| Course title <English> | 統計遺伝学基礎　ＩＩ<br>Introductory Genetics-Statistics II | | Affiliated department, Job title,Name | Graduate School of Medicine<br>Professor,YAMADA RIYOU |
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| Grade alloted | Professional degree students | Number of credits | 2 | Course offered year/period | 2015/Irregular, Second semester |
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| Day/period | 月6 | Class style | Lecture | Language | Japanese and English |
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## [Outline and Purpose of the Course]

Large-scale data science is one of the most striking features of the current life science. Basics of statistical tests and estimation are fundamental for the study area. The goal of the lectures in the 1st and 2nd semesters aim that the participants understand methods and their backgrounds and master the practical skills to perform the methods with computers.

This year's lectures are most fundamental among the lecture series provided by the unit of statistical genetics, medicine that are consisted of 3-4 year cyclic components.

The topics are selected from the genetic epidemiology field.

## [Course Goals]

Goals are to understand:
-basics of regression
-basics of clustering methods
-basics of Bayesian network
and to master:
-the skill to find appropriate functions in R
-the skill to run the functions and handles the outputs.
and to master:
-the skill to handle various phenotypes in the context of data-handling.

## [Course Schedule and Contents]

Introductory Genetics-Statistics are consisted of I in the 1st semester and II in the 2nd semester.
The contents are as below. Participants need knowledge and skill in the 1st semeter's class.
-Statistics (Regression, clustering and Bayesian network)
-Computer skills(Usage of various methods in free software R, handling of command-line applications)
-Handling of various data types (Phenotypes and intermediate phenotypes)

# Subject to change to optimize participants' progresses

**統計遺伝学基礎　ⅠⅠ (2)**

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**[Class requirement]**

Basics of biology and genetics are desirable but not compulsory if willing.
Needs a laptop PC with WiFi access. Knowledge/skill in computation is not necessary but the participants without them will need to spend time to get familiar at home along the course.
Participation to both I and II is desirable but not compulsory.

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

Discussion in the classes
Homeworks
Exam on the last day

**[Textbook]**

Not used

**[Reference books, etc.]**

**（Reference books）**

山田　亮 『遺伝統計学の基礎』（オーム社）ISBN:978-4-274-06822-5
ryamada(山田　亮) 『発病リスク推定のためのベイジアンネットワーク~オミックス統計学2014_6』（kindle）ISBN:B00IHP1ON2（"http://d.hatena.ne.jp/ryamada22/20141224" is the site to get one.）
ryamada(山田　亮) 『ジェノタイプ推定で学ぶベイジアンネットワーク』（kindle）ISBN:B00PMKZOXQ（"http://d.hatena.ne.jp/ryamada22/20141224" is the site to get one.）

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

Homeworks will be offered to facilitate participants' understanding contents.

**（Others (office hour, etc.)）**

Class language is mixture of Japanese and English depending on the participants.

*Please visit KULASIS to find out about office hours.