COMPBIO 293B Doctoral Seminar in Computational Biology
Weds from 12-2pm for Fall 2018. The seminar will be held in 321 Stanley.

Instructor: Priya Moorjani, Dan Rokhsar (Fall)
Offered: FALL SEMESTER
Units: 2.0 (Letter Grade)
Course Format: Seminar
CCN#: CCB 293/ MCB 296
Class size: 22

Course Description: This one-year interactive seminar builds skills, knowledge and community in computational biology for first year PhD and second year Designated Emphasis students. Topics covered include concepts in human population genetics and evolutionary biology, statistical and computational methods for data analysis, critical review and discussion of current research studies and methods, preparation for success in the PhD program and career development. Faculty members of the graduate program in computational biology and scientists from other institutions will participate. Topics will vary each semester.

Syllabus:

Week	Date	Subject	Instructors
1	8/22	Topics in Human Evolutionary Genetics Concepts in Population Genetics	Priya Moorjani Dan Rokhsar
2	8/29	Ancient DNA and human evolution	Priya Moorjani
3	9/5	Concepts in Population Genetics 2	Dan Rokhsar
4	9/12	Making inferences about human history and evolution from genetic data *Hands-on data analysis for ancestry inference*	Priya Moorjani
5	9/19	**Student presentation/ Journal club** Origin of modern humans and Out of Africa migration	Students
6	9/26	**Student presentation/ Journal club** Human-Neanderthals: species or populations?	Students
7	10/3	**Student presentation/ Journal club** Genetic uniqueness of humans	Students
8	10/10	**Student presentation/ Journal club** Recent human prehistory: Migrations, replacements and mixtures	Students
9	10/17	**No class for ASHG**	

10	10/24	**Student presentation/ Journal club** Human Adaptation and Selection	Students
11	10/31	**Student presentation/ Journal club** Genetic basis of Phenotypic variation	Students
12	11/7	**Student presentation/ Journal club** Disease mapping	Students
13	11/14	**Student presentation/ Journal club** Consumer genomics	Students
14	11/21	**No Class/Thanksgiving Holiday**	
15	11/28	**Student presentation/ Journal club** Implication of genetic inferences or TBD	Students

Grading:
- Homework Assignments: 40%
- Student Presentations: 40%
- Participation: 20%

Instructor Contact Information:

Professor: Priya Moorjani
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Professor: Dan Rokhsar
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Graduate Student Instructor: Sandra Hui
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Attendance: Attendance (sign-in) is taken each week. If you are going to miss a class you are encouraged to contact the instructors ahead of time. Attendance each week of the semester is critical to success in the course. **If you miss more than two classes, you will be dropped from the course.**

Lecture Slides and Course Reading Assignments: Slides will be posted on bCourses *after* each class. All Reading Assignments will be posted on bCourses. Don't get behind on reading! Reading is required ahead of the assigned class.

Homework Assignments: These will be posted on bCourses and are due before class begins on dates listed in syllabus. Assignments should be submitted via the bCourses site as pdf or word document submission through bCourses. Last name must be included in file name as

shown: (LASTNAME_COMPBIO293_Homework1_2018.pdf). In addition, First and Last name should be included at the top of the document. There will be a place for you to insert this information in each homework assignment.

Location: 321 Stanley Hall

Recommended Textbook: For reference, please use the following two textbooks:
1. Human Evolutionary Genetics (second edition) by Jobling, Hurles, and Tyler-Smith;
2. Population Genetics, A Concise Guide" by John Gillespie 2nd edition.

Attendance: Attendance (sign-in) is taken each week. If you are going to miss a class you are encouraged to contact the instructors ahead of time. Attendance each week of the semester is critical to success in the course. **If you miss more than two classes, you will be dropped from the course.**

Mental Health:

If you are experiencing stress, anxiety, or other forms of distress during the semester, we hope to be a resource for you. Please reach out to the GSI or Professor if you need support. There are also many resources available to you. All registered Berkeley students are eligible to use Counseling Psychological Services. You do not have to purchase the Student Health Insurance Plan to use these services. The first five counseling sessions are free for registered Berkeley students. Counselors can provide support in academic success, life management, career and life planning, and personal growth and development.

UC Berkeley, Counseling Psychological Services:

- Please call (510) 642-9494 or stop by the office on the 3rd floor of the Tang Center to make an appointment with a counselor.
- Drop-in counseling for emergencies: Monday - Friday, 10:00AM - 4:30PM
- After hours counseling: In the case of emergencies at night or on weekends, call (855) 817-5667 for free assistance and referrals. Request to speak with a counselor.
- For emergency support: Call UCPD 911 or (510) 642-3333

24 Hour Crisis Hotlines:

- Alameda County Crisis Line: (offers confidentiality, TDD services for deaf and hearing impaired callers and translation in 140 languages) Call 1-800-309-2131
- National Crisis Help Line: Call 1-800-273-TALK
- National HopeLine Network: Call 1-800-SUICIDE

We also ask that you look out for your fellow peers. If you see any of the signs below that may indicate your classmate may need assistance, please use the resources above or reach out to the GSI or Professors.
- Withdrawing from other people
- Changes in weight or eating patterns
- Changes in sleeping patterns
- Fatigue or lack of energy

- Increased anxiety or irritability
- Feeling worthless or hopeless

<u>Academic Dishonesty</u>:

Academic dishonesty is not acceptable at UC Berkeley. Academic dishonesty is any action that may result in creating an unfair academic advantage for oneself or unfair academic disadvantage for another member of the academic community. Therefore, any exam, quiz, paper, and/or homework assignment submitted by you that bears your name should be your own original work. In all of your assignments, including your homework or drafts of papers, you may use words or ideas written by other individuals in publications, web sites, or other sources, but only with proper attribution. 'Proper attribution' means that you have fully identified the original source and extent of your use of the words or ideas of others that you reproduce in your work for this course, usually in the form of a footnote, parentheses or quotations. If you are not clear about the expectations for completing an assignment or taking a test or examination, be sure to seek clarification from the instructors or GSI beforehand. Cheating and plagiarism are forms of academic dishonesty and are NOT TOLERATED under any circumstance. Any evidence of academic dishonesty will result in a score of zero (0) on that assignment or exam, and will be reported as soon as possible to the Center for Student Conduct (http://sa.berkeley.edu/conduct). This will result in a permanent scar on your academic record. In 2015, UC Berkeley launched the Turnitin service (https://asuc.org/honorcode/index.php) to support academic integrity and the campus honor code. Turnitin is an opt-in tool enabled through bCourses that allows Instructors and GSIs to check student assignments for originality. We will use Turnitin in this course for all written assignments. The consequences of cheating and academic dishonesty are substantial, including a formal discipline file, possible loss of future internship, scholarship, or employment opportunities, and denial of admission to graduate or medical school.

Reading List for Fall Semester 2018 (Tentative):

Week 1 **Date 8/22** **Concepts in Population Genetics (Dan)**
Readings:
  1. Chapter 2, "Population Genetics, A Concise Guide" by John Gillespie 2nd edition.
  2. 1000 Genomes Project Consortium. "An integrated map of genetic variation from 1,092
    human genomes." Nature 491.7422 (2012): 56.
  3. Lek et al. Analysis of protein-coding genetic variation in 60,706 humans.
    https://www.ncbi.nlm.nih.gov/pubmed/27535533

Week 2 **Date 8/29** **Archaic genomes: Neanderthals and Denisova (Priya)**
Readings:
  1. Novembre, John, and Sohini Ramachandran. "Perspectives on human population
    structure at the cusp of the sequencing era." Annual review of genomics and
    human genetics 12 (2011): 245-274.
  2. Slatkin, Montgomery, and Fernando Racimo. "Ancient DNA and human
    history." *Proceedings of the National Academy of Sciences* 113.23 (2016):
    6380-6387.

Week 3 **Date 9/5** **Concepts in Population Genetics 2 (Dan)**
Readings:
  1. Chapter 3-5, "Population Genetics, A Concise Guide" by John Gillespie 2nd edition.

Week 4 **Date 9/12** **Making inferences about human history and evolution from genetic data**
Readings:
  1. Novembre et al. Genes mirror geography within Europe. Nature. (2008) Nov 6;
    456(7218): 98–101.
  2. Li, Jun Z., et al. "Worldwide human relationships inferred from genome-wide patterns
    of variation." *science* 319.5866 (2008): 1100-1104.
  3. Loh P-R, Lipson M, Patterson N, Moorjani P, Pickrell JK, Reich D, and Berger B.
    Inferring Admixture Histories of Human Populations Using Linkage Disequilibrium.
    Genetics, 2013.

Week 5 **Date 9/19** **Origin of Modern Humans and Out of Africa Migration**
Readings:
  1. Cann RL, Stoneking M, Wilson AC. 1987. Mitochondrial DNA and human evolution.
    Nature 325:31–36.
  2. Ramachandran et al. 2005. *Proceedings of the National Academy of Sciences*.102 (44)
    15942-15947 https://doi.org/10.1073/pnas.0507611102
  3. Screrri et al. "Did Our Species Evolve in Subdivided Populations across Africa, and
    Why Does It Matter?" *Trends in ecology & evolution* (2018).

Week 6 **Date 9/26** **Human-Neanderthals: species or populations?**
Readings:
  1. The complete genome sequence of a Neanderthal from the Altai Mountains
  https://www.nature.com/articles/nature12886
  2. Sankararaman, S., et al. (2014). The genomic landscape of Neanderthal ancestry in
    present-day humans. Nature 507, 354-7.

3. Juric et al. (2016). The Strength of Selection against Neanderthal Introgression. Plos Genetics.
4. Harris and Nielsen. (2016). The Genetic Cost of Neanderthal Introgression. Genetics.

Week 7   Date 10/3   Genetic uniqueness of humans
Readings:
1. Sassa, Takayuki. "The role of human-specific gene duplications during brain development and evolution." *Journal of neurogenetics* 27.3 (2013): 86-96.
2. Enard, W., et al. (2002). Molecular evolution of FOXP2, a gene involved in speech and language. Nature 418, 869-72.
3. Hubisz, Melissa J., and Katherine S. Pollard. "Exploring the genesis and functions of Human Accelerated Regions sheds light on their role in human evolution." *Current opinion in genetics & development* 29 (2014): 15-21.

Week 8   Date 10/10   Recent human prehistory: Migrations, replacements and mixtures
Readings:
1. Haak et al. (2016) Massive migration from the steppe was a source for Indo-European languages in Europe. Nature.
2. Skoglund et al. (2017) Reconstructing Prehistoric African Population Structure. Cell
3. Yang and Fu. (2018). Insights into Modern Human Prehistory Using Ancient Genomes. Trends in Genetics. https://doi.org/10.1016/j.tig.2017.11.008.

Week 9   Date 10/17   no class (ASHG)

Week 10   Date 10/24   Human Adaptation and Selection
Readings:
1. Pritchard, JK., Pickrell, JK., Coop, G. (2010). The genetics of human adaptation: hard sweeps, soft sweeps, and polygenic adaptation. Curr Biol. 20, R208-15.
2. Sabeti, Pardis C., et al. "Detecting recent positive selection in the human genome from haplotype structure." Nature 419.6909 (2002): 832.
3. Huerta-Sánchez, Emilia, et al. "Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA." *Nature* 512.7513 (2014): 194.
4. Mathieson, Iain, et al. "Genome-wide patterns of selection in 230 ancient Eurasians." *Nature* 528.7583 (2015): 499.

Week 11   Date 10/31   Disease mapping
Readings:
1. Vischer et al. (2006) Assumption-Free Estimation of Heritability from Genome-Wide Identity-by-Descent Sharing between Full Siblings. https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.0020041.
2. Wellcome Trust Case Control Consortium. "Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls." *Nature* 447.7145 (2007): 661.
3. Boyle, Evan A., Yang I. Li, and Jonathan K. Pritchard. "An expanded view of complex traits: from polygenic to omnigenic." Cell 169.7 (2017): 1177-1186. https://doi.org/10.1016/j.cell.2017.05.038

Week 12   Date 11/7   Polygenic risk estimation
Readings:

1. Lee et al. Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature. https://www.nature.com/articles/s41588-018-0147-3
2. Kong, Augustine, et al. "The nature of nurture: Effects of parental genotypes." *Science* 359.6374 (2018): 424-428.

Week 13   Date 11/14   Personal genomics
Readings:
1. Han et al. 2017. Clustering of 770,000 genomes reveals post-colonial population structure of North America. https://www.nature.com/articles/ncomms14238
2. Bryc, Katarzyna, et al. "The genetic ancestry of african americans, latinos, and european Americans across the United States." The American Journal of Human Genetics 96.1 (2015): 37-53.

Week 14   Date 11/21   No Class/Thanksgiving Holiday

Week 15   Date 11/28   Implication of genetic inferences on Personal genomics
Ideas:
1. Lorenzen, Eline D., et al. "Species-specific responses of Late Quaternary megafauna to climate and humans." *Nature* 479.7373 (2011): 359.
2. Bycroft, Clare, et al. "The UK Biobank resource with deep phenotyping and genomic data." *Nature* 562.7726 (2018): 203.

Exercise
4 questions each week (2 per paper)