Contents

1	Gen 1.1 1.2	ne Genealogies and Genetic Data Genealogies and Genealogical Thinking	1 4 7
	1.3	Measures of DNA Sequence Polymorphism	9
	1.4	Variation at the PDHA1 Locus in Humans	12
	1.5	Exercises	16
2	Pro	bability Theory for the Coalescent	17
_	2.1	Fundamentals of Probability Theory	17
		2.1.1 Events, Probabilities, and Random Variables	17
		2.1.2 Four Famous Probability Distributions	26
	2.2	Poisson Processes	33
		2.2.1 Poisson Process Results for the Coalescent	35
		2.2.2 Convolutions of Exponential Distributions	37
	2.3	Exercises	39
3	The	e Coalescent	41
	3.1	Population Genetic Models	41
		3.1.1 The Wright-Fisher Model	42
		3.1.2 The Moran Model	43
	3.2	The Standard Coalescent Model	45
		3.2.1 Wright-Fisher Model Derivation	47
		3.2.2 Moran Model Derivation	51
		3.2.3 Breeding Structure and Exchangeability	53
	3.3	Some Properties of Coalescent Genealogies	57
		3.3.1 Two Measures of the Size of a Genealogy	57
		3.3.2 The Branching Structure of Genealogies	61
	3.4	Human-Neanderthal Couples?	63
	3.5	Exercises	69
4	Neu	atral Mutations and Genetic Polymorphisms	71
	4.1	The Infinite Sites Model and DNA Sequence Polymorphism	72
		4.1.1 The Number Segregating Sites	73
		4.1.2 Pairwise Differences	75
		4.1.3 Site Frequencies	79
	4.2	The Infinite Alleles Model and the Ewens Sampling Formula	83
	4.3	Deviations from the Standard Model: Testing "Neutrality"	86
		4.3.1 Test Statistics Based on Site Frequencies	87
		4.3.2 Demographic History and Patterns of Polymorphism	90
	4 4	A Footprint of Positive Selection Drosonhila simulans	94

5	Population Structure 101				
	5.1 Markov Processes	10			
	5.2 The Structured Coalescent				
	5.3 Geographic Structure				
	5.3.1 Subdivision with Migration				
	5.3.2 Divergence without Gene Flow				
	5.3.3 More Complicated Histories				
	5.4 Strong Natural Selection	10			
	5.4.1 Selective Sweeps				
	5.4.2 Balancing Selection				
	5.5 Gene Trees versus Species Trees in the Great Apes	10			
	5.6 Exercises				
6 Splitting Lineages: Recombination and Weak Selection 10					
•	6.1 Branching Processes and Branching-Coalescing Graphs				
	6.2 The Ancestral Recombination Graph				
	6.2.1 Breaking up the Sequence				
	6.2.2 Expectations and Variances				
	6.2.3 Comparing Patterns within and between Loci				
	6.3 The Ancestral Selection Graph				
	6.4 Correlation of Polymorphism Levels across the Human Genome				
	6.5 Exercises				
	7.1 Markov Processes with Two Time Scales	10 10			
	7.2.3 Age Structure	10 10 10			
0	7.2.3 Age Structure	10 10 10			
8	7.2.3 Age Structure	10 10 10 10			
8	7.2.3 Age Structure	10 10 10 10 10			
8	7.2.3 Age Structure	10 10 10 10 10 10			
8	7.2.3 Age Structure	10 10 10 10 10 10 10			
8	7.2.3 Age Structure	10 10 10 10 10 10 10 10			
8	7.2.3 Age Structure	10 10 10 10 10 10 10 10 10			
8	7.2.3 Age Structure	10 10 10 10 10 10 10 10 10			
	7.2.3 Age Structure	10 10 10 10 10 10 10 10 10			
So	7.2.3 Age Structure 7.2.4 Metapopulation Structure 7.3 Effective Population Size in Drosophila 7.4 Exercises Simulations and Simulation-based Methods 8.1 Simulating Genealogies: Monte-Carlo Integration 8.2 Computing Likelihoods of Full Data Patterns 8.2.1 Importance Sampling Methods 8.2.2 Markov Chain Monte Carlo Methods 8.3 The Bayesian Approach to Inference 8.4 Human Migrations into the Americas 8.5 Exercises	10 10 10 10 10 10 10 10 10			
So Bi	7.2.3 Age Structure 7.2.4 Metapopulation Structure 7.3 Effective Population Size in Drosophila 7.4 Exercises Simulations and Simulation-based Methods 8.1 Simulating Genealogies: Monte-Carlo Integration 8.2 Computing Likelihoods of Full Data Patterns 8.2.1 Importance Sampling Methods 8.2.2 Markov Chain Monte Carlo Methods 8.3 The Bayesian Approach to Inference 8.4 Human Migrations into the Americas 8.5 Exercises	10 10 10 10 10 10 10 10 10			