

# Syllabus of Fudan University

**Department: School of Life Sciences**

**Date: January 04, 2024**

<b>Course Code</b>	<b>BIOL130073</b>				
<b>Course Title</b>	<b>Human Evolutionary Genetics</b>				
<b>Credit</b>	<b>2</b>	<b>Practice Credit</b>	<b>2</b>	<b>Experiment (including computer) Credit</b>	<b>TBD</b>
<b>Credit Hours/Week</b>	<b>2</b>	<b>Practice Credit Hours</b>	<b>2</b>	<b>Experiment (including computer)Credit Hours</b>	<b>TBD</b>
<b>Course Nature</b>	<input type="checkbox"/> Specific General Education Courses <input type="checkbox"/> Core Courses <input type="checkbox"/> General Education Elective Courses <input type="checkbox"/> Basic Courses in General Discipline <input type="checkbox"/> Professional Compulsory Courses <input checked="" type="checkbox"/> Professional Elective Courses <input type="checkbox"/> Others				
<b>Course Objectives</b>	<p>"Human Evolutionary Genetics" is one of the most ideal courses that can naturally integrate the theoretical methods of natural science and humanistic ideas into classroom teaching. Through the systematic description of the genetic laws in the origin and evolution of human beings, discuss the theories, principles and methods, keep up with the frontiers and trends of cutting-edge technology development, and combine the major life and health issues facing human beings, combine the grand narrative with Micro-mechanism analysis is organically combined to cultivate students' critical thinking ability, cognitive structure, and humanistic feelings.</p>				
<b>Course Description</b>	<p><b>Evolutionary genetics</b> is founded on the principle that the genetic record of life is contained in the genomes of living species and it reveals evolutionary processes and relationships all the way back to the last universal common ancestor of all species. To find out about this ancestral organism we have to compare and contrast the most distantly related branches on the tree of life. Comparisons among much more closely related individuals, such as those from the same species, provide evidence on much more recent evolutionary processes. Our ability to read this genetic record has developed enormously in the last few years, although our confidence that information on our past exists within our heritable material is somewhat older. Genetic evidence comes from two main sources:</p> <ul style="list-style-type: none"> <li>• The genomes of living individuals that must have been passed down from ancestors</li> <li>• Ancient DNA from well-preserved organic remains, which may or may not be represented now in living descendants</li> </ul> <p><b>Human evolutionary genetics</b> involves the study of how different copies of the</p>				

	<p>human genome differ from one another, and from those of our closest relatives, other primates. Differences between genomes also form the basis of anthropological, medical, and forensic genetics. All of these fields are experiencing massive advances as a result of two developments. First, the public availability of human and nonhuman genome sequences, annotated with important functional elements such as genes, and with sites of genetic variation. Second, technology allowing analysis of most of this genetic variation across the genome, initially with the development of hybridization microarrays (or chips), followed by the development of methods to sequence whole genomes rapidly and cheaply (so-called next-generation sequencing). This explosion of information is driving an unprecedented period of innovation that gives us the tools to analyze huge datasets of unparalleled quality and quantity. This wealth of data is itself catalyzing the development of new interpretative methods. In addition, with the publication of genome sequences from other extant primates, as well as data from the genomes of extinct members of the genus <i>Homo</i>, we can now comprehensively catalog the genetic differences between humans and our closest relatives. As we shall see in this course, these impressive developments are allowing us to answer some of the most fundamental questions regarding human origins. These are indeed exciting times for human evolutionary genetics.</p> <p>Extracting information on any one past period or event requires careful interpretation to isolate it from previous and subsequent processes. This information can tell us not only about the demographic history and origins of populations but also something about the environmental challenges faced by those populations, through the influence of natural selection on genetic variation.</p> <p>It is said that “<b>the past is the source of the present</b>” and this is true in the academic field of human evolutionary genetics as much as elsewhere. This exciting subject owes its current status to developments and debates over the last 170 years in genetics, paleontology, archaeology, anthropology, and linguistics. In this course we have avoided cataloging this history, instead taking a twenty-first-century perspective.</p>
<p><b>Course Requirements:</b></p> <p>The students are anticipated to establish a basic concept of human evolutionary genetics, including the theories, principles, methodologies, and discoveries in the field. More importantly, the students are expected to improve their ability of critical thinking and communications. The students should be not only able to answer questions based on the known facts, but also capable of asking meaningful questions, writing summaries of literature, and doing presentations as well.</p>	
<p><b>Teaching Methods:</b></p> <p>Class teaching is accompanied with intensive Q&amp;A interactions, and classical &amp; latest literature reading, as well as presentation and practice involved all of the students.</p>	

**Instructor's Academic Background:**

Dr. **Shuhua Xu** is professor of human population genetics and Principal Investigator of Population Omics Group at Fudan University. He joined Chinese Academy of Sciences (CAS) and Max-Planck Partner Institute for Computational Biology (PICB) in 2006 after he received his PhD at Fudan University. He was appointed the position of Principal Investigator in 2009 and led the Population Genomics Group (PGG). He was appointed the position of Max-Planck Independent Research Group Leader in 2011, and supported by both Max-Planck and CAS from 2012 to 2018. He is currently holding a Distinguished Professorship at Fudan University and a Distinguished Adjunct Professorship at ShanghaiTech University, China. The Population Omics Group led by Dr. Xu is using computational approaches and developing new methods to dissect genetic architecture of human populations, quantitatively characterize their admixture features, and reveal their migration history and adaptive divergence. Dr. Xu has authored many scientific papers published in *Science*, *Nature*, *Cell*, *PNAS*, *Nature Genetics*, *Nature Communications*, *Genome Biology*, *The American Journal of Human Genetics*, *Nucleic Acids Research*, *Genome Research*, *Molecular Biology and Evolution*, *the PLoS* and *the BMC* series. Dr. Xu serves as Editorial Board member of several international peer-reviewed journals such as *JGG*, *Hereditas*, *Human Genomics*, *Molecular Genetics and Genomics* (co-Editor-in-Chief), *Frontier in Genetics*, *Scientific Reports*, *BMC Genetics* (Section Editor), *BMC Genomic Data* (Senior Editor).

**Members of Teaching Team**

<b>Name</b>	<b>Gender</b>	<b>Professional Title</b>	<b>Department</b>	<b>Responsibility</b>
<b>Lu Chen</b>	<b>Female</b>	<b>Assoc Prof.</b>	School of Life Sciences	Co-teaching
<b>Lian Deng</b>	<b>Female</b>	<b>Assoc Prof.</b>	School of Life Sciences	Co-teaching
<b>Ke Wang</b>	<b>Female</b>	<b>Assoc Prof.</b>	School of Life Sciences	Co-teaching
<b>Shaohua Fan</b>	<b>Male</b>	<b>Assoc Prof.</b>	School of Life Sciences	Co-teaching

**Course Schedule (Please supply the details about each lesson):**

课次 No.	教学周 Week	教学内容及预期效果 Content & Expected Achievement	作业/实验/实践 Assignment
1	1	A brief guide to the course design & An introduction to Human Evolutionary Genetics	Literature Reading
2	2	Facts about the human genome and genomics	Literature Reading
3	3	Human genome variation	Literature Reading
4	4	Finding, assaying, and analyzing genome diversity	Literature Reading
5	5	Processes shaping human genetic diversity	Literature Reading
6	6	Making inferences from diversity	Literature Reading
7	7	Humans as Apes	Literature Reading & Preparing for presentation
8	8	What genetic changes have made us human?	Literature Reading& Preparing for presentation
9	9	Origins of Modern Humans	Literature Reading& Preparing for presentation
10	10	The Distribution of Diversity	Literature Reading& Preparing for presentation
11	11	The Colonization of the Old World and Australia	Literature Reading& Preparing for presentation
12	12	Agricultural Expansions	Presentation & Discussion
13	13	Into New-Found Lands	Presentation & Discussion
14	14	Genetic structure and admixture	Presentation & Discussion
15	15	Adaptive evolution of human populations	Presentation & Discussion
16	16	Evolution and human diseases	Presentation & Discussion
17	17	All attendees	Final Exam

**The design of class discussion or exercise, practice, experience and so on:**

The class discussion and practice are designed to diversify the teaching approaches and delivery skills as much as possible, and involve students into intensive interactions, by this way motivates students to do the best that they can, giving students the opportunity to develop their ability to read, understand, communicate, and deliver in the context of a research field like Human Evolutionary Genetics.

**If you need a TA, please indicate the assignment of assistant:**

- (1) check on class attendance;
- (2) keep a record of and summarize Q&A response and performance;
- (3) assist to organize the students' presentations & practices;
- (4) collect exam papers and assist to check answers and give marks;
- (5) carry out administrative duties, such as preparing the classroom and clearing away after class to ensure effective teaching can take place;
- (6) monitor and record students' progress and provide detailed and regular feedback to teachers;

(7) Be aware and take care of students who have difficulties, administering first aid where necessary;

The TAs receive course credits in return for their assistance.

**Grading & Evaluation (Provide a final grade that reflects the formative evaluation process):**

考核形式 Assessment Criteria	权重 Percentage	评定标准 Assessment Standard
出勤/Attendance	10	签到记录
课堂表现/Participation	10	师生互动过程中的响应积极性、对待问题的态度、回答问题质量等
作业/实验/实践/ Assignment(s)	30	独立思考与合作实践（30%）；积极态度与投入程度（30%）；口头与书面报告质量（40%）
课程论文/Course Paper	30	文献调研（20%）；正确引用（10%）；认知深度（30%）；批判性思维（20%）；篇幅（10%）；行文规范（10%）
开卷考试/Open-book exam	20	按照卷面分统计
闭卷考试/Close-book exam	0	无
其他/Other(s)		

### 1. Oral presentation

An oral presentation can be done by a group of students collaboratively, students can choose or propose topics related to the content of the course.

**Basic requirement:**

- Maximal 3 team members
- Sufficient contribution of each team member
- Face the audience
- No reading
- **Context** of communication
- **Communication content**
- **Content delivery**

### 2. Term paper

A set of subjects for term papers will be offered, but students can also propose their own topics. A term paper can be written by a team, in particular, a term paper can be a summary of the oral presentation done by the same team. In this case, each team member co-authored the term paper must explicitly specific his/her contribution to the paper.

- literature coverage (20%)
- appropriate citation (10%)
- breath (30%)

- critical thinking (20%)
- length (10%)
- language (10%)

### 3. Open exam

About 10-20 questions will be provided, students are required to give back their answers in the given time.

**Teaching Materials & References (Including Author, Title, Publisher and Publishing time):**

#### 1. References of textbooks

《Human Evolutionary Genetics》(2nd Edition), Mark Jobling, Edward Hollox, Matthew Hurles, Toomas Kivisild, Chris Tyler-Smith, 2014 by Garland Science, Taylor & Francis Group, LLC. ISBN: 978-0-8153-4148-2

# HUMAN EVOLUTIONARY GENETICS second edition

Mark Jobling

Edward Hollox

Matthew Hurles

Toomas Kivisild

Chris Tyler-Smith

 **Garland Science**  
Taylor & Francis Group  
NEW YORK AND LONDON

#### 2. Human genome data resources, Computer tools, Database

PGG.population: [www.pgpopulation.org](http://www.pgpopulation.org)

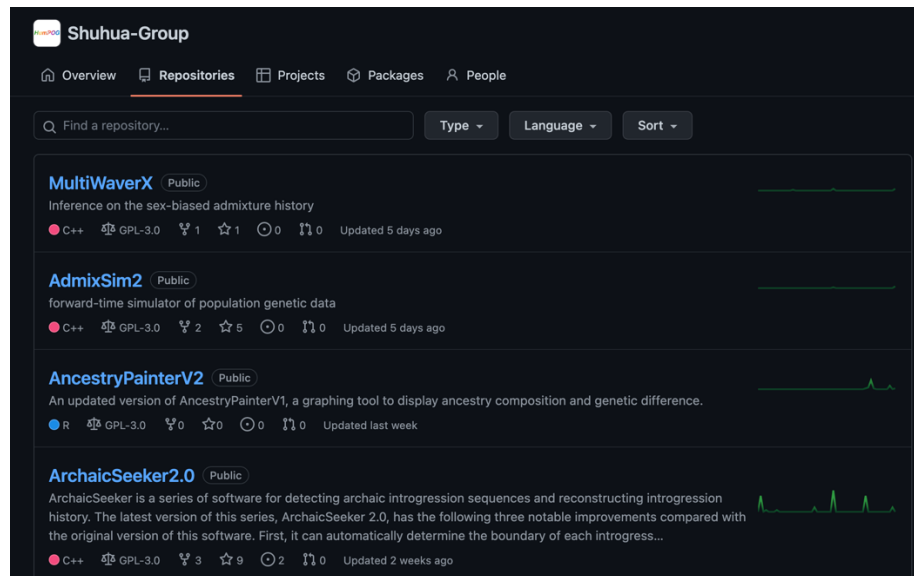
PGG.SNV: [www.pggsnv.org](http://www.pggsnv.org)

PGG.Han: [www.pgghan.org](http://www.pgghan.org)

PGG.SV: [www.biosino.org/pggsv](http://www.biosino.org/pggsv)

PGG.MHC: <https://pog.fudan.edu.cn/pggmhc>

GitHub: <https://github.com/orgs/Shuhua-Group/repositories>



1000 genomes Project: <http://www.internationalgenome.org>

<https://www.ncbi.nlm.nih.gov/variation/tools/1000genomes/>

MEGA: <http://www.megasoftware.net/>

PHYLIP: <http://evolution.genetics.washington.edu/phylip.html>

Arlequin: <http://cmpg.unibe.ch/software/arlequin35/>

### 3. References of Articles and Documents etc.

Human Population Omics Group: <http://pog.fudan.edu.cn/#/home>



