AN 333: Human Population Genetics

Fall 2018

Lecture is held on MWF, 1:25 – 2:15 pm in CAS 237

Faculty Instructor:

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Course Description: This course uses human genomic and population variation as a framework within which to better understand human evolutionary history. We do this by familiarizing ourselves with the methods, techniques, and biology that allow us to understand human variation at its most basic level: the genome. Throughout the course, we will download, analyze, and draw conclusions about human evolutionary and population history from open-source human genomic datasets derived from the 1000 Genomes Project. From there, we expand our view to better grasp human diversity and what it can tell us about our evolutionary history from our last common ancestor with other apes to how modern human populations have diverged, specialized and then interacted during our spread from East Africa to every part of the globe. Finally, we take a close look at the biological underpinnings of contemporary human variation and what impact our knowledge of these systems can have on our conceptions of public policy, health and disease.

Prerequisites: CAS AN 102, or AN 233; or CAS BI 107 and either BI 119, BI 211, or BI 303; or consent of instructor.

Course Format: This is a 4-unit lecture course with some lab-like classes held in lieu of lecture. Lectures will be held three times a week for a total of 3 hours.

Grading: Performance will be based on a total of 500 possible points distributed across five assessments:

1)	Exam 1	100 points	Wednesday, 10 October, 2018, 1:25-2:15pm (CAS 237)
2)	Exam 2	100 points	Friday, 09 November, 2018, 1:25-2:15pm (CAS 237)
3)	Exam 3	100 points	Monday, 12 December, 2018, 1:25-2:15pm (CAS 237)
4)	Lab Homework	60 points	See Lab Syllabus
5)	Final Project	140 points	Monday, 17 December, 2018 (hardcopy to STO 247E, by 5pm)

Final grades will be calculated as the total number of points earned divided by the total possible (510). Final grades are determined as:

93-100%	A	83-87%	B	73-77%	C	<60%	F
90-92%	A-	80-82%	B-	70-72%	C-		
88-89%	B+	78-79%	C+	60-69%	D		

Exams will be entirely multiple choice. If necessary, exam grades will be scaled, but not curved (this is to your advantage). **There will be NO extra credit.**

Required texts: The course text will be available for purchase at Barnes & Noble / BU, and also on library reserve at the Science and Engineering Library.

Principles of Population Genetics, Fourth Edition, by DL Hartl & AG Clark ISBN 978-0-87893-308-2

Course website: There is a web site for the course available to enrolled students through Blackboard at https://learn.bu.edu. Abbreviated lecture slides will be posted by 8pm the night before each class meeting. Reading assignments and required readings outside of the required text will be posted on Blackboard.

Course hashtag: Online content relevant to the course will be disseminated via Twitter and demarcated using the hashtag **#AN333BU18**. Note that you need not register with Twitter or have a smart phone to view content. Simply search for the hashtag on www.twitter.com. Although not all online content will be discussed, hashtagged items may be incorporated into lecture to provide contemporary commentary on issues discussed.

The community at Boston University has adopted the following Academic Conduct Code: "All students entering Boston University are expected to maintain high standards of academic honesty and integrity." Obviously, the full text is more detailed. The expectation is that you will adhere to this code, as your instructor pledges to do as well. For more information, please visit this website: http://www.bu.edu/academics/policies/academic-conduct-code/. In keeping with this code, cheating, plagiarism, or any other form of academic dishonesty will not be tolerated (ACC III) and will be referred to the Dean's Office.

Email policy: The instructor will respond to emails within 24 hours from 8am on Monday through 5pm on Friday. You will not receive email replies over the weekend. Although email is available to you 24 hours a day 7 days a week, I unfortunately cannot be. Please keep this in mind. If you would like to discuss a confidential issue with Dr. Schmitt, please request a meeting via email or set up a meeting in person.

You must sign your email with the official name you use with the University and/or use your email address registered with the University. If I cannot tell that you are officially a student at BU and enrolled in AN233 this semester, I will not reply to your email. THIS INCLUDES MESSAGES SENT FROM CELL PHONES.

Please use proper grammar and complete sentences so that your request is clearly understandable.

Policy on accommodation of religious holidays and other scheduling conflicts: In compliance with Massachusetts General Laws Chapter 151C, Section 2B, it is the official policy of Boston University to permit any student to undergo a test or examination, without penalty, at a time when that activity would not violate the student's religious creed.

All deadlines and exam dates are noted on this syllabus. It is your responsibility to note any conflicts with exams and due dates and let the instructor know. If you have other scheduling conflicts, please see the guidelines at: http://www.bu.edu/cfa/files/pdf/BUPolicyonstudentabsenceduetoreligiousobservance.pdf

Policy on exams: I will not administer make-up exams. If you have to miss an exam for a valid, unforeseeable and urgent reason, one of your other exams will be counted twice. For example, if you have a valid family emergency and miss exam 1, you may choose either exam 2 or exam 3 to count twice. If you do find yourself facing an unforeseen emergency, please contact us as soon as possible to let us know. Please note: this policy is for valid emergencies (i.e., illness, death in the family, need to attend a legal proceeding, your apartment burned down, etc.). Students are otherwise expected to take all three exams.

While I will remind you about exam logistics, you are responsible for making sure that you complete every question and turn in the exam before you leave the room in which it is administered. I will not accept your exam after you have left the classroom.

Policy on the paper/project assignment: Only illness or some other unforeseeable emergency will allow us to grant you a later due date for the paper than what is posted on this syllabus. Anticipated events do not count as acceptable reasons for turning in your paper late (even if it is a University-approved one), as you can and should plan ahead and turn your paper in early.

Policy on attendance for lecture: We do not enforce attendance. That said, be advised that exam content will primarily derive from lectures. The reading material is additional information that supplements but does not repeat what is presented in class. You are responsible for both. It is **strongly** recommended that you do not skip lecture.

Policy on attendance for discussion section: Again, we do not enforce attendance. That said, be aware that there will be an activity in each section worth 10 points of your final grade. There are 12 discussion section meetings. Your lowest section score will be dropped, for a maximum discussion section score of 110 out of 110. Another way to think of it is that each section meeting is worth about 2% of your final grade, outside of the pedagogical value. Material presented in section will be included on the exams. It is **strongly** recommended that you do not skip your discussion section.

Policy on laptop use in class: Laptops will be permitted in class for the purposes of statistical programming and data downloads from online repositories, but students are strongly encouraged to take notes by hand. In years past, laptop use has led to an abuse of the privilege and resulted in class disruption. For example, students who use class time to catch up on Facebook or to watch movies distract the students around them. This negatively impacts the learning environment. Recent research has strongly shown that note taking done by hand leads to better retention and learning outcomes. This is for the benefit and quality of your personal learning and the learning environment.

Policy on cell phones: All cell phones need to be silenced during class. Keep in mind that excessive texting or other use of your phones is distracting to other people in the class. If your cell phone activity becomes disruptive, you will be asked to leave the class. Cell phones must be turned off and put away during all exams. If you use your phone (even if it just rings) during an exam you will be asked to leave and you will receive a zero on the exam.

Policy for students requiring accommodation of disabilities: In order to adequately accommodate students with disabilities that require additional services, I need to know who you are and what your needs are by **September 21st**. If you delay processing your paperwork, I will not be able to accommodate you for the semester. Do not delay in finalizing and confirming your accommodations. For more information, visit their website: http://www.bu.edu/disability/

Policy on recording lectures: Lectures may NOT be recorded using audio or photographic equipment without the prior written permission of Dr. Schmitt or by formal recommendation of the Office of Disability Services. Lectures are comprised of copyrighted intellectual material, and the recording and sharing of that material without express permission is a violation of copyright and personal privacy. Additionally, the discussion of potentially sensitive issues in class requires that students feel safe to express their opinions without fear of future reprisal or exposure. Students who record course lectures using cameras, audio, or video equipment without prior notification and permission will be asked to leave.

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Course Outline and Due Dates:

Exams and the paper assignment due dates are in **bold**. Discussion section topics are in *italics*.
** Reading assignments will be posted on the course website.**

SECTION I: Understanding Allele Frequencies in Human Populations

W Sep 05	Class 1:	Introduction and basic review
F Sep 07	Class 2:	On discrete traits
M Sep 10	Class 3:	On continuous traits and the normal distribution
W Sep 12	Class 4:	One allele in a population
F Sep 14	Class 5:	Multiple alleles in populations
M Sep 17	Class 6:	Organization of the genome I: Recombination, linkage, and more
W Sep 19	Class 7:	Organization of the genome II: Linkage disequilibrium
F Sep 21	**Class 8:**	**Pre-lab: Shared Computing Cluster Tutorial**
M Sep 24		**NO CLASS**
W Sep 26	Class 9:	The Hardy Weinburg Model (and its violations)
F Sep 28	**Class 10:**	**Lab 1**
M Oct 01	Class 11:	On genetic drift
W Oct 03	Class 12:	Mutations and heterozygosity
F Oct 05	**Class 13:**	**Lab 2**
M Oct 08		**NO CLASS**
Tu Oct 09	Class 14:	Exam Review 1
W Oct 10	**Class 15:**	**Exam 1**

SECTION II: Measuring Evolutionary Change at the Gene Level in Human Populations

F Oct 12	**Class 16:**	**Lab 3**
M Oct 15	Class 17:	Measuring selection I
W Oct 17	Class 18:	Measuring selection II
F Oct 19	**Class 19:**	**Lab 4**
M Oct 22	Class 19:	Measuring selection III
W Oct 24	Class 20:	Measuring selection IV
F Oct 26	**Class 21:**	**Lab 5**
M Oct 29	Class 22:	Quantitative genetics I
W Oct 31	Class 23:	Quantitative genetics II
F Nov 02	**Class 24:**	**Lab 6**
M Nov 05	Class 25:	Gene regulation, epigenetics, gene/environment interactions
W Nov 07	Class 26:	Exam Review 2
F Nov 09	**Class 27:**	**Exam 2**

SECTION III: Measuring Evolutionary Change at the Organismal Level in Human Populations

M Nov 12	Class 28:	Migration history: Gene flow current and ancient
W Nov 14	Class 29:	Phenotypic variation: skin color, altitude, nutrition, climate
F Nov 16	**Class 30:**	**Lab 7**
M Nov 19	Class 31:	Reproductive strategy: aspects and consequences of mate choice
W Nov 21		**NO CLASS, Thanksgiving Break**
F Nov 23		**NO CLASS, Thanksgiving Break**
M Nov 26	Class 32:	Growth and Development: biological basis of behavioral and phenotypic plasticity
W Nov 28	Class 33:	Health and Disease: evolutionary medicine, energetics, longevity
F Nov 30	Class 34:	Climate change and its genotypic and phenotypic effects on human biology
M Dec 03	Class 35:	Diet change and its genotypic and phenotypic effects on human biology
W Dec 05	Class 36:	Coevolution of pathogen and host: SIV and HIV
F Dec 07	Class 37:	Social epidemiology: Genomics and public health
M Dec 10	Class 38:	Exam Review 3
W Dec 12	Class 39:	**Exam 3**
M Dec 17		**FINAL PAPER/PROJECT DUE**

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Readings from the Primary Textbook:

Please have readings finished by the date listed! The course text is on hold at the Science and Engineering Library.

W Sep 05	Class 1:	No readings.
F Sep 07	Class 2:	Review readings posted on Blackboard.
Week 1 (Sep 10-14)		Hartl & Clark, Chapter 1
Week 2 (Sep 17-21)		Hartl & Clark, Chapter 2 Optional Readings posted on Blackboard.
Week 3 (Sep 24-28)		Hartl & Clark, Chapter 2.2, 2.4
M Oct 01	Class 11:	Hartl & Clark, Chapter 3
W Oct 03	Class 12:	Hartl & Clark, Chapter 4
F Oct 05	Class 13:	Lab 2: Associated readings (see lab syllabus and Blackboard)
Week 5 (Oct 8-10)		Exam Review 1 (Hartl & Clark, Chapters 1-4)
F Oct 12	Class 16:	Lab 3: Associated readings (see lab syllabus and Blackboard)
Week 6 (Oct 15-19)		Hartl & Clark, Chapter 5, 9
F Oct 19	Class 19:	Lab 4: Associated readings (see lab syllabus and Blackboard)
Week 7 (Oct 22-26)		Hartl & Clark, Chapter 5, 10
F Oct 26	Class 21:	Lab 5: Associated readings (see lab syllabus and Blackboard)
Week 8 (Oct 29-Nov 2)		Hartl & Clark, Chapter 8
F Nov 02	Class 24:	Lab 6: Associated readings (see lab syllabus and Blackboard)
M Nov 05	Class 25:	TBD
W Nov 07	Class 26:	Exam Review 2 (Hartl & Clark, Chapters 5, 8, 9, 10)
M Nov 12	Class 28:	Hartl & Clark, Chapter 6
F Nov 16	Class 30:	Lab 7: Associated readings (see lab syllabus and Blackboard)
M Nov 19	Class 31:	Reproductive strategy: aspects and consequences of mate choice
W Nov 21		**NO CLASS, Thanksgiving Break**
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M Nov 26	Class 32:	Growth and Development: biological basis of behavioral and phenotypic plasticity
W Nov 28	Class 33:	Health and Disease: evolutionary medicine, energetics, longevity
F Nov 30	Class 34:	Climate change and its genotypic and phenotypic effects on human biology
M Dec 03	Class 35:	Diet change and its genotypic and phenotypic effects on human biology

W Dec 05	Class 36:	Coevolution of pathogen and host: SIV and HIV
F Dec 07	Class 37:	Social epidemiology: Genomics and public health
M Dec 10	Class 38:	Exam Review 3
W Dec 12	Class 39:	**Exam 3**

M Dec 17

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Readings, Exercises, and Due Dates:

These dates and topics are subject to change. Email your instructor or come to office hours if in doubt regarding any assignment.

Sep 21 Pre-Lab: BU Shared Computing Cluster Tutorial

Material covered: Introduction to and tutorial on using the BU Shared Computing Cluster, via Linux Virtual Lab *SCC*.

Readings: None.

Activities: We will create personal profiles using the *SCC* interface with the help of a representative from Research Computing. We'll learn how to connect to *SCC* and some basic commands that will help us navigate the interface and access analytical software that will be used in the course.

Assignment: In-class worksheet based on activities will be graded.

Learning Outcomes:

- Learn how to access your *SCC* profile and data storage, and become familiar with analytical software and data download and storage commands.
- Learn basic command-line tools, vocabulary, and syntax.
- Learn how to access analytical software such as R and RStudio, which we will be using to do real-life population genetic analyses.
- If we have time, we will begin using these tools to get a head start on Lab 1!

Sep 28 Lab 1: Accessing Human Candidate Gene Region Data – UCP1

Material covered: Introduction to the 1000 Genomes Project dataset, and tutorial on using *Ensembl* to access the 1000 Genomes dataset. For illustrative purposes, we'll focus on the *UCP1* gene, a candidate gene implicated in human obesity and metabolic disorders, which is specifically implicated in metabolic processes in humans related to the activation of brown adipose tissue (these are fat cells that actually generate heat, to keep us warm in cold weather).

Readings:

The 1000 Genomes Project Consortium. 2015. A global reference for human genetic variation. *Nature* 526: 68-74.

Danecek P, Auton A, Abecasis G, Albers CA, Banks E, DePristo MA, Handsaker RE, Lunter G, Marth GT, Sherry ST, McVean G, Durbin R, 1000 Genomes Project Analysis Group. 2011. The variant call format and VCFtools. *Bioinformatics App Note* 27: 2156-2158.

Gonzalez-Barroso MDM, Ricquier D, Cassard-Doulcier AM. 2000. The human uncoupling protein-1 gene (UCP1): present status and perspectives in obesity research. *Obesity Rev* 1: 61-72.

Activities: We'll learn how to use the *Ensembl* database to navigate our candidate gene, UCP1, and find more information about it. Each student will be assigned a 1000 Genomes population that they will look at over the course of the labs, and we will use the *Ensembl* data slicer to download data for those populations into our *SCC* accounts.

Assignment: Students must turn in a worksheet – with questions related to *UCP1* variation in humans and related to the downloaded dataset – in class the following Monday. **Pre-Lab Homework Assignment is due today.**

Learning Outcomes:

- Learn about the basics of bioinformatics and how genetic data is transformed from raw sequencing reads in to a VCF file, which is the file type we will be working with.
- Learn about the public data on human genomes available via the 1000 Genomes Project, and how to access it via *Ensembl*.
- Learn about the role of *UCP1* variation in humans, and how it is implicated in thermoregulation, brown adipose tissue, and whether and how it may be involved in human evolution and clinical medicine.
- Learn how to download specific regions of genomic data – or candidate gene regions – from 1000 Genome populations in VCF format from the *Ensembl Data Slicer* and move them on to the *SCC*

Oct 05 Lab 2: UCP1 *Variants and Hardy-Weinberg Equilibrium*

Material covered: Using *R* and *RStudio* via the *SCC* to run pre-written code that will perform our analyses. Assessing allelic variation in SNPs within and across populations. Testing Hardy-Weinberg equilibrium (HWE) and understanding what it means if violated, which involves knowing the assumptions of the model. Using downloaded candidate region data from 1000 Genomes Project to assess HWE in living human populations using a Chi Squared test. Using *Ensembl* to obtain genotype count information in order to use the Wigginton and Cutler method of HWE calculation on selected SNPs.

Readings:

Chen, J. The Hardy-Weinberg Principle and Its Applications in Modern Population Genetics. *Frontiers in Biology* 5(4): 348-53.

Rose, Giuseppina, *et al*. Two variants located in the upstream enhancer region of human *UCP1* gene affect gene expression and are correlated with human longevity. *Experimental Gerontology* 46(11): 897-904.

Wigginton JE, Cutler DJ, Abecasis GR. 2005. A note on exact tests of Hardy-Weinberg equilibrium. *Am J Hum Genet* 76: 887-893.

Activities: We will use the *R* coding language to test HWE in the dataset on *UCP1* we downloaded from *Ensembl*. We will assess whether or not SNPs in this genomic region are in Hardy-Weinberg equilibrium based on a Chi Square test in assigned human populations. We will then re-test selected SNPs using the "True HWE" method described in Wigginton and Cutler. We will then discuss what our results mean, in accordance with what we know about those populations, HWE, and the phenotypic effects of *UCP1*.

Assignment: Students must turn in a worksheet – with questions related to *UCP1* variation in humans and related to the downloaded dataset – in class the following Monday. **Lab 1 Homework Assignment is due today.**

Learning Outcomes:

- Learn how to use the *SCC* and *R* coding language to observe and understand population differences in UCP1 variation.
- Calculate Hardy-Weinberg Equilibrium for all UCP1 SNPs in individual populations using a traditional Chi Square test.
- Perform a check on all SNPs not in Hardy-Weinberg Equilibrium by calculating "True" Hardy-Weinberg with the built-in Shiny App.

- Research the consequence types of these SNPs in order to understand how these SNPs might affect the genome itself, and how they might affect genotype.
- Calculate the "True" Hardy-Weinberg Equilibrium using the Shiny App for A-3826G (SNP ID rs1800592), an upstream SNP that has known phenotypic consequences, and determine what the Hardy-Weinberg Equilibrium says about the population.

Oct 12 Lab 3: Linkage Disequilibrium in UCP1

Material covered: Assessing linkage disequilibrium (LD) in genomic regions using *R* coding language. Calculating LD by hand between two known loci in *UCP1*. Understanding factors that increase LD.

Readings:

Ramos, Aduato, *et al*. 2012. The contribution of FTO and UCP-1cSNPs to extreme obesity, diabetes and cardiovascular risk in Brazilian individuals. *BMC Med Genet* 13(101) (November 7, 2012).

Slatkin M. 2008. Linkage disequilibrium – understanding the evolutionary past and mapping the medical future. *Nat Rev Genet* 9: 477-485.

Stephens, J. Claireborn *et al*. Haplotype variation and linkage disequilibrium in 313 human genes. *Science* 293: 489-93.

Activities: We will assess linkage disequilibrium across the *UCP1* locus using with our dataset downloaded from *Ensembl*, with a focus on the SNPs that are defined in Ramos et al. We will then discuss what high linkage disequilibrium in our populations could mean for the selection within our population.

Assignment: Students must turn in a worksheet – with questions related to *UCP1* variation in humans and related to the downloaded dataset – in class the following Monday. **Lab 2 Homework Assignment is due today.**

Learning Outcomes:

- Learn about the SNPs rs6536991, rs35243591, rs2270565, and rs12502572 and their roles in obesity.
- Learn how to use the package *SNPStats* to perform LD analysis in a population, including constructing LD matrices and LD heatmaps.
- Learn about the two statistics D' and R^2, which are the most commonly used statistics to evaluate LD between SNPs. Learn what each can tell us about a population, and apply the two statistics to our own populations.
- Learn how to use *Ensembl* to look at long-distance LD between SNPs in UCP1 and SNPs in other genes.

Oct 19 Lab 4: Nearest-Neighbor Joining and Intro to Phylogeny

Material covered: Using Nearest Neighbor Joining to see which individuals within the population are most related to each other. Plotting trees to better understand the patterns of molecular variation and amount of diversity within the population.

Readings:

Kimura, M. 1980. A simple method for estimating evolutionary rates of base substitutions through ` comparative studies of nucleotide sequences. *J Mol Evol* 16: 111–120.

Saitou, N. and Nei, M. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* 4: 406–425.

Activities: We will learn how to create a phylogenetic tree with simple neighbor-joining methods using the *ape* package in *R.* We will then learn how to make a comparative tree that will allow us to compare three different

populations' structures in a qualitative way. We will also use these phylogenetic trees to assess the diversity of UCP1 in each population, and discuss what that means.

Assignment: Students must turn in a worksheet – with questions related to *UCP1* variation in humans and related to the downloaded dataset – in class the following Monday. **Lab 3 Homework Assignment is due today.**

Learning Outcomes:

- Learn how to apply Kimura's Neutral Theory to our populations to create a matrix of genetic distances between individuals in a population
- Learn how to use the *ape* package's Nearest Neighbor Joining algorithm to create a Nearest Neighbor Joining tree, and learn how to use the package *phangorn* to manipulate phylogenetic trees.
- Learn how to interpret a phylogenetic tree, and learn what it can tell us about molecular diversity within our populations

Oct 26 Lab 5: Introduction to Neutrality Statistics and Signs of Selective Sweeps

Material covered: Introduction to statistical tests of neutrality that can be used in genetic studies. Tajima's D, Fu and Li's D and F, and iHS scores will be covered. Understanding what each of these tests do to measure selection, and what these statistics can tell us about a population.

Readings:

Garrigan, Daniel, Richard, and John Wakeley. 2010. Measuring the sensitivity of single-locus "neutrality tests" using a direct perturbation approach. *Mol Biol Evol* 27(1): 73-89.

Southam L, Soranzo N, Montgomery SB. et al. 2009. Is the thrifty genotype hypothesis supported by evidence based on confirmed type 2 diabetes- and obesity-susceptibility variants? *Diabetologia* 52: 1846.

Tajima F. 1989. Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics* 123(3): 585–95.

Activities: We will use the packages *PopGenome* and *pegas* to cauclate Fu and Li's D and F, as well as Tajima's D. We will also look at an *example* of an iHS score with the example data from the *rehh* package. Finally, we will take ample time to understand what the Fu and Li's D and F and Tajima's D test results tell us about how our populations are evolving, and use the example of iHS to predict whether or not our populations underwent a selective sweep in the UCP1 region.

Assignment: Students must turn in a worksheet – with questions related to *UCP1* variation in humans and related to the downloaded dataset – in class the following Monday. **Lab 4 Homework Assignment is due today.**

Learning Outcomes:

- Learn what Fu and Li's D and F, Tajima's D, and iHS scores mean, and how to interpret them.
- Learn to use the *PopGenome* package to calculate neutrality stats such as Fu and Li's D and F, and Tajima's D.
- Learn to use the *pegas* package to explore our Tajima's D statistic further.
- Learn about iHS by looking at an example of how to calculate iHS in R, and reflect on what the iHS score for our population's UCP1 haplotype might look like.

- Learn about whether or not selection is happening in our populations based on these statistics, and relate it back to what may be happening in the environment to cause these alleles to be selected for/against.

Nov 02 Lab 6: A Brief Digression from UCP1 *for Quantitative Genetics*

Material covered: Quantitative genetics and partitioning variance in phenotypes between genetic and environmental signals. The *SOLAR* work environment. The quantitative genetics of BMI.

Readings:

Almasy L, Blangero J. 1998. Multipoint quantitative-trait linkage analysis in general pedigrees. *Am J Hum Genet* 62: 1198–1211.

Schmitt CA, Service S, Cantor RM, Jasinska AJ, Jorgensen MJ, Kaplan JR, and Freimer NB. 2018. High heritability of obesity and obesogenic growth are both highly heritable and modified by diet in a nonhuman primate model, the African green monkey (*Chlorocebus aethiops sabaeus*). *Int J Obesity* 42: 765-774.

Hill WG. 2012. Quantitative genetics in the genomics era. *Curr Genomics* 13(3): 196-206.

Activities: There will be a brief discussion of quantitative genetics and the vervet monkey (*Chlorocebus sabaeus*) model as implemented in SOLAR using the Almasy & Blangero terminology and orientation to using *SOLAR* in the Terminal environment. We will conduct in class exercises that will be used to answer questions in the Lab 6 homework.

Assignment: Students must turn in a worksheet – with questions related to BMI variation and heritability in vervet monkeys and related to the downloaded dataset – in class the following Monday. **Lab 5 Homework Assignment is due today.**

Learning Outcomes: TBD

Nov 16 Lab 7: Finding a New Locus…

Material covered: We will discuss the process of finding a new locus to do a population genetics study on.

Readings: None

Activities: There will be a brief tutorial on how to think about finding a new locus of interest to study on your own, and we will have a class discussion on final project topic ideas.

Assignment: Students must turn in a worksheet – with questions related to *UCP1* variation in humans and related to the downloaded dataset – in class the following Monday. **Lab 6 Homework Assignment is due today.**

Learning Outcomes:

- Learn how to use the resources provided to you in this class to find a new genetic locus for study