Course title <English>	統計遺伝学 II Statistical Genetics II				Affiliated department, Job title,Name	Graduate School of Medicine Professor,YAMADA RIYOU	
Grade alloted	Professional degree students	**Number of credits**		2	**Course offered year/period**	2016/Irregular, Second semester	
Day/period	月 6	**Class style**		Lecture		**Language**	Japanese and English

[Outline and Purpose of the Course]

Statistical genetics is based on mathematical evaluation of genetic heterogeneity. It is important to realize precision medicine particularly for the following two aspects:
-(1) Development of data analysis-methods of knoeledge discovery in genome and all the other omics data that are the basis of precision medicine.
-(2) Development of methods how to provide probabilistic information to assist desicion-makings.

This course handles fundamental ideas for data analysis, including, statistics, comparison, order, distance, dimension, space, graph, probability/likelihood and enumeration. These are essential to understand various analysis methods precisely and to become researchers on theories of staitstical genetics.
In this course, description of the ideas in natural and computer languages that strengthen learners' understanding is prompted with verbal communication in the class hours and homework.
The course language is bilingual with English and Japanese.

[Course Goals]

-Understand fundamental ideas (statistics, comparison, order, distance, dimension, space, graph, probability/ likelihood and enumeration).
-Be able to describe the above mentioned ideas in natural language appropriately.
-Be able to describe the above mentioned ideas in computer language.
-Understand methods in papers at the level of the fundamental ideas above.
-Be able to generate simulational datasets of models.
-Be able to write program functions of basic statistical methods.

[Course Schedule and Contents]

The following schedule is subject to be changed.

Oct 3 Probability and Likelihood
Oct 17 Likelihood and variables in linkage analysis
Oct 24 ditto
Oct 31 Indices
Nov 7 Estimation
Nov 14 ditto
Nov 21 No class
Nov 28 Rejection and statistical tests
Dec 5 Association and causal association
Dec 12 Enumeration
Dec 18 ditto
Dec 26 Sampling
Jan 4(Wed) For catching up for any delay.
Jan 16 Many tests
Jan 23 ditto

統計遺伝学 II(2)

Jan 30 Exam

[Class requirement]

Basics of medicine/biology, or basics of computer science/informatics is recommended but not required.
Bring your own laptop PC with wifi access.
Be able to finish EdX/MOOC course "Introduction to Statistical Methods for Gene Mapping" https://www.edx.org/course/introduction-statistical-methods-gene-kyotoux-005x .
Basics of free application R is required.

[Method, Point of view, and Attainment levels of Evaluation]

Comments in class hours, homeworks and the exam on the last day will be integrated.

[Textbook]

山田　亮『統計遺伝学の基礎』（オーム社）ISBN:978-4274068225（Unfortunately no English version. The codes in the book will be still useful.）

[Reference books, etc.]

　（Reference books）
Take EdX/MOOC "Introduction to Statistical Methods for Gene Mapping" (https://www.edx.org/course/introduction-statistical-methods-gene-kyotoux-005x) .

　（Related URLs）
https://statgenetkyotou.moodlecloud.com/course/view.php?id=9(Course site for instructions, homeworks and so on. Login as "guestsan" with password "guestsan".)

[Regarding studies out of class (preparation and review)]

Homework is must, that is linked to the following class content.

　（Others (office hour, etc.) ）
*Please visit KULASIS to find out about office hours.