

Anthro 5221 & Biol 5221
Lecture: MWF 10:45–11:35AM
Lab: F 1–3PM
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<http://content.csbs.utah.edu/~rogers/ant5221/index.php>

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 web site. 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,

Gillespie, John. 2004. *Population Genetics, a Concise Guide*, 2nd edition

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.

Recommended readings Hetland, Magnus L. 2005. *Beginning Python: From Novice to Professional*, 1st Edn.

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.

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 21 M	Introduction to the course, and to variation	RS
23 W	Describing and partitioning phenotypic variation	S
25 F	Genomes and their variation	S [3, sec. 1.0–1.3]
28 M	Probability 1	R [11, sec. 1–2]
30 W	Probability 2	R [11, sec. 3]
Sep 01 F	Probability 3	R [11, sec. 3]
	Homework 1 due.	
04 M	*** NO CLASS	
06 W	Python	S [14]
08 F	Random mating	R [3, sec. 1.4]
	Homework 2 due.	
11 M	Genetic drift and heterozygosity	R [3, sec. 2.0–2.2; 12, Ch. 1]
13 W	Mutation versus drift	R [3, sec. 2.3; 12, Ch. 1]
15 F	DNA sequence variation	R [12, Ch. 1]
	Homework 3 due.	
18 M	Gene genealogies	R [12, Ch. 4]
20 W	Catch-up and review	
22 F	Exam 1	
25 M	Connecting gene genealogies to genetics	R [12, Ch. 5; 3, sec. 2.6]
27 W	Site frequency spectrum	R [12, Ch. 6]
29 F	Mismatch distribution	R [12, Ch. 7]
	Homework 4 due.	
Oct 02 M	Population growth and gene genealogies	R [4]
04 W	Molecular evolution	S [3, sec. 2.4]
06 F	Molecular variation and neutral theory 1	S [3, sec. 2.5]
	Homework 5 due.	
09 M	*** NO CLASS	
11 W	*** NO CLASS	
13 F	*** NO CLASS	
16 M	Molecular variation and neutral theory 2	S [3, sec. 2.5]

	Extra credit assignment due.	
18 W	Selection 1	S [3, sec. 3.0–3.3]
20 F	Selection 2	S
	Homework 6 due.	
23 M	Mutation versus selection	S [3, sec. 3.4; 2]
25 W	Genetic load	S [3, sec. 3.5]
27 F	Fixation of advantageous mutations	S [3, sec. 3.9–3.10]
	Homework 7 due.	
30 M	Two-locus dynamics	R [3, sec. 4.0–4.1]
Nov 01 W	Catch-up and review	
03 F	Exam 2	
06 M	Two-locus selection	R [3, sec. 4.2]
	Homework 8 due.	
08 W	Inbreeding 1	R [3, sec. 5.0–5.3]
10 F	Inbreeding 2	R
	Homework 9 due.	
13 M	Population subdivision	R [3, sec. 5.5; 9]
15 W	Genomic traces of selective sweeps	R [13; 10]
17 F	Genetic draft	S [3, sec. 4.3]
	Homework 10 due.	
20 M	Population history from whole genomes	R [5]
22 W	Neolithic adaptations	R [1]
24 F	*** NO CLASS	
27 M	Archaic admixture	R [6, 15]
29 W	Quantitative Genetics: genes and environment	S [3, sec. 6.0–6.1]
Dec 01 F	Quantitative Genetics: heritability	S [3, sec. 6.2]
	Homework 11 due.	
	Homework 12 due.	
04 M	Quantitative Genetics: evolution in nature	S [3, sec. 6.3]
06 W	QTL mapping and “missing” heritability	S [8, 7]
	Homework 13 due.	
Dec 14 H	Final exam 10:30AM–12:30PM	

References

- [1] Todd Bersaglieri, Pardis C. Sabeti, Nick Patterson, Trisha Vanderploeg, Steve F. Schaffner, Jared A. Drake, Matthew Rhodes, David E. Reich, and Joel N. Hirschhorn. Genetic signatures of strong recent positive selection at the lactase gene. *American Journal of Human Genetics*, 74:1111–1120, 2004.
- [2] Wenqing Fu, Timothy D O’Connor, Goo Jun, Hyun Min Kang, Goncalo Abecasis, Suzanne M Leal, Stacey Gabriel, Mark J. Rieder, David Altshuler, Jay Shendure, Deborah A Nickerson, Michael J. Bamshad, NHLBI Exome Sequencing Project, and Joshua M. Akey. Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. *Nature*, 493:216–270, 2012.

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- [4] Chad D. Huff, Jinchuan Xing, Alan R. Rogers, David Witherspoon, and Lynn B. Jorde. Mobile elements reveal small population size in the ancient ancestors of *Homo sapiens*. *Proceedings of the National Academy of Sciences, USA*, 107(5):2147–2152, 2010.
- [5] Heng Li and Richard Durbin. Inference of human population history from individual whole-genome sequences. *Nature*, 475(7357):493–496, 2011.
- [6] Fernando L Mendez, Joseph C Watkins, and Michael F Hammer. Global genetic variation at OAS1 provides evidence of archaic admixture in Melanesian populations. *Molecular Biology and Evolution*, 29(6):1513–1520, 2012.
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- [9] Alan R. Rogers. Geographic population structure. <http://content.csbs.utah.edu/~rogers/ant5221/unprotected/popstruc.pdf>, 2009.
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- [12] Alan R. Rogers. Lecture notes on gene genealogies. <http://content.csbs.utah.edu/~rogers/ant5221/ggeneal.pdf>, 2013.
- [13] P. C. Sabeti, S. F. Schaffner, B. Fry, J. Lohmueller, P. Varilly, O. Shamovsky, A. Palma, T. S. Mikkelsen, D. Altshuler, and E. S. Lander. Positive natural selection in the human lineage. *Science*, 312:1614–1620, 2006.
- [14] Jon Seger. Just enough Python. <http://content.csbs.utah.edu/~rogers/ant5221/jepy.pdf>, 2013.
- [15] Benjamin Vernot and Joshua M Akey. Resurrecting surviving Neandertal lineages from modern human genomes. *Science*, 343(6174):1017–1021, 2014.