

(faculty stamp)

## COURSE DESCRIPTION

Z1-PU7

WYDANIE N1

Strona 1 z 3

<b>1. Course title: POPULATION GENETICS</b>		<b>2. Course code</b>		
<b>3. Validity of course description: 2012/2013</b>				
<b>4. Level of studies: 2<sup>nd</sup> cycle of higher education</b>				
<b>5. Mode of studies: intramural studies</b>				
<b>6. Field of study: BIOTECHNOLOGY</b>			RAU-1	
<b>7. Profile of studies: general</b>				
<b>8. Programme: Bioinformatics</b>				
<b>9. Semester: 3</b>				
<b>10. Faculty teaching the course: Institute of Automatic Control</b>				
<b>11. Course instructor: prof. dr hab. inż. Marek Kimmel</b>				
<b>12. Course classification: profile course (?)</b>				
<b>13. Course status: elective</b>				
<b>14. Language of instruction: English</b>				
<b>15. Pre-requisite qualifications: Calculus, statistics, bioinformatics. It is assumed that before starting the course student is familiar with distributions of random variables, statistical hypothesis testing, linear equations, genetics and bioinformatics.</b>				
<b>16. Course objectives: The goal of the course is to give students knowledge concerning basic models of population genetics, i.e. Wright-Fisher model of genetic drift, mutation-drift equilibrium model, natural selection models (underdominance, overdominance, directional) as well as coalescence, in particular in applications to generation artificial samples composed of genomic sequences with distributions comparable to those present in natural populations. Additionally, the course shows importance of genetic diversity in natural samples and its sources in population demography, when the population is subject to evolution process responsible for variation observed</b>				
<b>17. Description of learning outcomes:</b>				
Nr	Learning outcomes description	Method of assessment	Teaching methods	Learning outcomes reference code
1.	The student knows Wright-Fisher model of genetic drift	PS	WM, L	K_W19
2.	The student knows basic concepts in population analysis: genetic drift, mutation, selection, coalescence, effective population size	PS	WM, L	K_W04, K_W10
3.	The student knows the influence of the reproduction models on the effective population size	PS	WM, L	K_W03, K_W19
4.	The student knows types and properties of natural selection working at the molecular level	PS	WM, L	K_W04
5.	The student can determine the type of selection on the basis of model parameters	PS, CL	L	K_U07
6.	The student can determine the distribution of coalescence time for constant population	PS, CL	L	K_U08
7.	The student can run computer simulations for coalescence models aiming at generating samples of artificial genetic sequences	PS, CL	L	K_U07, K_U10
8.	The student can efficiently use English literature sources	PS	WM	K_U02, K_U03, K_U06
9.	The student can make independent decisions about the choice of an appropriate model describing evolutionary forces in natural populations	PS, CL	L	K_K03, K_K04

**18. Teaching modes and hours**

Lecture / BA /MA Seminar / Class / Project / Laboratory

Lecture - 30 h., Laboratory - 15 h

**19. Syllabus description:****Lectures**

- 1) Introduction to population genetics
- 2) Nature of genetic variation, Hardy-Weinberg equilibrium, Linkage disequilibrium, mutation models (MK)
- 3) Random genetic drift – Wright-Fisher model
- 4) Mutation-drift equilibrium
- 5) Effective population size
- 6) Natural selection 1
- 7) Natural selection 2
- 8) Coalescent theory 1
- 9) Analysis of DNA polymorphism 1: Do humans evolve faster than chimps? (MK)
- 10) Analysis of DNA polymorphism 2: When did Mitochondrial Eve live?
- 11) Coalescent theory 2
- 12) Mutation – selection balance
- 13) Case study: H. sapiens – H. neanderthalensis interactions
- 14) Models of population growths
- 15) Final remarks

**Laboratory**

- 1) Simulating logistic growth of populations (continuous, discrete, with time-delay)
- 2) Simulating the effect of the random genetic drift
- 3) Simulating population of RNA-World package model
- 4) Simulating population samples using coalescent algorithm
- 5) Simulating coalescence distributions on populations modeled by branching processes

**20. Examination: No****21. Primary sources:**Gillespie J.H., *Population Genetics – A Concise Guide*, The John Hopkins University Press, Baltimore and London, 1998**22. Secondary sources:**Hartl D.L., Clark A.G., *Principles of Population Genetics*, Sinauer Associates, Inc. Publishers, Sunderland, Massachusetts, 3rd Edition, 1997**23. Total workload required to achieve learning outcomes**

Lp.	Teaching mode :	Contact hours / Student workload hours
1	Lecture	30/10
2	Classes	0/0
3	Laboratory	15/15
4	Project	0/0
5	BA/ MA Seminar	0/0
6	Other	15/5
	Total number of hours	60/30

**24. Total hours:90****25. Number of ECTS credits: 3****26. Number of ECTS credits allocated for contact hours: 2****27. Number of ECTS credits allocated for in-practice hours (laboratory classes, projects):1****26. Comments:**

Approved:

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(date, Instructor's signature)

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(date , the Director of the Faculty Unit signature)