Programming Python by Mark Lutz, Laura Lewin and Frank Willison, O’Reilly Publication.
5. R Programming for Bioinformatics by Robert Gentleman, CRC Press

DBI-103 DBMS & DATA WAREHOUSE 4CH

Objective: To develop the ability to rationally design and implement suitable databases for addressing problems relating to storage, retrieval and management of biological data.

Learning Outcome:
By the end of the course a student acquires knowledge to choose suitable data structures, database models and apply skills to design and manage databases for storage and management of given biological data.

Course Description

Unit-I
Introduction – Database System Versus File Systems, Characteristics of Database, Database Concepts, Schemas & Instances, DBMS architecture and Data Independence, Data Models, Database Languages & Interfaces, View of Data, Database users and Administrators, Database System Structure, Database System Applications. **Data models** – ER Model: Keys, Constraints, Design Issues, Extended ER features, Reductions of ER Schema to Tables. Relational Model: Structure, Relational Algebra, Hierarchical Model, Network Model, Object Oriented Model

Unit-II
Structured Query Language – Basic Structure, Set Operations, Aggregate Functions, Null Values, Nested Sub queries, Views, Integrity: Domain constraints, Joined Relations, Data-Definition Language

Unit-III
Relational Database and Storage – Pitfalls in Relational Design Database, Functional dependencies, Decomposition Normal Forms – 1NF, 2NF, 3NF & Boyce-Codd NF, Data Storage – Ordered indices, Hashing concepts - Security and Authorization.

Unit-IV
Introduction to Data warehousing – concept of data warehouse and its advantages, components of data warehouse, architecture and lifecycle of a data warehouse,
Types of Data warehouse design methodologies–top down approach, bottom down approach, hybrid design Approach. **Data Models** - dimensional data modeling (Star Schema, Snowflake Schema); relational data modeling; conceptual, physical & logical data model. Multidimensional Analysis – OLAP & OLTP approaches. **Building & Maintaining the data warehouse** – ETL design & development; ETL application.

Suggested readings:

1. Database system Concepts (4th Ed.) by Silberschatz A., Korth H.F. and Sudarshan S., McGraw Hill Publishers.
2. An introduction to Database systems (7th Ed.) by Date C.J., Addison Wesley Publishers.
3. Fundamentals of Database systems (4th Ed.) by Elmasri and Navathe, Addison Wesley Publishers.
4. Principles of Database systems (2nd Ed.) by Ullman J.D., Galgotia Publications.
5. The Data Warehouse Lifecycle Toolkit by Ralph Kimball, Wiley Publishers.
6. Data Warehousing, Data Mining and OLAP by Alex Berson, MGH Publishers.
7. Building the Data Warehouse by Bill Inmon, Wiley Publishers.
8. Building the Data Warehouse (3rd Ed.) by Inmon W.H., Wiley Publishers.

DBI-104 MOLECULAR MODELING & SIMULATION 4CH

Objective:

To develop the ability to model and analyse computationally the structure and function of target proteins.

Learning Outcome:

- Ability to decipher information from the protein and drug molecules using visualization tools.
- Understanding the theoretical, experimental and computational approach of protein design.
- Ability to compare, classify, analyse protein structure and predict the function of proteins.

Course Description

Unit-I

Principles of protein structure (Motifs and domains), principles of DNA structure, RNA secondary and tertiary structures. Structural databases (PDB, SCOP, CATH and other structure based databases). Computational methods for secondary structure prediction of protein (Chou-Fasman, GOR and Neural Networks) and reliability (Q3 value and SOV score).

Unit-II

Tertiary structure predictions of proteins: types of predictions methods, homology protein modeling, fold recognition method, validation of protein structure (Ramachandran plot analysis, ERRAT score, VERIFY3D), Identifying structural domains in protein: first and second generation algorithms for domain assignments, domain assignment based on graph theoretical methods, prediction of binding sites and characterization.

Unit-III

Analysis of 3D structures: secondary structure assignment, assignment of hydrogen bonds, coulomb hydrogen bond calculation, empirical hydrogen bond calculation, assignment methods of secondary structure (DSSP, STRIDE, DEFINE, P-Curve).

Protein structures comparison and alignment: general approach, comparison algorithm & optimization (CE, VAST, DALI), concept of coordinate transformation, RMSD, Z score for structural comparison.

Unit-IV

Ab initio protein structure prediction: Empirical force field for biomolecular simulations, Potential Energy Function (bond length potential, bond angle potential, torsional potential, van der wals potential and coulomb potential), classical representations of electrostatics (Poisson-Boltzmann, Generalized Born and Colombic). Energy minimization techniques: concept of local and global minima, energy minimization protocol, energy minimization algorithms (steepest descent, conjugate gradient, Newton Raphson). Molecular Dynamics simulations.

Suggested readings:

1. Introduction to Protein Structure, Branden & Tooze, Garland Publishing, Inc, New York
2. Molecular Moelling : Principles & Applications, Andrew R. Leach, Prentice Hall
3. Molecular Modeling and Simulation by Tamar Schlick, Springer Publishers.
4. Molecular Modeling: Basic Principle and Application (3rd Ed.) by Holtje H.D. and Sippl W, Wiley Publishers.
5. Structural Bioinformatics by Bourne and Weissig, Wiley Publishers.

DBI-105	**Practical (Bioinformatics Programming, DBMS & Data Warehouse)**	**2 CH**	**50**
DBI-106	**Practical (Bioinformatics Resources, Molecular Modeling & Simulation)**	**2 CH**	**50**

SECOND SEMESTER

DBI-201 COMPUTATIONAL BIOLOGY 4CH

Objective:

To develop the ability to implement various algorithms and use of bioinformatics tools to annotate the sequences of DNA, RNA and proteins.

Learning outcomes:

- Students should be able to understand several biocomputing techniques.
- Apply biocomputing techniques to analyse DNA, RNA and protein sequence.
- Can predict genes and corresponding protein from raw DNA sequence.

Course Description

Unit-I

Introduction to sequence similarity, homology, alignment, Pairwise Sequence Alignment: Different scoring models, Substitution matrices (PAM and BLOSUM), Pairwise Alignment: Concept of Global and Local Alignment, Dot matrix method, Dynamic programming (Needleman-Wunsch algorithm, Smith-Waterman algorithm, gap penalties, Significance of score, FASTA and BLAST algorithms and types.

Unit-II

Multiple Sequence alignment: Multiple Sequence Alignment methods (MSA), Scoring of a MSA, Progressive (CLUSTALW, CLUSTALX and PILEUP), Gibbs Sampler.

Phylogenetic Analysis: Phylogenetic tree and terminology, Distances measures: Nucleotide distance measures (simple counts method, Jukes-Cantor correction, Kimura 2 parameter correction), different methods of Phylogenetic tree prediction: maximum parsimony, distance (UPGMA, NJ), maximum likelihood methods, bootstrapping.

Unit-III

Sequence Analysis: DNA sequencing & Human Genome Project, Dinucleotide abundance, Codon biases, GC reach prediction and relationship to gene density, GC and AT skewness and prediction of Ori and Ter site, Pattern searches, Primer design for PCR, Promoter analysis using PSSM, Methods for gene finding.

Unit-IV

RNA Structure Analysis: terminology of RNA secondary structure, RNA secondary structure prediction, Nussinov folding algorithm, energy minimization and Zuker folding algorithm.

Protein sequence analysis: compute pI/MW, RADAR, hydrophobic cluster analysis, pattern and profile search, Expasy tools for sequence analysis

Suggested Readings:

1. Bioinformatics: Genome and Sequence Analysis by Mount D.W., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.
2. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids by Durbin R., Eddy S., Krogh A. and Mitchison G., Cambridge University Press.
3. Bioinformatics and Functional Genomics by Pevsner J., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.
4. Bioinformatics – A practical guide to the Analysis of Genes and Proteins by Baxevanis A.D. & Oulette B.F.F., Willey International publishers.
5. DNA and Protein Sequence Analysis-A Practical Approach by Bishop M.J. and Rawlings C.J., Oxford University Press, ISBN 0 19 963464 7

DBI-202 COMPUTATIONAL GENOMICS & PROTEOMICS 4CH

Objective: To develop the skills for functional annotation of the novel DNA sequences and gene expression data.

Learning Outcome:

- Students will have a thorough understanding of genomic technologies pertaining to whole genome sequencing and annotation.
- The students will know the vast amount of genome information in publically available databases and how to access and best utilize for practical purposes.

Course Description

Unit-I

Genome sequencing: Genes and Genomes, gene sequencing methods (Sanger and PyroSequencing), protein sequencing method (EDMAN sequencing), genome sequencing strategies (Shortgun and Clone-by-clone approach), human genome project, sequence assembly and filling gaps, cDNA sequencing and EST, DNA editing, RNA editing, types of RNA editing, identification of various types of RNAs

Unit-II

Genome analysis: Genome structure analysis by genome browser and BLAT, gene sorter, in silico PCR, DNA duster, quantitative real time PCR, PCR applications, primer design. Gene predictions: prokaryotic and eukaryotic genome features for gene prediction, methods of gene prediction, algorithms of gene predictions (GRAIL, FGENESH, GENSCAN, etc), strategies and considerations

Unit-III

Comparative genome analysis: basic concepts and application, BLAST2, MegaBlast PipMarker, AVID, Vista, MUMmer, applications of suffix tree, synteny and gene order comparisons, COGs), application of comparative genomics, reconstruction of metabolic pathways, DNA profiling techniques and genetic diversity analysis, RAPD, ISSR, SSR, AFLP, popgene, AMOVA, dendrogram analysis, chromosome map construction, QTL mapping,

Unit-IV

MicroRNA and genomewide profiling: miRNA and human disease, significance of miRNA profiling, genomewide profiling of miRNA by microarray. RNAi: what are RNAi and siRNA, discovery of siRNA, RNAi mechanism, siRNA applications, siRNA design, siRNA resources, siRNA information. Proteomic data analysis: analyzing 2DE derived proteomics data, analyzing mass-spectrometry derived data, protein array and analyzing data derived from protein microarray

Suggested Readings:

1. Analysis of Genes and Genomes by Richard J. Reece, Wiley Publishers.
2. Bioinformatics and Functional Genomics by Jonatham Pevsner, Wiley Publishers
3. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (3rd Ed.) by Andreas D. Baxevanis & B.F. Francis Ouellette, Wiley Publishers.
4. Discovering Genomics, Proteomics and Bioinformatics (2 Ed.) by A Malcolm Campbell, Davidson College and Laurie J. Heyer, Pearson Publishers.
5. Introduction to Proteomics by Daniel C. Liebler and John R. Yates, Humana Press

DBI-203A COMPUTER AIDED DRUG DESIGN 4CH

Objective: To design potential lead molecules that may be explored further as a potential candidate for the drug.

Learning Outcome:

- The students have the ability to design and optimize lead molecules against drug targets.
- Able to develop QSAR model and pharmacophore hypothesis for virtual screening
- Working capability in drug designing software like, Discovery Studio, HyperChem, Schrodinger and molecular dynamics software like AMBER 8.0, etc.

Course Description

Unit-I

Introduction to the world of chemical informatics: defining chemical informatics; a glimpse of the future of chemical informatics. Representing 2D structures: Kinds of 2D structure representation; atom lookup and connection tables; graph theory; SMILES; SD files; Fragment codes & Fingerprints; Measuring of similarity and dissimilarity between drug molecules.

Unit-II

2D chemical database applications. Types of searching; substructure searching with SMARTS; similarity searching with fingerprints; demonstrations of searching systems (Molinspiration). Representing 3D structures. Sources of 3D information; experimental 3D databases; conformational flexibility; distance matrices; estimation of 3D structure; conformational search and minimization; 3D descriptors and fingerprint; representation of proteins

Unit-III

Molecular Descriptors: 2D descriptors. Kinds of descriptor; “mathematical” and topological indices; biological descriptors and their application in ADME/Tox; biological properties; property prediction software, 3D descriptors, data verification and manipulation. Quantitative structure-property relationships (QSPR): Feature selection, Model building, examples of QSPR studies and application. QSAR in drug design: QSAR methodology, QSAR applications in drug design, QSAR model selection and validation, CoMFA, 3D and nD-QSAR methods

Unit-IV

Pharmacophore and Drug Discovery: pharmacophore generation, searches in the database, software for pharmacophore generation, application and limitation of pharmacophore concept Computational models for ADME/Tox. The application of predictive models to pharmacology and toxicity testing. Target identification and characterization, structure based process for designing drug molecules (docking algorithms, MM-GBSA, MM-PBSA, LIE-SGB, free energy perturbation, thermodynamics integration, refinement methods)

Suggested Readings:

1. A.R. Leach and V.J. Gillet: An Introduction to Chemoinformatics, Kluwer Academic Publishers, The Netherland.
2. Chemoinformatics: A Textbook by John Gasteiger and Thomas Engel, Wiley Publisher.
3. Drug Design: Structure- and Ligand-based Approaches by Merz KM, D Ringe, Reynolds CH Cambridge University Press.
4. Guide Book on Modeling in Drug Design by Clauden Cohen N., Academic Press

DBI-203B CLINICAL DATA WAREHOUSE AND DATA MINING 4CH

Objective: To develop the clinical data warehouse for the electronic repository of multidimensional clinical data and analysis using data mining techniques.

Learning Outcome: Students will understand the mathematical foundations of knowledge-based systems, learn to identify areas that might benefit from a decision support system and evaluate the challenges surrounding development and implementation. By the end of the course students will be equipped with knowledge about design and implementation of a clinical data warehouse with decision support system and participate in strategic planning activities.

Course Description

Unit-I

Electronic Health Records - EHR Technology; Evolution of EHR; EHR adoption and usability; Scenario of EHR implementation in India, **Clinical data management** - Specialized form of clinical databases; Clinical data model and its implementation; Clinical data warehouse.

Unit-II

Data Mining and CDS - Statistical pattern recognition techniques; Supervised learning - Decision trees, Logistic regression, Neural networks, Nearest neighbor approach, Support vector machine, Evaluation of classifiers - ROC Graphs, Kolmogorov-Smirnov Test; Unsupervised learning - Cluster analysis; Genetic algorithm; Temporal mining algorithm.

Unit-III

Introduction to Image Processing – Fundamentals & applications of image processing; Human visual perception; Components of an image processing system.

Biomedical Image Processing – Macroscopic and microscopic image analysis; Biometric pattern recognition, Sampling and Quantization; Binary Image; 3-D Imaging; Image File formats, Image segmentation (Point and line detection, region growing and object segmentation)

Unit-IV

Case study - Mammogram Image Analysis (Steps involved – enhancement of mammogram, suspicious area detection, LESION segmentation, feature selection and extraction, wavelet analysis).

Suggested readings:

1. The Data Warehouse Toolkit, 2nd Edition: The Complete Guide to Dimensional Modeling by Kimball, Ralph; Ross, Margy, John Wiley & Sons Publisher.
2. Building the Data Warehouse by Bill Inmon, Wiley and Sons Publication.
3. Mastering Data Warehouse Design by Imhoff C, Galemmo N, Giger J.G., Wiley Publication.
4. DW 2.0 - Architecture for the Next Generation of Data Warehousing by Bill Inmon, Derek Strauss and Genia Neushloss, Elsevier Press.
5. Data Mining and Analysis: Fundamental Concepts and Algorithms by Zaki, Mohammed J., Cambridge University Press.
6. Data Mining: Concepts and Techniques by Jiawei Han and Micheline Kamber, Morgan Kaufmann Publisher.
7. Digital Image Processing (2nd Ed.) by Rafael C Gonzalez and Richard E Woods, Pearson Publisher.

DBI-203C NGS AND MICROARRAY DATA ANALYSIS 4CH

Objective:

To enable the students to analyze and infer information from whole genome sequence data and high through put gene expression data of microorganisms, plants and animals.

Learning outcome:

- The students will acquire knowledge and skills to analyze large scale genome data and infer needed information from the genomes of eukaryotes and prokaryotes.
- Students will learn to analyze the gene expression data sets to derive the biologically meaning information applicable to human health.

Course Description

Unit-I

Overview of next generation sequencing technology (Roche/454 FLX, Illumina Genome Analyzer, SOLiD™ Sequencing, Ion Torrent™, Nanopore), data processing, NGS and genetics of complex disease, exome sequencing, RNA-seq experiments and data analysis, differential expression analysis, chip-seq analysis, sequencing mappability.

Unit-II

NGS Data Quality Control methods, NGS Data Structure, Resources and Repositories, genome annotations, haplotyping (concepts and application), SNP technologies (platforms and analysis), Trascriptome Preparation and Annotation, Transcriptome Abundancy calculation and pathway mapping, pharmacogenomics (concepts and application in healthcare).

Unit-III

Metabolic pathway analysis: macromolecular networks, topology of macromolecular networks, modulatory and dynamics of macromolecular networks, inference of regulatory networks, simulation of molecular networks, simulation of biological processes.

Unit-IV

DNA and protein microarray: Fabrication of microarray, printing of DNA, sample preparation and hybridization, image segmentation and data acquisition, data normalization, data analysis and clustering, case studies, Screening of proteins: protein array, antibody array, case studies.

Suggested Readings:

1. Next Generation DNA Sequencing Informatics by Stuart M. Brown, Cold Spring Harbor Laboratory.
2. Network Analysis and Synthesis by Franklin F. Kuo, Wiley Publisher.
3. RNA-seq Data Analysis: A Practical Approach by Eija Korpelainen, CRC Press.
4. Bioinformatics: Genomics and post-genomics, Noah Hardy, John Wiley & Sons, Ltd
5. Microarray Bioinformatics, by Dov Stekel, Cambridge University Press
6. Protein Arrays – Method and Protocols by Fung, Human Press
7. Next-Generation DNA Sequencing Informatics, Stuart M. Brown, New York University School of Medicine, Cold spring Harbor Laboratory.

DBI-204	**Practical (Computational Biology, Computational Genomics and Proteomics)**	**2 CH**	**50**
DBI-205	**Practical (Based on Elective Paper, Linux Operating System)**	**2 CH**	**50**
DBI-206	**Review and Seminar (2 CH + 2 CH)**	**4 CH**	**100**