## BMB497B Comparative Genomics, Spring 2012, Tues and Thur 2:30-3:45 pm, 112 Thomas Building

Day, Date	Торіс	H'son HG	Readings	Assignment	Due
T, Jan 10	I. Is creative pedagogy an oxymoron? Goals and procedures in the class. What do students want to get from the class?			Examples of creative learning or what do you want to accomplish	F, Jan 13
R, Jan 12	2. Fundamentals of genomics	1	Lander 1996, Lander 2011		
T, Jan 17	3. Resources for functional genomics: Browsers, Galaxy, Blast	6	Kuhn 2007, Galaxy 2010	2. Browser, Galaxy exercises	F, Jan 20
R, Jan 19	4. Aligning biological sequences	1,2	Altschul et al. 1990		
T, Jan 24	Jan 24 No class				
R, Jan 26	5. Arc of genomics from bench to bedside		Green et al 2011	3. Will genomics really improve my health?	F, Jan 27
R, Jan 26	Eric Green, Director, National Human Genome Research Institute, NIH: The Future is Bright: Charting a Course for Genomic Medicine, 4:00 PM, 100 LSB Berg Auditorium				
T, Jan 31	Finding protein-coding genes within genomes: How many are there? How are they distributed along chromosomes? How do you find out what function they have? Evolution of protein-coding genes	3, 5	Ensembl gene set article, Lander_human 2001, Waterston_mouse 2002	4. Gene annotations	F, Feb 03
R, Feb 02					
T, Feb 07	7. Finding genes that do not code for proteins: How much of the genome is transcribed? Do they produce stable noncoding RNAs? What roles do they play in the cell (regulatory and enzymatic)?		ENCODE_pilot 2007, Rinn_Guttman 2009	5. long noncoding RNAs	F, Feb 10
R, Feb 09					
T, Feb 14	8. Finding evolutionary signatures of function: How can you use genome comparisons between species to estimate the amount of functional sequence – and to identify it? Inferring positive and negative selection from comparative genomics. Ultraconserved elements. Do protein-coding genes account for all or most of the functional sequences? This non-coding DNA inferred to be functional can be considered "dark matter" of the genome.	4	Waterston_ mouse 2002, Bejerano 2004	6. Constraint in noncoding sequences	F, Feb 17
R, Feb 16					
T, Feb 21	9. Recent selection - which genetic variants are adaptive?	4	Neilsen et al, Nature Reviews Genetics	7. Tools and resources for recent selection	F, Feb 24
R, Feb 23	10. How do human genes become maladaptive? 11. Genomics of Gene Regulation. Finding non-genic functional sequences: How can we		DiRienzo et al	Tot Todalic Scienciali	
T, Feb 28	illuminate the dark matter? How do you use high throughput genomics to find DNA sequences likely to be involved in gene regulation?	5	ENCODE_pilot 2007		
R, Mar 01				8. Gene expression	
<b>Mar 05-09</b> T, Mar 13	Spring Break Genomic approaches to mapping epigenetic features associated with gene regulation, such as histone modifications, DNase hypersensitive sites, and transcription factor occupancy.		Wold_Myers 2007	and regulation	F, Mar 16
R, Mar 15					
T, Mar 20	Prediction and tests of gene regulatory sequences		Hardison_Taylor 2012, Pennacchio et al Nature		
W, Mar 21	Steve Henikoff Marker Lecture 1, 6 pm 100 LSB				
R, Mar 22 T, Mar 27	Steve Henikoff Marker Lecture 2, 3 pm 100 LSB Finding function by phenotype: Genetic association studies are currently identifying with high precision and statistical support loci that contribute to complex traits, such as disease susceptibility. How can you find these results easily? How can you use the data and insights from the earlier topics to develop testable hypotheses about how variation among humans at these loci lead to increased susceptibility to disease?		1000Genomes 2010, Manolio 2009	9. Interpreting GWAS SNPs	F, Mar 30
R, Mar 29	Phenotype-associated SNPs not in coding regions		ENCODE_User's_Guide 2011		
T, Apr 03					
R, Apr 05					
T, Apr 10			-		
R, Apr 12 T, Apr 17			-		
	Project presentations				
R. Apr 19			+		
R, Apr 19 T, Apr 24	Project presentations				