

Course title <English>	統計遺伝学基礎 I Introductory Genetics-Statistics I		Affiliated department, Job title,Name	Graduate School of Medicine Professor, YAMADA RIYOU	
Grade allotted	Professional degree students	Number of credits	2	Course offered year/period	2015/Irregular, First semester
Day/period	月 6	Class style	Lecture	Language	Japanese and English
[Outline and Purpose of the Course]					
<p>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.</p> <p>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.</p> <p>The topics are selected from the genetic epidemiology field.</p>					
[Course Goals]					
<p>Goals are to understand:</p> <ul style="list-style-type: none"> -2x2 contingency table, odds ratio, confidence interval -statistical tests and estimation -uniform distribution -basics of 2x3 contingency table -trend test and logistic regression test for 2x3 tables -genetic models and their tests -multiple testings and types 1 and 2 error -exact probability -randomization/permutation method -linkage disequilibrium -Hardy-Weinberg equilibrium -genomic control method and FDR method for non-uniform p-values <p>and to master basic free software R skills to handle the above mentioned contents.</p> <p># Subject to change to optimize participants' progresses</p>					
[Course Schedule and Contents]					
<p>Introductory Genetics-Statistics are consisted of I in the 1st semester and II in the 2nd semester.</p> <ul style="list-style-type: none"> -The first two months in the 1st semester: <ul style="list-style-type: none"> --Basics of statistical tests (contingency table tests, multiple testings, genetic models) --Basics of free software R (Uni-variate and bi-variate data, plots, packages) -The later two months in the 2nd semester: <ul style="list-style-type: none"> --Apply the methods in the first two months to genetic heterogeneity topics with R. 					
Continue to 統計遺伝学基礎 I (2) ↓ ↓ ↓					

統計遺伝学基礎 I (2)

[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]

Instructed during class

[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) 『遺伝子多型のためのp値の話』 (kindle) ISBN:B00OY4Q994 (<http://www.genome.med.kyoto-u.ac.jp/StatGenetCourse/course/view.php?id=33> is the site to get one.)
ryamada(山田 亮) 『マルチプルテストとFDR~オミックス統計学2014_4~ 統計遺伝学』 ISBN: B00IBGKUN2 ("<http://d.hatena.ne.jp/ryamada22/20141224>" is the site to get one.)

(Related URLs)

<http://www.genome.med.kyoto-u.ac.jp/StatGenetCourse/course/view.php?id=33>(Access through the icon "login as a guest" until registration)

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

Usage of R in daily activities is highly recommended to facilitate the understanding of the course.

(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.