



COURSE: COMPUTATIONAL BIOLOGY		
DEGREE: BIOMEDICAL ENGINEERING	YEAR: 2020-2021	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.	X					1,6	6
W1	2 T	Unit 1_Databases and sequence retrieval. Databases and tools: NCBI interface. The ENCODE project, scientific publications. Structural, expression and functional databases. mRNA sequence retrieval: FASTA vs. GENE BANK format. Identification	X	X		YES		1,6	

		of CDS/ORFs. UniSTS database. ORF finder program. Unit 1_ Exercises 1							
W2	3 M	Unit 1_ Databases and sequence retrieval. Genome data viewer: graphical view of data al genome level. Annotation and Build versions. dbSNP: single nucleotide polymorphism database. Searching information in Genome Data Viewer: track options.	X					1,6	6
W2	4 T	Unit 1_ Exercises 2		X		YES		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	Unit 2_ Exercises 1		X		YES		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	Unit 2_ Exercises 2		X		YES		1,6	
W5	9 T	Unit 2_ Sequence analysis. Pairwise alignments. Introduction to Dynamic programming. Alignments based on dynamic programming Unit 2_ Exercises 3	X	X		YES		1,6	6
W6	10 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	11 T	Unit 3_ Exercises 1		X		YES		1,6	
W7	12 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	13 T	Unit 3_ Exercises 2		X		YES		1,6	
W8	14 T	Continuous evaluation 1 (Units 1, 2 and 3)		X		YES	REDUCED GROUPS G48 &G49	1,6	
W9	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	6
W9	16 T	Unit 4_ Exercises 1		X		YES		1,6	
W10	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	
W10	18 T	Unit 4_ Exercises 2		X		YES		1,6	
W11	19 M	Unit 5_ Structure analysis. RNA secondary structure prediction. Dot matrix analysis. Minimum Free-energy Method (MFE). MFOLD program. MicroRNAs analysis. miRBase database. Protein analysis: ExpASy. Protein primary analysis: ProtParam, ProtScale. Protein secondary prediction: CFSSP. Tertiary structure prediction: Swiss Model, NCBI structure.	X					1,6	6
W11	20 T	Unit 5_ Exercises 1		X		YES		1,6	
W12	21 M	Unit 5_ Structure analysis. Evolutionary conserved regions (ECR browser). Protein advanced analysis: Generation of recombinant vectors in silico. Enzyme restriction sites. Restriction analysis. Artificial expression vectors: PUC19, pLuescript. Promoter region and Multicloning site (MCS). Generation of recombinant mutant proteins by genetic engineering.		X				1,6	6
W12	22 T	Unit 5_ Exercises 2		X		YES		1,6	6

W13	23	Resolution of doubts						1,6	
W14	24 M	Continuous evaluation 2 (Units 4 & 5)				CE2	FOR REDUCED GROUP G48		
W14	25 T	Continuous evaluation 2 (Units 4 & 5)				CE2	FOR REDUCED GROUP G49		

Subtotal 1 **43,2** **81**

Total 1 (<i>Hours of class plus student homework hours between weeks 1-14</i>)	124,2
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15		Tutorials, handing in, etc						1,5	
16		Assessment						3	6
17									
18									

Subtotal 2 **3** **7,5**

Total 2 (<i>Hours of class plus student homework hours between weeks 15-18</i>)	10,5
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TOTAL (<i>Total 1 + Total 2</i>)	134,7
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