COURSE: BIOINFORMATICS		
DEGREE: BIOMEDICAL ENGINEERING	**YEAR: 2018-2019**	**TERM: 1st semester**

WEEKLY PLANNING

WEEK	**SESSION**	**DESCRIPTION**	**GROUPS (mark X)**		**SPECIAL ROOM FOR SESSION (Computer class room, audio-visual class room)**	**Indicate YES/NO If the session needs 2 teachers**	**WEEKLY PROGRAMMING FOR STUDENT**		
			LECTURES	SEMINARS			DESCRIPTION	CLASS HOURS	HOMEWORK HOURS (Max. 7h week)
W1	1 M	**Course overview** **Unit 0_Introduction to Bioinformatics:** Observables and data archives. The World Wide Web. Genomes and proteomes. Genes and inherited diseases. Electronic publication. Computer Science. Use of sequences to determine phylogenetic relationships. Searching for similar sequences in data bases. Protein structure prediction and engineering. Proteomics. Clinical implications. **Unit 1_Databases and sequence retrieval.** Databases and tools: NCBI and 123 genomics interfaces. The ENCODE project, scientific publications. Structural, expression and functional databases. mRNA sequence retrieval: FASTA vs. GENEBANK format. Identification of CDS/ORFs. UniSTS database. ORF	X					1,6	6

		finder program.							
W1	2 T F	**Unit 1_Exercises**		X	Computer room			1,6	
W2	3 M	**Unit 1_ Databases and sequence retrieval.** MAP VIEWER: graphical view of data al genome level. Annotation and Build versions. Map viewer tools. Definition of contig, clone and chromosomal sequences. dbSNP: single nucleotide polymorphism database. Searching information in Map Viewer: maps options. UniGENE, Hs_RNA, Gene and Contig Maps. Data as a table view. Glosary terms.	X					1,6	6
W2	4 T F	**Unit 1_Exercises**		X	Computer room			1,6	
W3	5 M	**Unit 2_ Sequence analysis: Pairwise alignments**. Sensitive and selective searching methods. Alignment and comparison of sequences. Picking out genes in genomes. Pairwise sequence alignments: BLASTA (BLASTn, BLASTp, BLASTx, TBLASTn, TBLASTx, PSI-BLAST). Dotplots graphics. and CLUSTAL-W.	X					1,6	6
W3	6 T F	**Unit 2_ Exercises**		X	Computer room			1,6	
W4	7 M	**Unit 2_ Sequence analysis. Pairwise alignments.** Evaluation of identity among sequences. Measures of sequence similarity: Hamming and Levenshtein distance. Scoring schemes. PAM and BLOSUM scoring matrices. Approximate searching algorithms.	X					1,6	6
W4	8 T F	**Unit 2_Exercises**		X	Computer room			1,6	
W5	9 M	**Unit 2_ Sequence analysis. Pairwise alignments.** Introduction to Dynamic programming. Alignments based on dynamic programming	X					1,6	6
W5	10 T F	**Unit 2_Exercises 2**		X	Computer room			1,6	
W6	11 M	**Unit 3_ Sequence analysis: Multiple alignments.** Structural inferences from multiple sequence analysis. Applications of multiple sequence analysis and data base searching. Profiles, PSI-BLAST. Hidden Markov Models	X					1,6	6
W6	12 T F	**Unit 3 _ Exercises**		X	Computer room			1,6	

W7	13 M	**Unit 3_ Sequence analysis: phylogeny.** Introduction. Time scale of earth history. Phylogenetics trees. Rooted and unrooted trees. Phylogenetic prediction methods: Clustering and cladistic methods**.** Clustering methods: distances. UPGMA and FITCH. Cladistic methods: maximum parsimony (MP) and maximum likelihood (ML). ML and reconstruction of ancestral sequences.	X					1,6	
W7	14 TF	**Unit 3_Exercises 2**		X	Computer room			1,6	
W8	15 M	**Unit 4_ Genome analysis.** Genome organization. Prokaryotic and Eukaryotic genomes. Inheritance patterns. SNPs and dBSNP. Sequence repeats and satellite DNA, Mini and Microsatellites. Transposable elements (TEs): Class I (LTR, SINE, LINE); Class II (DNA based mechanisms); Class III (MITEs). Genotyping. Haplotyping. Linkage analysis. Candidate gene approach.	X					1,6	
W8	16 TF	**Continuos evaluation 1 (Units 1, 2 and 3)**		X	Computer room	CE1		1,6	6
W9	17 M	**Unit 4_ Genome analysis**. Repeat masker. Alignment, table, masked and annotation files. Evaluation of the pathogenicity of disease variants: OMIM, Polyphen2, Sift,.	X					1,6	
W9	18 TF	**Unit 4 _Exercises**		X	Computer room			1,6	6
W10	19 M	**Unit 5_ Structure analysis. RNA secondary structure prediction.** Dot matrix analysis. Minimum Free-energy Method (MFE). MFOLD program. MicroRNAs analysis. miRBase database.	X					1,6	
W10	20 TF	**Unit 4 _Exercises 2**		X	Computer room			1,6	6
W11	21 M	**Unit 5_ Structure analysis.** Protein analysis: ExPASy. Protein primary analysis: ProtParam, ProtScale. Protein secondary prediction: CFSSP. Tertiary structure prediction: Swiss Model, NCBI structure. Evolutionary conserved regions (ECR browser) .	X					1,6	
W11	22 TF	. **Unit 5_ Exercises**		X	Computer room			1,6	6
W12	23 M	**Unit 5_Structure analysis. Protein advanced analysis.** Generation of recombinant vectors in silico. Enzyme restriction sites. Restriction analysis. Artificial expression vectors: PUC19, pBLuescript. Promoter region and Multicloning site (MCS).		X				1,6	

		Generation of recombinant mutant proteins by genetic engineering.							
W12	24 T F	**Unit 5_ Exercises**		X	Computer room			1,6	6
W13	25 M T	Continuous evaluation 2 (Units 4 & 5)			Computer room	CE2		1,6	
							Subtotal 1	**43,2**	**81**
							Total 1 *(Hours of class plus student homework hours between weeks 1-14)*	124,2	

15		Tutorials, handing in, etc						1,5	
16		Assessment						3	6
17									
18									
							Subtotal 2	**3**	**7,5**
							Total 2 *(Hours of class plus student homework hours between weeks 15-18)*	10,5	

TOTAL *(Total 1 + Total 2)*	**134,7**