Human Evolutionary Genetics

Description  Theories and methods of molecular population genetics, with emphasis on human examples. Using these tools, genetic data can inform us about population history and adaptive evolution. Laboratory exercises with the Python programming language connect theory to data. Satisfies Quantitative Intensive Requirement.

Prerequisites  You should be comfortable with algebra and first-semester calculus. No prior knowledge of Python is needed.

Grading  two midterm exams and a cumulative final (17% each), weekly labs (25% total), and weekly homeworks (25% total). Grades are curved as explained on the website.

Extra credit  An extra credit assignment is available on the course website. It provides practice in algebra and is available only during the first half of the semester. The due date is listed in the syllabus below.

Exams  are paper-and-pencil and take place in the lecture room. You may bring one 3X5 card containing handwritten notes on both sides. You may bring a calculator, but do not load notes onto the calculator.

Weekly computer lab  In this lab, students do projects using the Python computer language. The lab assignments are short enough to complete during the two-hour lab. The lab syllabus is available on the class website. The projects themselves are described in JEPy and in the Lab Manual for Anth/Biol 5221, which is also available on the website or the Copy Center at Olpin Student Union.

Homework  There are also paper-and-pencil homework assignments, which are due at roughly weekly intervals as indicated in the syllabus below. The homework assignments are available on the class website or the Copy Center at Olpin Student Union. Answers to even-numbered problems are in the back of the book of assignments. Only odd-numbered problems will be graded.

Required readings  are listed in the outline below and in the list of references. The main text,


is available at the bookstore. All other readings are on the class website. In addition, we will occasionally assign other published papers and notes of our own. When we do, they will be available either on paper or on the course web site.

**Discussion list**  All students should enroll in the class email list, which is a place to ask questions about the course (and also to answer them). We often use the list for important announcements involving review sessions, homework, and exams. To enroll, point your browser at http://lists.csbs.utah.edu, and follow the link to EvGen. To post a question to the list, you must use the email account with which you enrolled in the list. Just send your question by email to evgen@lists.csbs.utah.edu.

**Contact**  For questions of general interest—the subject matter of the course, what the exam will be like, etc.—please use the class discussion list (see above). For private discussions, all of us are available after class and by appointment.  *Rogers:* 206a Stewart Bldg., 801-581-5529, rogers@anthro.utah.edu;  *Stark* derek.stark@utah.edu;  *Torosin* nicole.torosin@anthro.utah.edu.

**Equal access provisions**  The University seeks to provide equal access to its programs, services and activities for people with disabilities. If you will need accommodations in this class, then reasonable prior notice must be given to the instructor and to the Center for Disability Services, 162 Olpin Union. Call 581-5020 to make arrangements.

**Date**  |  **Lecture**  |  **Reading**
---|---|---
Aug 20 M  |  Introduction to the course, and to variation  |  RS
22 W  |  Describing and partitioning phenotypic variation  |  S
24 F  |  Genomes and their variation  |  S [3, sec. 1.0–1.3]
27 M  |  More genomes and their variation  |  S
29 W  |  Probability 1  |  R [11, sec. 1–2]
31 F  |  Probability 2  |  R [11, sec. 3]
Sep 03 M  |  *** NO CLASS  |  
05 W  |  Probability 3  |  R [11, sec. 3]
07 F  |  Python  |  S [14]
10 M  |  Random mating  |  R [3, sec. 1.4]
12 W  |  Genetic drift and heterozygosity  |  R [3, sec. 2.0–2.2; 12, Ch. 1]
Homework 2 due.
14 F  |  Mutation versus drift  |  R [3, sec. 2.3; 12, Ch. 1]
17 M  |  DNA sequence variation  |  S [12, Ch. 1]
19 W  |  Gene genealogies  |  S [12, Ch. 4]
Homework 3 due.
21 F  |  Exam 1  |  
24 M  |  Connecting gene genealogies to genetics  |  R [12, Ch. 5; 3, sec. 2.6]
26 W  |  Site frequency spectrum  |  R [12, Ch. 6]
28 F  |  Mismatch distribution  |  R [12, Ch. 7]
Homework 4 due.
03 W  |  Molecular evolution  |  S [3, sec. 2.4]
05 F  |  Molecular variation and neutral theory 1  |  S [3, sec. 2.5]
Homework 5 due.
08 M  |  *** NO CLASS  |  
10 W  |  *** NO CLASS  |  
12 F  |  *** NO CLASS  |  

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### Schedule

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<thead>
<tr>
<th>Date</th>
<th>Assignment/Topic</th>
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<tbody>
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<td>15 M</td>
<td>Molecular variation and neutral theory</td>
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<td>17 W</td>
<td>Selection 1</td>
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<td>19 F</td>
<td>Selection 2</td>
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<td>22 M</td>
<td>Mutation versus selection</td>
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<td>24 W</td>
<td>Genetic load</td>
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<td>26 F</td>
<td>Fixation of advantageous mutations</td>
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<td>29 M</td>
<td>Two-locus dynamics</td>
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<td>31 W</td>
<td>Catch-up and review</td>
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<td>Nov 02 F</td>
<td>Exam 2</td>
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<tr>
<td>05 M</td>
<td>Two-locus selection</td>
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<td>07 W</td>
<td>Inbreeding 1</td>
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<td>09 F</td>
<td>Inbreeding 2</td>
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<td>12 M</td>
<td>Population subdivision</td>
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<td>14 W</td>
<td>Genomic traces of selective sweeps</td>
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<td>16 F</td>
<td>Genetic draft</td>
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<td>19 M</td>
<td>Population history from whole genomes</td>
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<td>21 W</td>
<td>Neolithic adaptations</td>
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<td>23 F</td>
<td>*** NO CLASS</td>
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<td>26 M</td>
<td>Archaic admixture</td>
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<td>28 W</td>
<td>Quantitative Genetics: genes and environment</td>
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<td>30 F</td>
<td>Quantitative Genetics: heritability</td>
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<td>Dec 03 M</td>
<td>Quantitative Genetics: evolution in nature</td>
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<td>05 W</td>
<td>QTL mapping and “missing” heritability</td>
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<td>Dec 14 F</td>
<td>Final exam 10:30AM–12:30PM</td>
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### References


Learning outcomes

**Evolution** Students will be able to apply the principles of natural selection and mechanisms of genetic change, including trait variation and heritability, to explain the observed diversity of life that has arisen over the past several hundred thousand years.

**Scientific reasoning** Students will be able to apply the process of science to identify knowledge gaps, formulate hypotheses, and test them against experimental and observational data to advance an understanding of the natural world.

**Quantitative reasoning** Students will be able to use mathematical and computational methods and tools to describe living systems and be able to apply quantitative approaches, such as statistics, quantitative analysis of dynamic systems, or mathematical modeling.