UNIVERSITÀ
DEGLI STUDI DI MILANO-BICOCCA

COURSE SYLLABUS

Statistical Models For Genetics

2122-1-F8203B017

Learning objectives

The focus of the course will be on the methods for identification and mapping of susceptible genes for human diseases. Students will be exposed to the basic genetic epidemiology designs and methods, the standard statistical genetics models and at the end of the course they should had learned how to interpret results from statistical analyses of genetic data and also how to read and evaluate current statistical human genetics literature

Contents

Mendel vs Complex Diseases, Segregation and Linkage analysis, Genetic association, Sample size and power, Genome-wide and sequencing analyses

Detailed program

Mendel and the complex genetic diseases;

genetic confounding factors;

Hardy Weinberg euilibrium;

Genetic epidemiology study designs and teorethical statistical models applied to genetic studies:

Segregation analysis,

Linkage analysis (teorethical fundaments, mapping mendelian diseases, complex traits),

Association analysis (Linkage disequil

ibrium, case-control studies, family based studies);

Sample size and power;

GWA (Genome Wide) and next generation sequencing analyses

Prerequisites

None

Teaching methods

Lectures, article review, exercises, softwares tutorial

Assessment methods

problem solving approach

Textbooks and Reading Materials

Ziegler A, Konig IR. A Statistical Approach to Genetic Epidemiology; II edition, Wiley-Blackwell; 2010

P. Sham. Statistics in Human Genetics. Oxford University Press; 1997

Updated Scientific pubblications

Semester

second semester

Teaching language

Italian

Sustainable Development Goals

QUALITY EDUCATION