Course title <English>	統計遺伝学 I Statistical Genetics I			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, First 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]

授業計画と内容

The following schedule is subject to be changed.

Apr 11 The 1st week of EdX/MOOCコース "Introduction to Statistical Methods for Gene Mapping" (https://www.edx.org/course/introduction-statistical-methods-gene-kyotoux-005x)

Apr 18 Heredity

Apr 25 DNA, RNA, protein and traits

May 2 The 1st week of EdX/MOOCコース "Introduction to Statistical Methods for Gene Mapping" (https://www.edx.org/course/introduction-statistical-methods-gene-kyotoux-005x)

May 9 Various aspects of heterogeneity

May 16 ditto

May 23 Observation and evaluation

May 30 ditto

Jun 6 Treat samples individually

Jun 13 Treat samples as a population

Jun 20 ditto

Jun 27 Measures, variables, degrees of freedom, dimensions

統計遺伝学 I(2)

Jul 4 Distribution
Jul 11 ditto
Jul 25 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.