Załącznik nr 3 do:
do Wytycznych do tworzenia studiów oraz projektowania i modyfikacji
programów studiów

Course code: ………………..   **Plan position:**   ……………

1. INFORMATION ABOUT THE COURSE

A. Basic information

Name of course	Bioinformatics
Field of studies	
Level of studies	
Profile of studies	General academic
Form of studies	
Specialty	
Unit responsible for the field of studies	Faculty of Animal Breeding and Biology, Department of Biotechnology and Animal Genetics
Name and academic degree of teacher(s)	PhD Beata Sitkowska, prof. PBS; PhD Magdalena Kolenda
Introductory courses	Genetics, Chemistry
Introductory requirements	Basic knowledge in biology, genetics and IT

B. Semester/week schedule of classes

Semester	Lectures (W)	Auditorium classes (Ć)	Laboratory classes (L)	Project classes (P)	Seminar (S)	Field classes (T)	Number of ECTS points
Winter / summer			30				6

2. LEARNING OUTCOME

No.	Learning outcomes description	The reference to the learning outcomes of specific field of study	The reference to the learning outcomes for the area
KNOWLEDGE			
W1	One knows terminology connected to bioinformatics and phylogenetics.		
W2	One knows how to characterize organisms in relation to their genotypes.		
W3	One knows how to effectively search data in biological databases.		
SKILLS			
U1	One knows how to use advanced biological databases and their tools.		
SOCIAL COMPETENCES			

K1	One is aware of the collections of biological information, is keen on using these databases.		

3. TEACHING METHODS

Presentations, computer laboratories

4. METHODS OF EXAMINATION

Colloquium, project

5. SCOPE

Laboratories	Focus areas in bioinformatics and genomics. Content of biological databases. Structure of the most important bioinformatics databases (NCBI, ENSEMBL). Different effective searching techniques in these databases (genes, genomes, biological projects). Methods of sequences searching: sequences comparison and matching. DNA sequences and proteins analysis using advanced site search tools from the NCBI, ENSEMBL and EBI websites. A practical guide to genome browsing. BLAST, gene expression. Browsing genes and genomes with ENSEMBL. Gene Ontology Annotation (GOA). BIOMART. GENEBUILD, REACTOME. SNPs in cattle. Variation. Comparative genomics. Gene trees and homologues.

6. METHODS OF VERIFICATION OF LEARNING OUTCOMES

LEARNING OUTCOME	Form of assessment					
	Oral examination	Written exam	Colloquium	Project	Presentation	…………
W1			X			
W2			X	X		
U1			X	X		
K1			X	X		

7. LITERATURE

Basic literature	Jonathan, P. 2015. Bioinformatics and functional genomics. Wiley Blackwell. Xiong, J., 2006. Essential bioinformatics. Cambridge University Press.
Supplementary literature	https://www.ncbi.nlm.nih.gov/guide/training-tutorials/ http://www.ebi.ac.uk/ http://www.ensembl.org/index.html

8. TOTAL STUDENT WORKLOAD REQUIRED TO ACHIEVE EXPECTED LEARNING OUTCOMES EXPRESSED IN TIME AND ECTS CREDITS

Student's activity		Student workload– number of hours
Classes conducted under a direct supervision of an academic teacher or other persons responsible for classes	Participation in classes indicated in point 1B	30
	Supervision hours	5
Student's own work	Preparation for classes	30
	Reading assignments	40
	Other (preparation for exams, tests, carrying out a project etc)	45
Total student workload		150

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Number of ECTS points	6