



<b>Wednesday (August 26)</b>		<b>Association Analysis</b>	
9:00am	- 9:45am	16. Genetics and Linkage Equilibrium – Measures and Tests	[Cantor]
9:45am	- 10:45am	17. Case/Control Association Tests	[Sinsheimer]
10:45am	- 11:00am	<i>Break (tea, etc)</i>	
11:00am	- Noon	18. Haplotypes – Frequency Estimation and Genotype Imputation	[Lange]
Noon	- 1:30pm	<i>Lunch</i>	
1:30pm	- 2:15pm	19. Genome-wide Association Studies (GWAS) – Background and Study Design Issues	[Cantor]
2:15pm	- 3:15pm	20. Ethnic Admixture and Structure	[Alexander]
3:15pm	- 3:30pm	<i>Break (tea, etc)</i>	
3:30pm	- 5:00pm	21. GWAS and Extensions	[Lange]
<b>Thursday (August 27)</b>		<b>Association Analysis continued</b>	
9:00am	- 10:45am	22. Family-based Association Tests, including Gamete Competition	[Horvath]
10:45am	- 11:00am	<i>Break (tea, etc)</i>	
11:00am	- Noon	23. Association Tests given Linkage	[Sinsheimer]
Noon	- 1:30pm	<i>Lunch</i>	
<b>1:30pm</b>	<b>- 5:30pm</b>	<b>Local Excursion: Getty Museum and Gardens</b>	
	1:30pm	Pick up at UCLA	
	5:00pm	Pick up at Getty; return to UCLA	
<b>6:30pm</b>		<b>Course Dinner: Covel Commons Terrace</b>	
<b>Friday (August 28)</b>		<b>Quantitative Trait Loci (QTL) Analysis</b>	
9:00am	- 9:45am	24. Introduction to Quantitative Trait Analysis	[Sinsheimer]
9:45am	- 10:45am	25. Linkage Analysis for Quantitative Traits – Variance Component Analysis	[Sinsheimer]
10:45am	- 11:00am	<i>Break (tea, etc)</i>	
11:00am	- Noon	26. Association Tests for Quantitative Traits	[Sinsheimer]
Noon	- 1:30pm	<i>Lunch</i>	
1:30pm	- 3:15pm	27. Network Analysis: Integrating Expression Levels and Marker Data	[Horvath]
3:15pm	- 3:30pm	<i>Break (tea, etc)</i>	
3:30pm	- 4:15pm	28. Demonstration of Mendel Enterprise Clinical Components	[Papp]
4:15pm	- 5:00pm	29. Audience Questions Addressed, Future Directions, and Final Overview	[Lange]
<b>Saturday (August 29)</b>		<b>Check-out Day</b>	

## **Background Reading**

Suggested background reading in genetics includes Human Molecular Genetics (HMG), by Tom Strachan and Andrew Read. In the 3rd edition, the relevant chapters are: 4, 13, 14, and 15 (with chapter 18 also of interest to some participants). In the older 2nd edition, which is online at <[www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=hmg](http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=hmg)>, the relevant chapters are: 3, 11, 12, and 19 (chapters 15 and 17 also may be of interest to some).

Suggested background reading in statistics includes The Cartoon Guide to Statistics, by Larry Gonick and Woollcott Smith. A more theoretical work is Mathematical and Statistical Methods for Genetic Analysis, by Kenneth Lange, the lead instructor in this course. An alternative theory book is Statistical Methods in Genetic Epidemiology, by Duncan Thomas; in particular, chapter 4 provides an overview of relevant statistical principles. Finally, the chapters in HMG (see above) covering gene mapping are a good basic introduction to statistical genetics, particularly chapters 13, 14, and 15 in the 3<sup>rd</sup> edition.