AYDIN ADNAN MENDERES UNIVERSITY
GRADUATE SCHOOL OF HEALTH SCIENCES
BIOSTATISTICS
BIOSTATISTICS (MEDICAL)
BIOSTATISTICS (MEDICAL) MASTER
COURSE INFORMATION FORM

Course Title		Statistical Genetics						
Course Code		BİS536		Couse Level		Second Cycle (Master's Degree)		
ECTS Credit	6	Workload	152 *(Hours)*	Theory	3	Practice	0	Laboratory	0
Objectives of the Course		This course provides an introduction to the models and methods of Statistical Genetics for students with little Genetics background but with some knowledge of Probability and Statistics. The course provides a basis for further study in Statistical Genetics.						
Course Content		Mendelian genetic traits. Hardy-Weinberg, allelic variation, subdivision. Likelihood inference, latent variables and EM algorithm. Pedigree relationships and gene identity. Meiosis and recombination. Linkage detection. Multipoint linkage analysis.						
Work Placement		N/A						
Planned Learning Activities and Teaching Methods			Explanation (Presentation), Case Study, Project Based Study					
Name of Lecturer(s)								

Assessment Methods and Criteria

Method	Quantity	Percentage (%)
Midterm Examination	1	40
Final Examination	1	60

Recommended or Required Reading

1	Lange, K. (2003). Mathematical and statistical methods for genetic analysis. Springer Science & Business Media.
2	Weir, B. S. (1990). Genetic data analysis. Methods for discrete population genetic data. Sinauer Associates, Inc. Publishers.
3	Thompson, E. A. (2000). Statistical inference from genetic data on pedigrees. IMS.
4	Balding, D. J., Bishop, M., & Cannings, C. (Eds.). (2008). Handbook of statistical genetics. John Wiley & Sons.

Week	Weekly Detailed Course Contents	
1	Theoretical	Overview of genome mapping
2	Theoretical	Basic genetics: Mendelian genetics,Population & quantitative genetics,Marker segregation analysis
3	Theoretical	Simple Mendelian traits; Mendelian segregation, dominant and recessive traits, X-linked traits, patterns of inheritance.
4	Theoretical	Population genetic issues; testing Hardy-Weinberg equilibrium, likelihood estimation of allele frequencies, the EM algorithm
5	Theoretical	Haplotypes, allelic association and haplotyping. Likelihood estimation of haplotype frequencies. Mutation, selection, and random genetic drift.
6	Theoretical	Kinship and gene identity by descent; probabilities on pedigrees.
7	Theoretical	Genetic linkage; meiosis and recombination, twolocus kinship and gene identity, linkage disequilibrium, Two-locus linkage analysis, the probabilities of meiosis patterns-1
8	Intermediate Exam	Midterm exam
9	Theoretical	Genetic linkage; meiosis and recombination, twolocus kinship and gene identity, linkage disequilibrium, Two-locus linkage analysis, the probabilities of meiosis patterns-2
10	Theoretical	Simple designs for two-locus linkage; testing for linkage, expected lod scores and power to detect linkage, homozygosity mapping-1
11	Theoretical	Simple designs for two-locus linkage; testing for linkage, expected lod scores and power to detect linkage, homozygosity mapping-2
12	Theoretical	Meiosis, recombination and map functions.
13	Theoretical	Multipoint linkage analysis; the hidden Markov model for multipoint linkage.
14	Theoretical	The Baum algorithms; the EM algorithm for map estimation.
15	Theoretical	Literature review and discussion.
16	Final Exam	Final exam

Workload Calculation

Activity	Quantity	Preparation	Duration	Total Workload
Lecture - Theory	14	0	2	28
Assignment	1	10	0	10
Individual Work	14	0	2	28
Quiz	14	2	1	42
Midterm Examination	1	20	2	22
Final Examination	1	20	2	22
			Total Workload (Hours)	152
			[Total Workload (Hours) / 25*] = **ECTS**	6

*25 hour workload is accepted as 1 ECTS

Learning Outcomes

1	Be able to statistically relate genetic and environmental effects to a quantative trait
2	Be able to identify procedures for estimation of genetic and enviromental effects
3	Be able to identify methods for localization of genes that influence variation in quantitative traits
4	Be able to identify methods for quantifying the affects of genetic variants on quantitative traits
5	Be able to read/understand the current applied and theoretical literature involving genetic influences on quantitative traits

Programme Outcomes *(Biostatistics (Medical) Master)*

1	To be able to understand the interdisciplinary interaction releated with biostatistics.
2	to be able to use Theoretical and practical knowledge at the level of expertise.
3	To be able to nterpret the information by integrating information from different disciplines and create new information
4	To be able to nalyze the problems encountered by using research methods
5	to be able to conduct a study as an independent specialist
6	To be able to formulate solutions for complex unpredictable problems encountered by developing new approaches and taking responsibility.
7	To be able to resolve problems in environments that require leadership.
8	To be able to evaluate and direct knowledge and skills with a critical approach at the level of expertise.
9	To be able to to give statistical advise at the begining stages of preparing health related projects
10	To be able to get the knowledge and the ability of using statistical packages

Contribution of Learning Outcomes to Programme Outcomes *1:Very Low, 2:Low, 3:Medium, 4:High, 5:Very High*

	L1	L2	L3	L4	L5
P1	5	5	4	5	5
P2	5	5	5	3	4
P3	5	4	5	4	5
P4	5	5	5	5	4
P5	5	5	4	4	5
P6	5	5	4	5	4
P7	4	5	4	4	5
P8	5	5	4	5	4
P9	5	5	4	3	5
P10	5	4	3	4	4