



UNIVERSITÀ  
DEGLI STUDI DI MILANO-BICOCCA

## SYLLABUS DEL CORSO

### Modelli Statistici per la Genetica

2122-1-F8203B017

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#### 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 have 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 equilibrium;

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

Segregation analysis,

Linkage analysis (theoretical fundamentals, mapping mendelian diseases, complex traits),

Association analysis (Linkage disequilibrium, 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 publications

### **Semester**

second semester

### **Teaching language**

Italian

# Sustainable Development Goals

QUALITY EDUCATION

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